

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:31:07 ; Search time 142 Seconds
(without alignments)
18.565 Million cell updates/sec

Title: US-10-660-118a-2

Perfect score: 31
Sequence: 1 XGPKC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 244163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 244163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1980s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	4	2 AAR11508	Aar11508 Thioresox
2	31	100.0	4	2 AAR09052	Aar09052 Thioresox
3	31	100.0	4	3 AAB13337	Aab13337 Human Trx
4	31	100.0	4	3 AAY49348	Aay49348 Active-si
5	31	100.0	4	5 ABP56403	Abp56403 Thioresox
6	31	100.0	4	5 AAO22593	Aao22593 Redox act
7	31	100.0	4	5 ABG32509	Abg32509 M. tuberc
8	31	100.0	4	5 AAU97916	Aau97916 Tetrapept
9	31	100.0	4	5 ABB05573	Abb05573 Dithiol p
10	31	100.0	4	6 AAE37340	Aae37340 E. coli t
11	31	100.0	4	8 ADJ47607	Adj47607 Trx catal
12	31	100.0	4	8 ADM32927	Adm32927 Amino aci
13	31	100.0	4	8 ADRA6076	Adra6076 Antioxida
14	31	100.0	4	9 ADV11816	Adv11816 Thioresox
15	31	100.0	4	9 ADM97624	Adm97624 Human thi
16	31	100.0	4	9 ADY81685	Ady81685 Thioresox
17	31	100.0	5	3 AAY78911	Aay78911 Thioresox
18	31	100.0	5	4 AAB05156	Aae05156 Human thi
19	31	100.0	5	5 AAO21523	Aao21523 Wild type
20	31	100.0	5	5 ABG71301	Abg71301 Thioresox
21	31	100.0	6	1 AAP71087	Aap71087 Sequence
22	31	100.0	6	5 ABP54936	Abp54936 Active si
23	31	100.0	6	6 ADA08451	Ada08451 Mammalian
24	31	100.0	6	8 ADH05024	Adh05024 Target pe

25	31	100.0	6	8 ADM32929	Adm32929 Amino aci
26	31	100.0	6	8 ADM32928	Adm32928 Amino aci
27	31	100.0	6	8 ADP87509	Adp87509 Thioresox
28	31	100.0	6	8 ADP67423	Adp67423 Thioresox
29	31	100.0	6	8 ADP97008	Adp97008 Thioresox
30	31	100.0	6	8 AAF50203	Aaf50203 Sequence
31	31	100.0	8	1 ADC81369	Adc81369 Bovin THR
32	31	100.0	8	2 AAW05002	Aaw05002 Thymic hu
33	31	100.0	8	2 AAH041664	Aah041664 Immunomod
34	31	100.0	8	2 ADH05029	Adh05029 Target pe
35	31	100.0	8	9 ADV60194	Adv60194 VEGF pept
36	31	100.0	8	9 ADZ28911	Adz28911 Calmoduli
37	31	100.0	9	9 ADV60195	Adv60195 VEGF pept
38	31	100.0	10	2 AAR50846	Aar50846 Cyclic pe
39	31	100.0	10	2 AAR50868	Aar50868 Cyclic pe
40	31	100.0	10	2 AAR50834	Aar50834 Cyclic pe
41	31	100.0	10	2 AAR50895	Aar50895 Cyclic pe
42	31	100.0	10	2 AAR50830	Aar50830 Cyclic pe
43	31	100.0	10	4 AAG94724	Aag94724 Human com
44	31	100.0	10	4 AAG94776	Aag94776 Human com
45	31	100.0	10	4 AAG66916	Aag66916 Saccharom
46	31	100.0	10	4 AAG66918	Aag66918 Saccharom
47	31	100.0	10	9 ADV60196	Adv60196 VEGF pept
48	31	100.0	12	2 AAW45003	Aaw45003 Immunomod
49	31	100.0	12	2 AAY09429	Aay09429 Immunoad
50	31	100.0	12	9 ADV60191	Adv60191 VEGF pept
51	31	100.0	13	9 ADV60192	Adv60192 VEGF pept
52	31	100.0	14	9 ADV60193	Adv60193 VEGF pept
53	31	100.0	14	9 ADM28625	Adm28625 VEGF165 e
54	31	100.0	17	9 ADV54876	Adv54876 G protein
55	31	100.0	17	9 ADV54992	Adv54992 G protein
56	31	100.0	17	9 ADV55097	Adv55097 G protein
57	31	100.0	19	5 AAE23038	Aae23038 Human thi
58	31	100.0	20	9 ADV60188	Adv60188 VEGF pept
59	31	100.0	21	9 ADV60189	Adv60189 VEGF pept
60	31	100.0	23	3 AAB38160	Aab38160 Human sec
61	31	100.0	24	9 ADV55042	Adv55042 G protein
62	31	100.0	24	9 ADV56216	Adv56216 G protein
63	31	100.0	24	9 ADV53880	Adv53880 G protein
64	31	100.0	24	9 ADV54929	Adv54929 G protein
65	31	100.0	24	9 ADV55148	Adv55148 G protein
66	31	100.0	25	3 AAB38027	Aab38027 Fragment
67	31	100.0	25	9 ADV55146	Adv55146 G protein
68	31	100.0	25	9 ADV55040	Adv55040 G protein
69	31	100.0	25	9 ADV54928	Adv54928 G protein
70	31	100.0	28	7 ADC89744	Adc89744 Cyclic VE
71	31	100.0	29	5 AAU75045	Aau75045 Retrovira
72	31	100.0	29	9 ADV60190	Adv60190 VEGF pept
73	31	100.0	30	5 AAU75030	Aau75030 4070A amp
74	31	100.0	32	4 AAM20162	Aam20162 Peptide #
75	31	100.0	32	4 ABB40402	Abb40402 Peptide #
76	31	100.0	32	4 AAM34108	Aam34108 Peptide #
77	31	100.0	32	4 ABB24771	Abb24771 Protein #
78	31	100.0	32	4 AAM73929	Aam73929 Human bon
79	31	100.0	32	4 AAM61210	Aam61210 Human bira
80	31	100.0	32	4 ABG55681	Abg55681 Human liv
81	31	100.0	32	5 ABG43817	Abg43817 Human pep
82	31	100.0	35	4 AAB60793	Aab60793 Androcton
83	31	100.0	35	8 ADI12462	Adi12462 Moroccan
84	31	100.0	35	8 AAU08671	Aau08671 Moroccan
85	31	100.0	37	5 ABB07837	Abb07837 Thioresox
86	31	100.0	37	5 ADI12460	Adi12460 Moroccan
87	31	100.0	37	8 ADH89471	Adh89471 Moroccan
88	31	100.0	37	8 ABB21076	Abb21076 Novel hum
89	31	100.0	42	4 AAM15659	Aam15659 Peptide #
90	31	100.0	43	4 ABB34663	Abb34663 Peptide #
91	31	100.0	43	4 AAM28160	Aam28160 Peptide #
92	31	100.0	43	4 ABB29484	Abb29484 Peptide #
93	31	100.0	43	4 ABB20069	Abb20069 Protein #
94	31	100.0	43	4 AAM67841	Aam67841 Human bon
95	31	100.0	43	4 AAM55452	Aam55452 Human bira
96	31	100.0	43	4 ABB49482	Abb49482 Human liv
97	31	100.0	43	4	

244	31	100.0	103	6	ABR41607	Abi41607 Human DIT	317	100.0	106	5	ABP60721	ABP60721 Anacystis
245	31	100.0	103	8	ADK90669	Adk90669 Baker's Y	318	100.0	106	5	ABP60783	ABP60783 Penicillium
246	31	100.0	103	8	ADM32932	Adm32932 Amino aci	319	100.0	106	5	ABP60827	ABP60827 Manduca s
247	31	100.0	103	8	ADM32933	Adm32933 Amino aci	320	100.0	106	5	ABP60709	ABP60709 Anabaena
248	31	100.0	104	2	AAR42820	Aar42820 RECEF 104	321	100.0	106	5	ABP60778	ABP60778 Streptomy
249	31	100.0	104	2	AAR42820	Aar42820 RECEF 104	322	100.0	106	5	ABP60774	ABP60774 Helicobac
250	31	100.0	104	2	AAR72389	Aar72389 Recombina	323	100.0	106	5	ABP60764	ABP60764 Coprinus
251	31	100.0	104	2	ABP30470	Abp30470 Streptococ	324	100.0	106	7	ADJ70266	Adj70266 Human hea
252	31	100.0	104	5	ABP54990	Abp54990 Lactococc	325	100.0	106	8	ADJ79080	Adj79080 Plant ful
253	31	100.0	104	5	ABP60708	Abp60708 S. cerevi	326	100.0	107	4	AAW95351	Aaw95351 Human adu
254	31	100.0	104	5	ABP60927	Abp60927 Staphyloc	327	100.0	107	4	ABP60478	ABP60478 Drosophil
255	31	100.0	104	5	ABP60803	Abp60803 Homo sapi	328	100.0	107	4	AAW91786	Aaw91786 Human lim
256	31	100.0	104	5	ABP60785	Abp60785 Rhodospir	329	100.0	107	5	ABP60725	ABP60725 Porphyra
257	31	100.0	104	5	ABP60797	Abp60797 Bos tauru	330	100.0	107	5	ABP60790	ABP60790 Streptomy
258	31	100.0	104	5	ABP60812	Abp60812 Ovis arie	331	100.0	107	5	ABP60802	ABP60802 Drosophil
259	31	100.0	104	5	ABP60805	Abp60805 Macaca mu	332	100.0	107	5	ABP60722	ABP60722 Cyanidium
260	31	100.0	104	5	ABP60806	Abp60806 Mus muscu	333	100.0	107	5	ABP60726	ABP60726 Porphyra
261	31	100.0	104	5	ABP60809	Abp60809 Cryptolag	334	100.0	107	5	ABP60772	ABP60772 Haemophil
262	31	100.0	104	5	ABP60810	Abp60810 Rattus no	335	100.0	107	5	ABP60760	ABP60760 Chromatu
263	31	100.0	104	5	ABP60801	Abp60801 Gallus ga	336	100.0	107	6	ABW71327	Abw71327 Staphyloc
264	31	100.0	104	5	ABG93115	Abg93115 S. cerevi	337	100.0	107	7	ADA44976	Ada44976 Human pol
265	31	100.0	104	6	ABU02257	Abu02257 S. pneumo	338	100.0	108	5	ABP90010	ABP90010 Human pol
266	31	100.0	104	6	ABP81634	Abp81634 Streptococ	339	100.0	108	5	ABG70953	ABG70953 Escherich
267	31	100.0	104	8	ADK46563	Adk46563 Streptococ	340	100.0	108	5	ABG70952	ABG70952 Escherich
268	31	100.0	104	8	ADK90667	Adk90667 Baker's Y	341	100.0	108	5	ABP60784	ABP60784 Pseudomon
269	31	100.0	104	8	ADM32931	Adm32931 Amino aci	342	100.0	108	5	ABP60768	ABP60768 Escherich
270	31	100.0	104	8	ADOS9801	Ados9801 B. subtil	343	100.0	108	5	ABP60752	ABP60752 Chlorobiu
271	31	100.0	104	8	ADS88157	Ads88157 Human pro	344	100.0	108	5	ABP60793	ABP60793 Thiodacil
272	31	100.0	104	8	ADV82057	Adv82057 Streptococ	345	100.0	108	7	ABW73822	Abw73822 DNA clone
273	31	100.0	105	1	AAW92141	Aaw92141 Recombina	346	100.0	108	7	ABE42151	Aeb42151 L. pneumo
274	31	100.0	105	2	AAW92141	Aaw92141 RECEF/chio	347	100.0	109	2	AAW15646	Aar15646 Thiorodex
275	31	100.0	105	2	AAW37700	Aar37700 ADF, 11/1	348	100.0	109	2	AAW75767	Aar75767 His-patch
276	31	100.0	105	2	AAW47856	Aar47856 Human ADF	349	100.0	109	2	AAW75768	Aar75768 E. coli t
277	31	100.0	105	2	AAW72390	Aar72390 Recombina	350	100.0	109	2	AAW93015	Aar93015 Thiorodex
278	31	100.0	105	2	AAW69567	Aaw69567 Human thi	351	100.0	109	2	AAW25383	Aay25383 Plasmid p
279	31	100.0	105	3	AAW25908	Aay25908 Human thi	352	100.0	109	2	AAW02639	Aay02639 Thiorodex
280	31	100.0	105	3	AAW03956	Aaw03956 Human sec	353	100.0	109	3	AAW57199	Aau57199 Thiorodex
281	31	100.0	105	5	ABP60700	Abp60700 Human thi	354	100.0	109	3	AAW57199	Aau57199 Thiorodex
282	31	100.0	105	5	ABP60705	Abp60705 Dictyoste	355	100.0	109	4	ABP60744	ABP60744 Aspergill
283	31	100.0	105	5	ABP60835	Abp60835 Synechocy	356	100.0	109	5	ABP79749	ABP79749 Thiorodex
284	31	100.0	105	5	ABP60786	Abp60786 Rhodobact	357	100.0	109	5	ABP60792	ABP60792 Synechocy
285	31	100.0	105	5	ABP60757	Abp60757 Corynebact	358	100.0	109	5	ABP60698	ABP60698 Escherich
286	31	100.0	105	5	ABP60769	Abp60769 Synechocy	359	100.0	109	5	ABP60724	ABP60724 Griffiths
287	31	100.0	105	5	ABP60745	Abp60745 Alicyclob	360	100.0	109	5	ABP60836	ABP60836 Synechocy
288	31	100.0	105	5	ABG93353	Abg93353 Human BAX	361	100.0	109	5	ABP60744	ABP60744 Aspergill
289	31	100.0	105	6	ABO07225	Abp07225 Human p53	362	100.0	109	6	ABW53718	Abw53718 Propionib
290	31	100.0	105	6	ABR92158	Abi92158 Human cer	363	100.0	109	6	ABU26015	Abu26015 Aspergill
291	31	100.0	105	7	ADD67269	Adp67269 Thiorodex	364	100.0	109	7	ABU25415	Abu25415 Aspergill
292	31	100.0	105	7	ADP30728	Adp30728 Rat angio	365	100.0	109	7	ADP59277	Adp59277 E. coli t
293	31	100.0	105	7	ADJ70213	Adj70213 Human hea	366	100.0	109	8	ADJ57878	Adj57878 E. coli t
294	31	100.0	105	8	ADJ47593	Adj47593 Wild-type	367	100.0	109	8	ADM32930	Adm32930 Amino aci
295	31	100.0	105	8	ADJ48285	Adj48285 Human PRO	368	100.0	109	8	ADOS9803	Ados9803 E. coli m
296	31	100.0	105	8	ADM32938	Adm32938 Amino aci	369	100.0	109	9	ADP66900	Adp66900 Thiorodex
297	31	100.0	105	8	ADM32935	Adm32935 Amino aci	370	100.0	109	9	ABE68327	ABE68327 E. coli t
298	31	100.0	105	8	ADM32936	Adm32936 Amino aci	371	100.0	110	4	AAW21649	Aam21649 Peptide #
299	31	100.0	105	8	ADM32937	Adm32937 Amino aci	372	100.0	110	4	ABR44009	ABR44009 Peptide #
300	31	100.0	105	8	ADM32934	Adm32934 Amino aci	373	100.0	110	4	AAW37954	Aam37954 Peptide #
301	31	100.0	105	8	ADOS5473	Ados5473 D. discoi	374	100.0	110	4	ABR26917	ABR26917 Protein #
302	31	100.0	105	8	ADO19655	Ado19655 Human PRO	375	100.0	110	4	AAW77740	Aam77740 Human bon
303	31	100.0	105	8	ADP54775	Adp54775 Human PRO	376	100.0	110	4	AAW65055	Aaw65055 Propionib
304	31	100.0	105	8	ADRA9671	Adra9671 Murine th	377	100.0	110	4	AAW65023	Aam65023 Human bra
305	31	100.0	105	9	ADW97622	Adw97622 Human thi	378	100.0	110	6	ABW53024	ABW53024 Propionib
306	31	100.0	105	9	ADY16038	Ady16038 PRO poly	379	100.0	110	6	ADW86658	ADW86658 Streptococ
307	31	100.0	105	8	ADU06404	Adu06404 Novel bro	380	100.0	110	8	ADY79911	Ady79911 Streptococ
308	31	100.0	105	9	ADY19738	Ady19738 PRO poly	381	100.0	110	8	ABP60728	ABP60728 Anabaena
309	31	100.0	105	9	ADY16038	Ady16038 PRO poly	382	100.0	110	5	ABP60789	ABP60789 Streptomy
310	31	100.0	105	9	ADW97622	Adw97622 Human thi	383	100.0	110	6	ABW53024	ABW53024 Propionib
311	31	100.0	106	3	AAW30735	Aaw30735 Therapeut	384	100.0	110	8	ADW86658	ADW86658 Streptococ
312	31	100.0	106	3	AAW19105	Aaw19105 Polypepti	385	100.0	110	8	ADY79911	Ady79911 Streptococ
313	31	100.0	106	4	ABW60229	Abw60229 Drosophil	386	100.0	111	2	AAW76572	Aay76572 Human ova
314	31	100.0	106	4	AAW95038	Aaw95038 Human pro	387	100.0	111	3	AAW12494	Aag12494 Zea maye
315	31	100.0	106	5	AAO22592	Aao22592 106-mer H	388	100.0	111	4	ABW59805	ABW59805 Drosophil
316	31	100.0	106	5	ABP60791	Abp60791 Synechocy	389	100.0	111	5	ABP39014	ABP39014 Staphyloc

390	31	100.0	111	5	ABB77457	Abb77457	Fungi str	463	31	100.0	122	7	AAE39220	AAe39220	Barley th
391	31	100.0	111	7	ADM60195	Adm60195	Human NOV	464	31	100.0	122	7	AAE39223	AAe39223	Barley H-
392	31	100.0	111	8	ADM60336	Adm60336	Staphyloc	465	31	100.0	122	7	ADF04112	AdF04112	Bacterial
393	31	100.0	111	8	ADRA9062	Adra9062	Thioredox	466	31	100.0	122	7	ADO59274	AdO59274	Rice thio
394	31	100.0	111	9	AEBS39008	Aeb39008	L. pneumo	467	31	100.0	122	7	ADO59272	AdO59272	Barley ch
395	31	100.0	112	4	AAAM25652	Aam25652	Human pro	468	31	100.0	123	3	AAI70462	AAI70462	Glycine m
396	31	100.0	112	4	AAU32348	Aau32348	Novel hum	469	31	100.0	123	3	AAU626780	AAU626780	Zea maya
397	31	100.0	112	5	ABP60738	Abp60738	Chlamydom	470	31	100.0	123	4	AAU64279	AAU64279	Proplionib
398	31	100.0	112	5	ABP60780	Abp60780	Mycobacte	471	31	100.0	123	4	AAAB37102	AAAB37102	Wheat Tar
399	31	100.0	112	5	ABP60236	Abp60236	Human Th1	472	31	100.0	123	5	ABPE5992	ABPE5992	Bifidobac
400	31	100.0	112	5	AAU91276	Aau91276	Human NOV	473	31	100.0	123	6	ABM60798	ABM60798	Proplionib
401	31	100.0	112	5	AAU78664	Aau78664	Human NOV	474	31	100.0	124	4	AAE87895	AAE87895	C. glutam
402	31	100.0	112	7	ADU97112	Adc97112	E. faeciu	475	31	100.0	124	4	AAE93165	AAE93165	C. glutam
403	31	100.0	112	8	ADU04590	Adt04590	Luteinist	476	31	100.0	124	7	ADU13226	ADU13226	Abc13226
404	31	100.0	112	8	ADU07462	Adw07462	Human lut	477	31	100.0	124	7	ABO61500	ABO61500	Klebsiell
405	31	100.0	113	5	ABP52004	Abp52004	NOVGN ho	478	31	100.0	125	3	AAI17574	AAI17574	Arabidops
406	31	100.0	113	6	ABP56107	Abp56107	Human IGF	479	31	100.0	125	5	ABPE60741	ABPE60741	Picea mar
407	31	100.0	113	7	ADB65045	Adb65045	Human pro	480	31	100.0	125	7	ADOS9273	ADOS9273	Wheat th1
408	31	100.0	113	7	ADM04461	Adm04461	Human pro	481	31	100.0	125	7	ABM85633	ABM85633	Human pro
409	31	100.0	113	8	ADM04093	Adg82093	Equine g1	482	31	100.0	125	8	ADP07816	ADP07816	Human sec
410	31	100.0	114	3	AAAG08114	Aag08114	Arabidops	483	31	100.0	125	9	ABM95048	ABM95048	M. xanthu
411	31	100.0	114	3	AAAG54021	Aag54021	Arabidops	484	31	100.0	126	5	ABPE60743	ABPE60743	Trifolium
412	31	100.0	114	4	AAU04622	Aau04622	Human lut	485	31	100.0	126	5	ABPE60730	ABPE60730	Nicotiana
413	31	100.0	114	4	AAE04494	Aae04494	Human lut	486	31	100.0	126	5	ABPE9275	ABPE9275	Tobacco t
414	31	100.0	114	5	ABP60696	Abp60696	Arabidops	487	31	100.0	126	8	ADQ39499	ADQ39499	Human myo
415	31	100.0	114	5	ABP60680	Abp60680	Phaseolin	488	31	100.0	127	2	AAE93016	AAE93016	Soft whea
416	31	100.0	114	5	ABP60727	Abp60727	Arabidops	489	31	100.0	127	2	AAW44907	AAW44907	"polyprol
417	31	100.0	114	5	ABG32916	Abg32916	Arabidops	490	31	100.0	127	3	AAAB29248	AAAB29248	Wheat th1
418	31	100.0	114	7	ADOS8276	Ados8276	Arabidops	491	31	100.0	127	3	AAE36604	AAE36604	Arabidops
419	31	100.0	114	8	ADQ82092	Adq82092	Human gly	492	31	100.0	127	4	ABG18304	ABG18304	Novel hum
420	31	100.0	114	8	ADRA94295	Adra94295	Novel S.	493	31	100.0	127	5	ABPE60782	ABPE60782	Neurospor
421	31	100.0	114	9	AEAS8165	Aeas8165	Streptococ	494	31	100.0	128	8	ADY04690	ADY04690	Plant ful
422	31	100.0	115	3	AAAG12953	Aag12953	Arabidops	495	31	100.0	128	4	ABG23738	ABG23738	Novel hum
423	31	100.0	115	3	AAAG45020	Aag45020	Zea maya	496	31	100.0	129	6	ABP78912	ABP78912	N. gonorr
424	31	100.0	115	5	ABPE60781	Abp60781	Mycobacte	497	31	100.0	129	7	ADBE3991	ADBE3991	Human pro
425	31	100.0	115	5	ABPE60799	Abp60799	Caenorhab	498	31	100.0	129	7	ADBE39961	ADBE39961	C. neofo
426	31	100.0	116	5	ABPE60739	Abp60739	Fagopyrum	499	31	100.0	130	2	AAE93017	AAE93017	Hard whea
427	31	100.0	116	7	ABM85632	Abm85632	Mouse pro	500	31	100.0	130	2	AAW70535	AAW70535	Human th1
428	31	100.0	117	5	ABP60749	Abp60749	Borrelia	501	31	100.0	130	3	AAAB29249	AAAB29249	Wheat th1
429	31	100.0	118	3	AAAY70480	Aay70480	Calappa s	502	31	100.0	130	5	ABPE60787	ABPE60787	Rickettsi
430	31	100.0	118	3	AAAY70483	Aay70483	Vernonia	503	31	100.0	131	2	AAW47027	AAW47027	eCG hormo
431	31	100.0	118	5	ABP27942	Abp27942	Streptococ	504	31	100.0	131	4	AAAG3360	AAAG3360	P patens
432	31	100.0	118	5	ABP27941	Abp27941	Streptococ	505	31	100.0	131	4	AAU51778	AAU51778	Proplionib
433	31	100.0	118	5	ABP60733	Abp60733	Nicotiana	506	31	100.0	131	4	AAAG80910	AAAG80910	Co-factor
434	31	100.0	118	5	ABP60742	Abp60742	Ricinus c	507	31	100.0	131	5	ABPE60844	ABPE60844	Palari's
435	31	100.0	119	4	ABG01907	Abg01907	Novel hum	508	31	100.0	131	5	ABPE60821	ABPE60821	Hordeum b
436	31	100.0	119	5	ABPE60826	Abp60826	Secale ce	509	31	100.0	131	5	ABPE60822	ABPE60822	Lolium pe
437	31	100.0	120	4	AAAY70481	Aay70481	Glycine m	510	31	100.0	131	5	ABPE60823	ABPE60823	Oryza sat
438	31	100.0	120	4	AAAM41837	Aam41837	Human pol	511	31	100.0	131	5	ABPE60825	ABPE60825	Secale ce
439	31	100.0	120	7	ADP70794	Adp70794	Minicell	512	31	100.0	131	6	ABM48297	ABM48297	Proplionib
440	31	100.0	120	7	ADP70792	Adp70792	Minicell	513	31	100.0	131	7	ABM74315	ABM74315	DNA clone
441	31	100.0	120	7	ADP70791	Adp70791	Minicell	514	31	100.0	132	4	ABG13926	ABG13926	Novel hum
442	31	100.0	120	7	ADP70793	Adp70793	Minicell	515	31	100.0	132	5	ADK36696	ADK36696	Novel hum
443	31	100.0	120	8	ADNA49430	Adn49430	Seven-pas	516	31	100.0	132	7	ADG33012	ADG33012	Human nov
444	31	100.0	121	2	AAAR96043	Aar96043	Human vas	517	31	100.0	133	3	AAAG10853	AAAG10853	Arabidops
445	31	100.0	121	2	AAAR96043	Aar96043	Vascular	518	31	100.0	133	5	ABPE60731	ABPE60731	Arabidops
446	31	100.0	121	2	AAAR93977	Aar93977	Vascular	519	31	100.0	133	5	AAU72822	AAU72822	Human NKG
447	31	100.0	121	2	AAW09091	Aaw09091	Human VEG	520	31	100.0	133	7	ADP70773	ADP70773	Minicell
448	31	100.0	121	2	AAW40597	Aaw40597	VEGF/VPFI	521	31	100.0	133	8	ADY06180	ADY06180	Plant ful
449	31	100.0	121	3	AAAY9848	Aay9848	Human vas	522	31	100.0	134	2	AAW47025	AAW47025	eCG hormo
450	31	100.0	121	3	AAAY92001	Aay92001	Human lut	523	31	100.0	134	2	AAAG04653	AAAG04653	Arabidops
451	31	100.0	121	7	ADDA42004	Add42004	Human VEG	524	31	100.0	134	3	ADCI4128	ADCI4128	Human th1
452	31	100.0	121	7	ADME25402	Adme25402	Hyperther	525	31	100.0	134	8	ADMC12939	ADMC12939	Amino aci
453	31	100.0	121	8	ADL92176	Adl92176	Lutropin	526	31	100.0	135	4	AAAM5055	AAAM5055	Peptide #
454	31	100.0	122	2	AAAR15123	Aar15123	hCG/hhA c	527	31	100.0	135	4	ABE34043	ABE34043	Peptide #
455	31	100.0	122	2	AAAR65908	Aar65908	Protein f	528	31	100.0	135	4	AAAM7498	AAAM7498	Peptide #
456	31	100.0	122	2	AAAY29594	Aay29594	Human lut	529	31	100.0	135	4	ABBR28866	ABBR28866	Peptide #
457	31	100.0	122	3	AAAB19159	Aab19159	Amino aci	530	31	100.0	135	4	ABBI9484	ABBI9484	Protein #
458	31	100.0	122	3	AAAB29247	Aab29247	Barley th	531	31	100.0	135	4	AAAM67204	AAAM67204	Human bon
459	31	100.0	122	3	AAAY70479	Aay70479	Memordica	532	31	100.0	135	4	AAAM54823	AAAM54823	Human bra
460	31	100.0	122	3	AAAG03775	Aag03775	Human sec	533	31	100.0	135	4	ABG48868	ABG48868	Human liv
461	31	100.0	122	3	AAAB35810	Aab35810	Rice thio	534	31	100.0	135	4	AAW02790	AAW02790	Peptide #
462	31	100.0	122	5	ABP60740	Abp60740	Oryza sat	535	31	100.0	135	5	ABG36860	ABG36860	Human pep

536	31	100.0	136	2	AAV12478	Hay12478 Human 5'	609	31	100.0	144	3	AAAG54790	AAg54790 Arabidops
537	31	100.0	136	8	ADG16382	Adg16382 TRIAP-aldp	610	31	100.0	144	8	ADX79859	Adx79859 Plant ful
538	31	100.0	136	8	ADY06635	Ady06635 plant ful	611	31	100.0	145	2	AAAR15122	AAar15122 hCG/hLH c
539	31	100.0	137	2	AAW55082	Aaw55082 Streptoco	612	31	100.0	145	2	AAAR15106	AAar15106 hCG/BLH c
540	31	100.0	137	2	AAW47026	Aaw47026 eCG hormo	613	31	100.0	145	2	AAAR15124	AAar15124 hCG/BLH c
541	31	100.0	137	2	ABP54576	Abp54576 S. pneumo	614	31	100.0	145	2	AAAR15125	AAar15125 hCG/BLH c
542	31	100.0	137	7	ADCA5121	Adca5121 S. pneumo	615	31	100.0	145	2	AAAR15102	AAar15102 hCG/BLH c
543	31	100.0	137	8	ADP07819	Adp07819 Human sec	616	31	100.0	145	2	AAAR15118	AAar15118 hCG/BLH c
544	31	100.0	137	8	ADX90438	Adx90438 plant ful	617	31	100.0	145	2	AAAR15116	AAar15116 hCG/BLH c
545	31	100.0	137	8	ADY09660	Ady09660 plant ful	618	31	100.0	145	5	AAAB60759	AAb60759 Corynebac
546	31	100.0	137	8	ADY08622	Ady08622 plant ful	619	31	100.0	145	6	ADPA34073	ADp34073 Acinetoba
547	31	100.0	137	8	ADY78867	Ady78867 plant ful	620	31	100.0	146	7	ADL17747	ADl17747 Human TRP
548	31	100.0	137	8	ADY04779	Ady04779 Plant ful	621	31	100.0	146	8	ADY56820	ADy56820 Human TRP
549	31	100.0	138	4	AAU47482	Aau47482 Propionib	622	31	100.0	147	3	AAAB09393	AAa09393 Hepaticis
550	31	100.0	138	4	AAAB71791	Aab71791 Dog lutro	623	31	100.0	147	3	AAAC30361	AAc30361 Arabidops
551	31	100.0	138	5	AAUB3040	Aaub3040 Dog lutro	624	31	100.0	147	4	AAU55797	AAu55797 Propionib
552	31	100.0	138	6	ABM44001	Abm44001 Propionib	625	31	100.0	147	6	ABM52316	ABm52316 Propionib
553	31	100.0	138	6	ADG16354	Adg16354 TRIAP-aldp	626	31	100.0	147	8	ADY75484	ADy75484 Plant ful
554	31	100.0	139	1	AAPE6061	Aape6061 Sequence	627	31	100.0	148	8	ABG29964	ABg29964 Novel hum
555	31	100.0	139	1	AAW47024	Aaw47024 eCG hormo	628	31	100.0	148	9	ADX85123	ADx85123 Vascular
556	31	100.0	139	3	AAAG41167	Aag41167 Zea mays	629	31	100.0	148	9	ADZ79967	ADz79967 Human vas
557	31	100.0	139	4	ABBB68209	Abb68209 Drosophil	630	31	100.0	149	2	AAAR31001	AAar31001 Equine ch
558	31	100.0	139	4	AAU30551	Aau30551 Novel hum	631	31	100.0	149	4	AAAG93039	AAg93039 C glutami
559	31	100.0	139	5	ABPE60770	Abpe60770 Escherich	632	31	100.0	150	8	ADY09570	ADy09570 Plant ful
560	31	100.0	139	8	ADY10883	Ady10883 Plant ful	633	31	100.0	151	3	AAAG44847	AAg44847 Zea mays
561	31	100.0	140	3	AAAG09942	Aag09942 Arabidops	634	31	100.0	151	3	AAAB67468	AAb67468 Amino aci
562	31	100.0	140	3	AAAG37258	Aag37258 Arabidops	635	31	100.0	151	5	ABBP60819	ABp60819 Arabidops
563	31	100.0	140	3	AAAG37257	Aag37257 Arabidops	636	31	100.0	151	8	ADPP90872	ADp90872 Brevibaci
564	31	100.0	140	3	AAAG38662	Aag38662 Arabidops	637	31	100.0	152	3	AAAG41898	AAg41898 Arabidops
565	31	100.0	140	3	AAAG10594	Aag10594 Arabidops	638	31	100.0	152	3	AAAG26778	AAg26778 Zea mays
566	31	100.0	140	5	ABPE60814	Abpe60814 Arabidops	639	31	100.0	152	7	ABMB96502	ABm96502 Rice abio
567	31	100.0	140	5	ABPE60715	Abpe60715 Chlamydom	640	31	100.0	152	8	ADY06632	ADy06632 Plant ful
568	31	100.0	140	8	ADP24746	Adp24746 PRO polyp	641	31	100.0	153	8	ADX87889	ADx87889 Plant ful
569	31	100.0	140	8	ADY04782	Ady04782 Sequence	642	31	100.0	154	6	ABR62385	ABr62385 Secreted
570	31	100.0	141	1	AAPE6062	Aape6062 Sequence	643	31	100.0	154	7	ADP70797	ADp70797 PMPX-91 M
571	31	100.0	141	2	AAW99519	Aaw99519 Glycoprot	644	31	100.0	154	7	ADP70798	ADp70798 PMPX-96 M
572	31	100.0	141	2	AAW99548	Aaw99548 hLH-Delta	645	31	100.0	154	7	ADP70795	ADp70795 PMPX-80 M
573	31	100.0	141	2	AAW99516	Aaw99516 Glycoprot	646	31	100.0	155	7	ADP70796	ADp70796 PMPX-81 M
574	31	100.0	141	2	AAW99523	Aaw99523 Glycoprot	647	31	100.0	155	4	ABBB97761	ABb97761 Human sec
575	31	100.0	141	2	AAW99518	Aaw99518 Glycoprot	648	31	100.0	157	4	ABG11999	ABg11999 Novel hum
576	31	100.0	141	2	AAW99520	Aaw99520 Glycoprot	649	31	100.0	157	4	ABG22533	ABg22533 Novel hum
577	31	100.0	141	2	AAW99547	Aaw99547 hLH-Delta	650	31	100.0	157	8	ABO58969	ABo58969 Human gen
578	31	100.0	141	2	AAW99522	Aaw99522 Glycoprot	651	31	100.0	159	3	AAAG36125	AAg36125 Arabidops
579	31	100.0	141	2	AAW99525	Aaw99525 Glycoprot	652	31	100.0	159	5	ABBB97522	ABb97522 Thioresox
580	31	100.0	141	2	AAW99517	Aaw99517 Glycoprot	653	31	100.0	160	5	ABBP60832	ABp60832 Klebsiella
581	31	100.0	141	2	AAW99524	Aaw99524 Glycoprot	654	31	100.0	160	7	ABO65111	ABo65111 Protein k
582	31	100.0	141	2	AAW99521	Aaw99521 Glycoprot	655	31	100.0	161	5	ABBP59105	ABp59105 Thioresox
583	31	100.0	141	4	ABBB76824	Abb76824 Single ch	656	31	100.0	161	9	ADZ66921	ADz66921 Trx-DP-TM
584	31	100.0	141	4	ABBB71792	Aab71792 Bovine lu	657	31	100.0	161	9	ADZ66918	ADz66918 Trx-DP-TM
585	31	100.0	141	4	AAAB71790	Aab71790 Pig lutro	658	31	100.0	161	9	AAAG30360	AAg30360 Arabidops
586	31	100.0	141	4	AAAB71789	Aab71789 Sheep lut	659	31	100.0	162	5	AAU72820	AAu72820 Human NKG
587	31	100.0	141	4	AAAB71795	Aab71795 Human lut	660	31	100.0	162	5	AAU72820	AAu72820 Human NKG
588	31	100.0	141	4	AAAB71793	Aab71793 Rat lutel	661	31	100.0	163	8	ADSI10583	ADs10583 Human tne
589	31	100.0	141	4	AAU96132	Aau96132 Human lut	662	31	100.0	163	8	ADQ66065	ADq66065 Novel hum
590	31	100.0	141	5	AAU83039	Aau83039 Pig lutro	663	31	100.0	163	8	ADRO89588	ADr089588 Human pro
591	31	100.0	141	5	AAU83038	Aau83038 Sheep lut	664	31	100.0	163	8	ADX89993	ADx89993 Plant ful
592	31	100.0	141	5	AAU83042	Aau83042 Rat lutem	665	31	100.0	163	8	ADY72134	ADy72134 plant ful
593	31	100.0	141	5	AAU83041	Aau83041 Bovine lu	666	31	100.0	164	2	AAAR10911	AAar10911 Bovine va
594	31	100.0	141	5	AAU83044	Aau83044 Beta-chai	667	31	100.0	164	2	AAAR38920	AAar38920 Bovine VE
595	31	100.0	141	5	ABBP52007	Abbp52007 NOVCON ho	668	31	100.0	164	5	ABBP41742	ABp41742 Human ova
596	31	100.0	141	5	ABBP52008	Abbp52008 NOVCON ho	669	31	100.0	165	2	AAAR10917	AAar10917 Human vas
597	31	100.0	141	7	AAEA90318	Aaea90318 Human NOV	670	31	100.0	165	2	AAAR38921	AAar38921 Human VEG
598	31	100.0	141	8	ADZ820914	Adz820914 Boyine ju	671	31	100.0	165	2	AAW31085	AAw31085 Vascular
599	31	100.0	141	8	ADZ78767	Adz78767 Plant ful	672	31	100.0	165	2	AAW31088	AAw31088 Vascular
600	31	100.0	141	8	ADY06170	Ady06170 Plant ful	673	31	100.0	165	2	AAW31091	AAw31091 Vascular
601	31	100.0	141	8	ADY04783	Ady04783 Plant ful	674	31	100.0	165	2	AAW31095	AAw31095 Vascular
602	31	100.0	141	8	ADY78677	Ady78677 Plant ful	675	31	100.0	165	2	AAW31096	AAw31096 Vascular
603	31	100.0	143	4	AAAB71794	Aab71794 Cat lutel	676	31	100.0	165	2	AAW31087	AAw31087 Vascular
604	31	100.0	143	4	AAU83043	Aau83043 Cat lutem	677	31	100.0	165	2	AAW31089	AAw31089 Vascular
605	31	100.0	143	5	AAU72821	Aau72821 Human NKG	678	31	100.0	165	2	AAW31092	AAw31092 Vascular
606	31	100.0	143	8	ADP19385	Adp19385 Human sec	679	31	100.0	165	2	AAW31090	AAw31090 Vascular
607	31	100.0	144	3	AAAG20218	Aag20218 Arabidops	680	31	100.0	165	2	AAW31094	AAw31094 Vascular
608	31	100.0	144	3	AAAG20218	Aag20218 Arabidops	681	31	100.0	165	2	AAW31094	AAw31094 Vascular

682	31	100.0	165	2	AAW1086	AAW1086	Vascular	755	31	100.0	171	5	ABP06779	ABP06779	Human ORF
683	31	100.0	165	2	AAV08280	AAV08280	Human gyo	756	31	100.0	171	8	ADY07711	ADY07711	Plant ful
684	31	100.0	165	6	ABP56770	ABP56770	Human vas	757	31	100.0	171	8	ADX97324	ADX97324	Plant ful
685	31	100.0	165	6	ABR82055	ABR82055	Human VEG	758	31	100.0	172	1	AAV4809	AAV4809	Human int
686	31	100.0	165	7	ADD42006	ADD42006	Human VEG	759	31	100.0	172	3	AAI15597	AAI15597	Arabidops
687	31	100.0	165	8	ADI19317	ADI19317	Coccidiol	760	31	100.0	172	5	ABP60718	ABP60718	Pisum sat
688	31	100.0	165	8	ADJ47601	ADJ47601	Wld-type	761	31	100.0	172	5	ABP60717	Oryza sat	Arabidops
689	31	100.0	165	8	ADM24881	ADM24881	Human mat	762	31	100.0	172	7	ABM87854	Rice abio	Arabidops
690	31	100.0	165	8	ADR40207	ADR40207	Human VEG	763	31	100.0	172	8	ADM32941	Amino aci	Arabidops
691	31	100.0	165	8	ADU17883	ADU17883	Human vas	764	31	100.0	173	3	AAV45018	Zea mays	Arabidops
692	31	100.0	165	8	ADU07202	ADU07202	Human aci	765	31	100.0	173	5	ABP60712	Rice abio	Arabidops
693	31	100.0	165	8	ADT78147	ADT78147	Human VEG	766	31	100.0	173	7	ABM86658	Rice abio	Arabidops
694	31	100.0	165	8	ADT99246	ADT99246	Partial v	767	31	100.0	174	4	AAU17068	Novel sig	Arabidops
695	31	100.0	165	8	ADT36536	ADT36536	Partial v	768	31	100.0	174	4	AAV82531	Vascular	Arabidops
696	31	100.0	165	8	ADT98421	ADT98421	Human VEG	769	31	100.0	174	7	ADT84512	Mycobacte	Arabidops
697	31	100.0	165	8	ADU17609	ADU17609	Human VEG	770	31	100.0	174	7	ADT93776	Human nov	Arabidops
698	31	100.0	165	8	ADU17466	ADU17466	Human vas	771	31	100.0	174	9	ADT60207	VEGF isoC	Arabidops
699	31	100.0	165	8	ADU00628	ADU00628	Human vas	772	31	100.0	175	5	ABP60720	Triticum	Arabidops
700	31	100.0	165	8	ADT55064	ADT55064	Human vas	773	31	100.0	175	5	ABP60817	Arabidops	Arabidops
701	31	100.0	165	8	ADT55423	ADT55423	Human vas	774	31	100.0	175	8	ADT88193	Plant ful	Arabidops
702	31	100.0	165	8	ADT55424	ADT55424	Human vas	775	31	100.0	177	5	ADT14129	Chimeric	Arabidops
703	31	100.0	165	8	ADT85122	ADT85122	Vascular	776	31	100.0	177	5	ABP60714	Brassic	Arabidops
704	31	100.0	165	9	ADT79964	ADT79964	Human vas	777	31	100.0	177	8	ADT90870	Brevibac	Arabidops
705	31	100.0	166	2	AAW59885	AAW59885	Human aci	778	31	100.0	177	8	ADT17846	Plant ful	Arabidops
706	31	100.0	166	2	AAW59886	AAW59886	Human aci	779	31	100.0	178	3	AAV19366	Arabidops	Arabidops
707	31	100.0	166	2	AAW49006	AAW49006	Human thi	780	31	100.0	178	4	AAW95211	Human rep	Arabidops
708	31	100.0	166	4	AAU58218	AAU58218	Propionib	781	31	100.0	178	5	ABP60703	Arabidops	Arabidops
709	31	100.0	166	5	ABP41978	ABP41978	Human ova	782	31	100.0	178	8	ADT74765	Thale cre	Arabidops
710	31	100.0	166	5	ABP60804	ABP60804	Homo sapl	783	31	100.0	179	3	AAV30359	Arabidops	Arabidops
711	31	100.0	166	5	ABP60798	ABP60798	Bos tauri	784	31	100.0	179	5	ABP60710	Arabidops	Arabidops
712	31	100.0	166	5	ABP60807	ABP60807	Mus muscu	785	31	100.0	179	7	ADT64659	Arabidops	Arabidops
713	31	100.0	166	5	ABP60811	ABP60811	Rattus no	786	31	100.0	179	8	ADT06451	Plant ful	Arabidops
714	31	100.0	166	6	ABM54737	ABM54737	Propionib	787	31	100.0	179	8	ADT10996	Plant ful	Arabidops
715	31	100.0	166	7	ADT27624	ADT27624	Human col	788	31	100.0	180	8	ADT78704	Plant ful	Arabidops
716	31	100.0	166	7	ADT62952	ADT62952	Rat Prote	789	31	100.0	180	8	ADT99807	Plant ful	Arabidops
717	31	100.0	167	2	AAW44910	AAW44910	"polyprol	790	31	100.0	180	8	ADT10998	Plant ful	Arabidops
718	31	100.0	167	4	AAW85253	AAW85253	Thioredox	791	31	100.0	181	3	AAV09380	Arabidops	Arabidops
719	31	100.0	167	4	AAW85254	AAW85254	Thioredox	792	31	100.0	181	5	ABP60719	Spinacia	Arabidops
720	31	100.0	167	4	AAU17909	AAU17909	Novel hum	793	31	100.0	182	3	AAV52357	Arabidops	Arabidops
721	31	100.0	167	5	ABP60716	ABP60716	Zea mays	794	31	100.0	182	3	AAV77356	Arabidops	Arabidops
722	31	100.0	167	7	ADG41289	ADG41289	Human tes	795	31	100.0	182	5	ABP60707	Pisum sat	Arabidops
723	31	100.0	167	7	ADT197063	ADT197063	Human res	796	31	100.0	182	5	ABP60705	Brassic	Arabidops
724	31	100.0	167	8	ADM32940	ADM32940	Amino aci	797	31	100.0	182	8	ADN74793	Thale cre	Arabidops
725	31	100.0	168	3	AAV30217	AAV30217	Arabidops	798	31	100.0	182	8	ADT11299	Plant ful	Arabidops
726	31	100.0	169	2	AAW33773	AAW33773	Equine ch	799	31	100.0	183	4	AAV1492	Arabidops	Arabidops
727	31	100.0	169	2	AAW33775	AAW33775	Equine ch	800	31	100.0	183	4	AAU20503	Human sec	Arabidops
728	31	100.0	169	2	AAW33777	AAW33777	Equine ch	801	31	100.0	183	5	ABP99365	Arabidops	Arabidops
729	31	100.0	169	4	AAW65110	AAW65110	Equine ch	802	31	100.0	183	8	ADT72703	Trix-Conot	Arabidops
730	31	100.0	169	4	AAW65110	AAW65110	Equine ch	803	31	100.0	183	9	ADT85121	Vascular	Arabidops
731	31	100.0	169	4	AAW71788	AAW71788	Co-factor	804	31	100.0	183	9	ABM95783	M. xanthu	Arabidops
732	31	100.0	169	4	AAW80909	AAW80909	Co-factor	805	31	100.0	183	9	ADT79966	Human vas	Arabidops
733	31	100.0	169	5	AAU83037	AAU83037	Horbe cho	806	31	100.0	184	3	AAV38661	Arabidops	Arabidops
734	31	100.0	169	5	ABP60682	ABP60682	Phaseolin	807	31	100.0	184	4	AAV41965	Human pol	Arabidops
735	31	100.0	169	7	ABM73604	ABM73604	DNA clone	808	31	100.0	185	4	AAV80918	Thioredox	Arabidops
736	31	100.0	169	8	ADP18553	ADP18553	Horse pla	809	31	100.0	185	5	ABP60704	Arabidops	Arabidops
737	31	100.0	169	9	ABM91297	ABM91297	M. xanthu	810	31	100.0	185	6	ABU01415	S. pneumo	Arabidops
738	31	100.0	170	2	AAW63623	AAW63623	Human tum	811	31	100.0	187	7	ABM90060	Rice abio	Arabidops
739	31	100.0	170	2	AAV90358	AAV90358	Human tum	812	31	100.0	187	8	ADT648707	Streptoco	Arabidops
740	31	100.0	170	3	AAV90358	AAV90358	Human tum	813	31	100.0	187	8	ADT648707	Streptoco	Arabidops
741	31	100.0	170	3	AAV90358	AAV90358	Human tum	814	31	100.0	187	8	ADT648707	Streptoco	Arabidops
742	31	100.0	170	4	AAV90358	AAV90358	Human tum	815	31	100.0	187	8	ADT648707	Streptoco	Arabidops
743	31	100.0	170	5	AAE20849	AAE20849	Human tum	816	31	100.0	187	7	ABM90060	Rice abio	Arabidops
744	31	100.0	170	5	AAE20849	AAE20849	Human tum	817	31	100.0	187	7	ABM90060	Rice abio	Arabidops
745	31	100.0	170	8	ADT96153	ADT96153	Human tum	818	31	100.0	188	8	ADT96153	Rice abio	Arabidops
746	31	100.0	170	8	ADT96153	ADT96153	Human tum	819	31	100.0	188	8	ADT96153	Rice abio	Arabidops
747	31	100.0	170	9	ADT96153	ADT96153	Human tum	820	31	100.0	188	8	ADT96153	Rice abio	Arabidops
748	31	100.0	170	9	ADT96153	ADT96153	Human tum	821	31	100.0	188	8	ADT96153	Rice abio	Arabidops
749	31	100.0	170	9	ADT96153	ADT96153	Human tum	822	31	100.0	188	8	ADT96153	Rice abio	Arabidops
750	31	100.0	170	9	ADT96153	ADT96153	Human tum	823	31	100.0	189	4	AAV92005	Human vas	Arabidops
751	31	100.0	171	3	AAV92005	AAV92005	Human vas	824	31	100.0	189	4	AAV92005	Human vas	Arabidops
752	31	100.0	171	3	AAV92005	AAV92005	Human vas	825	31	100.0	189	6	AAV92005	Human vas	Arabidops
753	31	100.0	171	3	AAV92005	AAV92005	Human vas	826	31	100.0	189	8	ADN05035	Human pro	Arabidops
754	31	100.0	171	4	AAV92005	AAV92005	Human vas	827	31	100.0	189	9	ADN05035	Human pro	Arabidops

828	31	100.0	189	9	ADZ79963	Human vas	901	31	100.0	196	7	ADZ808098	Adz808098 Novel pro
829	31	100.0	190	2	AAZ808001	Parox v	902	31	100.0	196	7	ADZ808261	Adz808261 Novel pro
830	31	100.0	190	2	AAZ3440	Parox v	903	31	100.0	196	8	ADZ89354	Adz89354 Coliae eu
831	31	100.0	190	5	ABP60708	Abp60708 Spinacia	904	31	100.0	197	8	ADZ67695	Adz67695 Novel hum
832	31	100.0	191	2	AAZ808002	Human vas	905	31	100.0	199	3	AAZ42214	Adz42214 Human ORF
833	31	100.0	191	2	AAZ91076	Human vas	906	31	100.0	201	8	ADZ72965	Adz72965 Plant ful
834	31	100.0	191	2	AAZ00724	Human vas	907	31	100.0	203	3	AAZ39661	Adz39661 Arabidops
835	31	100.0	191	2	AAZ94002	Vasculat	908	31	100.0	204	8	ADZ77747	Adz77747 Plant ful
836	31	100.0	191	2	AAZ38242	Vasculat	909	31	100.0	205	8	ADZ67129	Adz67129 Hybrid pr
837	31	100.0	191	2	AAZ62525	Vasculat	910	31	100.0	205	8	ADZ10015	Adz10015 Human pro
838	31	100.0	191	2	AAZ69331	Human VEG	911	31	100.0	206	8	ADZ89864	Adz89864 Fusion pr
839	31	100.0	191	2	AAZ57398	Variant v	912	31	100.0	206	8	ADZ40208	Adz40208 Human VEG
840	31	100.0	191	2	AAZ57399	Variant v	913	31	100.0	206	9	ADZ90273	Adz90273 Protease-
841	31	100.0	191	2	AAZ3439	Parapox v	914	31	100.0	206	9	ADZ85119	Adz85119 Vasculat
842	31	100.0	191	2	AAZ07725	Human VEG	915	31	100.0	206	9	ADZ79962	Adz79962 Human vas
843	31	100.0	191	3	AAZ59414	Human vas	916	31	100.0	207	3	AAZ22069	Adz22069 Arabidops
844	31	100.0	191	3	AAZ18305	Human vas	917	31	100.0	207	3	AAZ38804	Adz38804 Arabidops
845	31	100.0	191	3	AAZ90403	VEGF enco	918	31	100.0	208	2	AAZ43483	Adz43483 Amino aci
846	31	100.0	191	3	AAZ82825	Mutant hu	919	31	100.0	209	2	AAZ1931	Adz1931 Human TC-
847	31	100.0	191	3	AAZ82823	Wild-type	920	31	100.0	209	2	AAZ04250	Adz04250 10A1 mutl
848	31	100.0	191	3	AAZ82823	Mutant hu	921	31	100.0	209	2	AAZ04249	Adz04249 4070A ret
849	31	100.0	191	3	AAZ82823	Mutant hu	922	31	100.0	209	5	AAZ79754	Adz79754 Thioresox
850	31	100.0	191	3	AAZ82823	Mutant hu	923	31	100.0	209	6	AAZ80982	Adz80982 N-gonort
851	31	100.0	191	4	AAZ84603	Amino aci	924	31	100.0	209	9	ADZ60205	Adz60205 VEGF isof
852	31	100.0	191	4	AAZ02856	Human vas	925	31	100.0	210	4	AAZ05136	Adz05136 Human T c
853	31	100.0	191	4	AAZ50433	Human VEG	926	31	100.0	211	3	AAZ28560	Adz28560 Human sol
854	31	100.0	191	4	AAZ97568	Human VEG	927	31	100.0	211	4	AAZ85678	Adz85678 Drosophil
855	31	100.0	191	4	AAZ31562	Amino aci	928	31	100.0	214	5	AAZ809175	Adz809175 Leptin-VE
856	31	100.0	191	4	AAZ08401	Human VEG	929	31	100.0	214	6	AAZ10041	Adz10041 Leptin-VE
857	31	100.0	191	5	AAZ19434	Human vas	930	31	100.0	214	8	ADZ00679	Adz00679 Leptin-VE
858	31	100.0	191	5	ABP60706	Mesembrya	931	31	100.0	215	2	AAZ05102	Adz05102 Human vas
859	31	100.0	191	5	ABP65133	Hypoxia-r	932	31	100.0	215	2	AAZ91077	Adz91077 Human vas
860	31	100.0	191	5	ABZ76301	Human vas	933	31	100.0	215	2	AAZ94003	Adz94003 VEGF189.
861	31	100.0	191	6	ABZ79137	Vasculat	934	31	100.0	215	2	AAZ62526	Adz62526 Amino aci
862	31	100.0	191	6	ABP1583	Streptoco	935	31	100.0	215	2	AAZ07726	Adz07726 Human VEG
863	31	100.0	191	6	ABZ80135	VEGF-165.	936	31	100.0	215	3	AAZ59415	Adz59415 Amino aci
864	31	100.0	191	6	ABP97880	Amino aci	937	31	100.0	215	3	AAZ10645	Adz10645 Human VEG
865	31	100.0	191	7	ABU62245	Human vas	938	31	100.0	215	3	AAZ90404	Adz90404 VEGF enco
866	31	100.0	191	7	ADZ34696	Human vas	939	31	100.0	215	3	AAZ94803	Adz94803 Human VEG
867	31	100.0	191	7	ADZ08994	Human VEG	940	31	100.0	215	3	AAZ57035	Adz57035 Human A21
868	31	100.0	191	7	ADZ25490	Binding d	941	31	100.0	215	4	AAZ37512	Adz37512 Human VEG
869	31	100.0	191	7	ADZ25492	Binding d	942	31	100.0	215	4	ABG10788	Adg10788 Novel hum
870	31	100.0	191	7	ADZ43402	VEGF poly	943	31	100.0	215	6	ADZ25611	Adz25611 Human VEG
871	31	100.0	191	7	ADZ92137	Human vas	944	31	100.0	215	7	ABU62246	Adz62246 Human vas
872	31	100.0	191	8	ADZ17128	Human vas	945	31	100.0	215	7	ADZ34697	Adz34697 Human vas
873	31	100.0	191	8	ADZ62205	Human vas	946	31	100.0	215	7	ADZ92128	Adz92128 Human vas
874	31	100.0	191	8	ADZ17222	Human nat	947	31	100.0	215	8	ADZ62207	Adz62207 Human vas
875	31	100.0	191	8	ADZ05122	Protein #	948	31	100.0	215	8	ADZ17224	Adz17224 Human nat
876	31	100.0	191	8	ADZ071599	Amino aci	949	31	100.0	215	8	ADZ73979	Adz73979 Vasculat
877	31	100.0	191	8	ADZ026337	Human vas	950	31	100.0	215	9	ADZ60204	Adz60204 VEGF isof
878	31	100.0	191	8	ADZ46385	Human vas	951	31	100.0	215	9	ADZ28638	Adz28638 VEGF, SER
879	31	100.0	191	8	ADZ31430	Human vas	952	31	100.0	215	9	ADZ81008	Adz81008 Human vas
880	31	100.0	191	8	ADZ54918	Human PRO	953	31	100.0	215	9	ADZ69290	Adz69290 Human VEG
881	31	100.0	191	8	ADZ18045	Human can	954	31	100.0	215	9	ADZ16584	Adz16584 PRO polyP
882	31	100.0	191	8	ADZ06703	Novel brc	955	31	100.0	215	9	ADZ59379	Adz59379 Human VEG
883	31	100.0	191	8	ADZ60206	VEGF isof	956	31	100.0	215	9	AAZ49900	Adz49900 Human VEG
884	31	100.0	191	9	ADZ8644	VEGF165.1	957	31	100.0	215	9	AAZ81220	Adz81220 Human vas
885	31	100.0	191	9	ADZ81007	Mature hu	958	31	100.0	216	2	AAZ28120	Adz28120 NKG2.1
886	31	100.0	191	9	ADZ69287	Human VEG	959	31	100.0	216	7	ADZ06452	Adz06452 Human MTC
887	31	100.0	191	9	ADZ16437	PRO polyP	960	31	100.0	216	8	ADZ93627	Adz93627 Human C-T
888	31	100.0	191	9	ADZ00436	VEGF-A. 6	961	31	100.0	216	8	ADZ182971	Adz182971 Human PRO
889	31	100.0	191	9	AAZ03073	IGF-1 rec	962	31	100.0	216	8	ADZ17796	Adz17796 Human soe
890	31	100.0	192	2	AAZ94040	VEGF165 C	963	31	100.0	216	8	ADZ56126	Adz56126 Human PRO
891	31	100.0	192	2	AAZ94039	VEGF165 C	964	31	100.0	216	8	ADZ10550	Adz10550 Plant ful
892	31	100.0	193	3	AAZ11491	Arabidops	965	31	100.0	216	9	ADZ19952	Adz19952 PRO polyP
893	31	100.0	193	3	AAZ37884	Arabidops	966	31	100.0	216	9	ADZ15632	Adz15632 PRO polyP
894	31	100.0	193	5	ABP60713	Arabidops	967	31	100.0	217	3	AAZ37883	Adz37883 Arabidops
895	31	100.0	194	3	AAZ4095	Arabidops	968	31	100.0	217	8	ADZ07461	Adz07461 Plant ful
896	31	100.0	194	3	AAZ32511	Arabidops	969	31	100.0	218	6	ABU27423	Abu27423 Protein e
897	31	100.0	194	3	AAZ67218	Arabidops	970	31	100.0	219	4	AAZ19517	Adz19517 Human dia
898	31	100.0	194	8	ADZ6469	Novel S.	971	31	100.0	219	7	ABZ74148	Abz74148 DNA clone
899	31	100.0	194	9	AAZ60339	Streptoco	972	31	100.0	221	3	AAZ61101	Adz61101 Arabidops
900	31	100.0	195	9	ABZ96249	M. xanthu	973	31	100.0	221	3	AAZ15609	Adz15609 Arabidops

974	31	100.0	221	8	ADN02744	Adn02744 Human rec
975	31	100.0	222	3	AAG38803	Aag38803 Arabidops
976	31	100.0	222	3	AAG15608	Aag15608 Arabidops
977	31	100.0	222	3	AAG61100	Aag61100 Arabidops
978	31	100.0	222	3	AAG22068	Aag22068 Arabidops
979	31	100.0	222	8	ADX90428	Adx90428 Plant ful
980	31	100.0	223	3	AAAB13572	Aab13572 Streptomy
981	31	100.0	223	4	ABAB1846	Abb1846 Human int
982	31	100.0	223	4	ADDA6716	Add6716 Rat Prote
983	31	100.0	223	7	ADDA6720	Add6720 Rat Prote
984	31	100.0	223	7	ADDE5402	Ades5402 Rat Prote
985	31	100.0	223	7	ADDE5406	Ades5406 Rat Prote
986	31	100.0	223	7	ADDA6724	Add6724 Rat Prote
987	31	100.0	223	7	ADDA6712	Add6712 Rat Prote
988	31	100.0	223	7	ADBO9087	Adeo9087 Novel pro
989	31	100.0	223	9	ADUA0604	Adu40604 Novel hum
990	31	100.0	224	6	ADA21146	Ada21146 Human sec
991	31	100.0	224	7	ADBE5189	Abg05189 Human pro
992	31	100.0	226	4	ABG09456	Abg09456 Novel hum
993	31	100.0	227	4	AAG34398	Aag34398 Arabidops
994	31	100.0	227	4	AA895374	Aab95374 Human pro
995	31	100.0	227	8	AD124503	Adi24503 Human mod
996	31	100.0	227	8	ADK60183	Adk60183 Angiogene
997	31	100.0	227	8	ADK60484	Adk60484 Angiogene
998	31	100.0	227	8	ADP73107	Adp73107 Angiogene
999	31	100.0	227	9	AEA21064	Aea21064 Novel hum
1000	31	100.0	228	4	AU55184	Aau55184 Propionib

ALIGNMENTS

RESULT 1

ID AAR11508 standard; peptide; 4 AA.

AC	XX	AA11508;	
AC	XX		
DT	09-JAN-2003 (revised)		
DT	12-JUN-1991 (first entry)		
XX			
DE	Thioredoxin active site.		
XX			
KM	thioredoxin; colon cancer; B-lymphocytic leukaemia; MP6/Trx.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PN	WO9104320-A.		
XX			
PD	04-APR-1991.		
XX			
PF	12-SEP-1989; 89SE-00003003.		
XX			
PR	12-SEP-1989; 89SR-00003003.		
XX			
PA	(ASTR) ASTRA AB.		
XX			
PI	Rosen A;		
XX			
DR	WPI; 1991-117511/16.		
XX			
PT	Use of thioredoxin alone or with co-factor(s) e.g. interferon(s) etc. -		
PT	for treatment of malignant cells e.g. B lymphocytic leukaemia, colon		
PT	cancer etc.		
XX			
PS	Claim 1; Page 27; 41pp; English.		
XX			
CC	Thioredoxin analogues containing this motif are used to treat malignantly		
CC	transformed cells. The analogue may be used with a co-factor such as		
CC	interleukin-1, -2, -3 or -4, interferons, TNF-alpha, etc. The preferred		
CC	thioredoxin analogue is derived from the MP6 human CD4+ T cell hybridoma		
CC	and is designated MP6/Trx. (Updated on 09-JAN-2003 to add missing OS		

CC field.)
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 31; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 1 CGPC 4

RESULT 2

ID AAW09052 standard; peptide; 4 AA.

AC	XX	AAW09052;	
AC	XX		
DT	20-AUG-1997 (first entry)		
XX			
DE	Thioredoxin motif of enzymes used in branched protein synthesis method.		
XX			
KM	Thioredoxin; protein folding; branched; disulphide bond;		
KM	prokaryotic recombinant production; biologically active;		
KM	protein disulphide oxidoreductase; glutaredoxin; redox buffer.		
XX			
OS	Synthetic.		
XX			
PN	SE9501285-A.		
XX			
PD	07-OCT-1996.		
XX			
PF	06-APR-1995; 95SE-00001285.		
XX			
PR	06-APR-1995; 95SE-00001285.		
XX			
PA	(LJUN/) LJUNG J.		
PA	(HOLM/) HOLMGREN A.		
PA	(ASLUD/) ASLUND F.		
XX			
PI	Ljung J, Holmgren A, Aslund F;		
XX			
DR	WPI; 1997-032920/03.		
XX			
PT	Preparing correctly branched proteins contg. disulphide linkages -		
PT	comprises reacting non-branched reduced protein with protein di:ulphide		
PT	oxido:reductase enzyme in glutaredoxin and redox buffer.		
XX			
PS	Claim 2; Page 16; 22pp; Swedish.		
XX			
CC	AAW09052-W09054 are motifs that are present in thioredoxin or enzymes		
CC	containing thioredoxin domains, e.g. protein-disulphide oxidoreductases.		
CC	These enzymes are used in a method for producing biologically active,		
CC	correctly branched, disulphide-bonded proteins. The method involves		
CC	reacting the corresponding non-branched, reduced protein with a protein-		
CC	disulphide oxidoreductase enzyme that allows correct disulphide bonding;		
CC	in the presence of glutaredoxin and redox buffer (glutathione disulphide)		
CC	with a redox potential of -270 to -140 mV to give protein with desired		
CC	biological activity. The method is used for producing human proteins in		
CC	bacteria (e.g. Escherichia coli) in the correct conformation. Proteins		
CC	such as (pro)insulin, IGF-I, IGF-II, t-PA, growth hormone, Factor VIII,		
CC	coagulation factors, interleukins, pancreatic mammalian ribonucleases,		
CC	lysosomes, pancreatic mammalian trypsin inhibitors, interferons, rennin,		
CC	prolactin and human alpha-1 trypsin inhibitors can be made in prokaryotic		
CC	cells in a biologically active form		
XX			
SQ	Sequence 4 AA;		

Query Match 100.0%; Score 31; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 3

AAAB13337
 ID AAB13337 standard; protein; 4 AA.

AC AAB13337;
 XX

DT 06-NOV-2000 (first entry)
 XX

DE Human Trx-homology domain conserved motif.
 XX

KW Human; thioredoxin; Trx; PICOT; PKC-interacting cousin of thioredoxin;
 KW Protein kinase C theta; PKCtheta; c-Jun N-terminal kinase; JNK; AP-1;
 KW NF-kappaB; interleukin-2; IL-2; TCR/CD28 signaling cascade;
 KW PICOT-homology domain; PIH domain; protein activity modulation; stress;
 KW inflammation.
 XX

OS Homo sapiens.
 XX

PN WO200036083-A2.
 XX

PD 22-JUN-2000.
 XX

PF 17-DEC-1999; 99WO-US030285.
 XX

PR 17-DEC-1998; 98US-00112649.
 XX

PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
 XX

PI Altman A, Witte S;
 XX

DR WPI; 2000-442379/38.
 XX

PT A PKC-interacting cousin of Trx (PICOT) polypeptides and the nucleic
 acids that encode it, useful e.g. for modulating Jun N-terminal kinase,
 AP-1 and/or nuclear factor-kappa-B expression and activity.
 PT

PS Example 4; Page 43; 68pp; English.
 XX

CC The present polypeptide is a conserved motif found in the Trx-homology
 domain of the thioredoxin (Trx) family of proteins. The motif is
 important for catalytic activity. The N-terminal region of PKC-
 interacting cousin of thioredoxin (PICOT) shows homology to the Trx-
 homology domain but it lacks the conserved motif and contains instead an
 Ala-Pro-Gln-Cys motif. PICOT modulates the function of PKCtheta and
 inhibits activation of c-Jun N-terminal kinase (JNK) and the
 transcription factors AP-1 and NF-kappaB. These polypeptides are involved
 in the TCR/CD28 signaling cascade which leads to IL-2 production. PICOT
 also modulates activity of the Trx system. PICOT may be useful for
 ameliorating physiological conditions, e.g. an inflammation or stress
 response, associated with these polypeptides. The cDNA encoding PICOT was
 isolated using yeast two-hybrid screening. PKCtheta polypeptides were
 screened for binding to polypeptides encoded by a Jurkat T lymphoma cDNA
 library. The two longest cDNAs from the PKCtheta-interacting positive
 clones were sequenced and the putative 37.5 kDa polypeptide encoded by
 the open reading frame was named PICOT
 CC

XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 31; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 4

AAAY9348
 ID AAAY9348 standard; peptide; 4 AA.
 XX

AC AAAY9348;
 XX

DT 14-MAR-2000 (first entry)
 XX

DE Active-site loop of E. coli thioredoxin.
 XX

KW Saccharomyces; mammalian; fusion protein; interactor peptide;
 KW conformation-constraining protein; DNA binding moiety; thioredoxin;
 KW gene activating moiety; protein interaction; gene purification.
 XX

OS Escherichia coli.
 XX

PN US6004746-A.
 XX

PD 21-DEC-1999.
 XX

PF 20-JUL-1995; 95US-00504538.
 XX

PR 20-JUL-1994; 94US-00278082.
 XX

PA (GEHO) GEN HOSPITAL CORP.
 XX

PI (GEMV) GENETICS INST INC.
 XX

PI McCoy JM, Jessen TH, Brent R;
 XX

DR WPI; 2000-072059/06.
 XX

PT Population of Saccharomyces and/or mammalian cells comprising recombinant
 DNA encoding fusion proteins, useful for detecting protein interactions.
 PT

PS Disclosure; Col 15; 24pp; English.
 XX

CC The invention relates to a population of Saccharomyces and/or mammalian
 cells comprising recombinant DNA molecules encoding fusion proteins, each
 consisting of a candidate interactor peptide, a conformation-constraining
 protein and a DNA binding moiety and/or gene activating moiety. The cells
 are useful for detecting protein interactions. The cells may also be used
 in a method for identifying and purifying genes encoding a wide range of
 useful proteins based on their physical interaction with a second
 polypeptide
 CC

XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 31; DB 3; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 5

ABP56403
 ID ABP56403 standard; peptide; 4 AA.

AC ABP56403;
 XX

DT 12-MAR-2003 (first entry)
 XX

DE Thioredoxin related peptide #2.
 XX

KW Thioredoxin; TrxA; fusion protein; allogenic protein.
 XX

OS Synthetic.
 XX

PN CN1189539-A.
 XX

PD 05-AUG-1998.
 XX

PF 31-JAN-1997; 97CN-00100362.
 XX
 PR 31-JAN-1997; 97CN-00100362.
 XX
 PA (BIOL-) BIOLOGICAL ENG INST ACAD MILITARY MEDICI.
 XX
 PI Cui L, Ma Q;
 XX
 DR WPI; 2002-733391/80.
 XX
 PT Soluble expression carrier and its fusion protein of novel thioredoxin.
 XX
 PS Disclosure; Page 2 (Disclosure); 14pp; Chinese.
 XX
 CC The present invention describes a DNA molecule of a fusion protein which
 CC is composed of the DNA sequence similar to encoded thioredoxin in
 CC structure and the DNA sequence of an encoded allogenic protein. The
 CC soluble expression of the fusion protein is efficient. The expressed
 CC fusion protein can be easily purified as several amino acid sequences are
 CC inserted at active sites of the thioredoxin gene sequence, and hydrolysed
 CC by a specific protease as the junction between the two encoded DNA
 CC sequences can be cut by the specific protease, obtaining a recombinant
 CC allogenic protein the same as the natural protein in one-class structure.
 CC The present sequence represents a peptide which is given in the
 CC exemplification of the present invention
 CC
 XX
 SO Sequence 4 AA;

Query Match 100.0%; Score 31; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 6
 AAO22593
 ID AAO22593 standard; peptide; 4 AA.
 XX
 AC AAO22593;
 XX
 DT 30-OCT-2002 (first entry)
 XX

DE Redox active peptide sequence CGPC.
 XX

KM Antiinflammatory; immunosuppressive; antiaesthetic; antibacterial;
 KM nephrotoxic; antiarteriosclerotic; antirheumatic; antiarthritic;
 KM Helicobacter pylori protein; inhibitor; activator; NF-kappaB; rheumatoid;
 KM inflammation; inflammatory bowel disease; autoimmune arthritis;
 KM chronic disease; autoimmune disease; asthma; septic shock; lung fibrosis;
 KM glomerulonephritis; atherosclerosis; autoimmune encephalomyelitis;
 KM soft tissue injury; reduction catalyst; chronic inflammatory disease;
 KM systemic inflammatory response; NF-kappaB-mediated inflammatory disease;
 KM inducible surface expression; CD44; intercellular adhesion molecule;
 KM ICAM-1; NF-kappaB activation; redox active peptide.
 XX

OS Unidentified.
 OS
 PN WO200260933-A2.
 XX
 PD 08-AUG-2002.
 XX

PF 30-JAN-2002; 2002WO-IE000011.
 XX
 PR 30-JAN-2001; 2001IE-00000069.
 XX

PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
 XX

PI Windle HJ, Dermot K, Dermot O, Abdel-Latif MM;
 XX
 DR WPI; 2002-627466/67.

XX
 PT Novel Helicobacter pylori protein useful for treating inflammation,
 PT autoimmune diseases, septic shock and glomerulonephritis, has redox
 PT active peptide sequence inhibiting activation of NF-kappaB.
 XX
 PS Claim 4; Page 22; 34pp; English.
 XX

CC The invention relates to a Helicobacter pylori protein, its derivatives,
 CC fragments, mutants and variants capable of inhibiting the activation of
 CC NF-kappaB and having a sequence of 106 amino acids defined in the
 CC specification. The protein is useful for preventing and/or treating
 CC inflammation, inflammatory bowel disease, rheumatoid/autoimmune
 CC arthritis, chronic disease where NF-kappaB is transcriptionally
 CC activated, autoimmune diseases, asthma, septic shock, lung fibrosis,
 CC glomerulonephritis, atherosclerosis or autoimmune encephalomyelitis, and
 CC soft tissue injury. The Helicobacter pylori protein is also used for
 CC treating chronic diseases where NF-kappaB is transcriptionally activated.
 CC The Helicobacter pylori protein catalyses the reduction of proteins. The
 CC H. pylori protein is also useful for treating chronic inflammatory
 CC diseases, particularly systemic inflammatory response syndrome or other
 CC NF-kappaB-mediated inflammatory disease states, down regulates the
 CC resting and inducible surface expression of CD44 and intercellular
 CC adhesion molecule (ICAM)-1, prevents NF-kappaB activation both prior to
 CC stimulation with inducers of NF-kappaB and secondary to induction of NF-
 CC kappaB, and prevents or inhibits constitutive NF-kappaB activity. This
 CC sequence represents the redox active peptide sequence CGPC relating to
 CC the invention
 CC
 XX
 SO Sequence 4 AA;

Query Match 100.0%; Score 31; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 7
 ABG32509
 ID ABG32509 standard; peptide; 4 AA.
 XX
 AC ABG32509;
 XX
 DT 15-NOV-2002 (first entry)
 XX

DE M. tuberculosis thioredoxin active site peptide.
 XX
 XX
 XX

KM Thioredoxin; TRX; tuberculosis; antibacterial; active site;
 KM tuberculostatic; vaccine; superoxide dismutase; SOD; bacterial infection;
 KM attenuated intracellular bacterium.
 KM

OS Mycobacterium tuberculosis.
 OS

PN WO200262298-A2.
 XX

PD 15-AUG-2002.
 XX

PF 07-FEB-2002; 2002WO-US003451.
 XX

PR 07-FEB-2001; 2001US-0267328P.
 XX

PR 18-SEP-2001; 2001US-0322989P.
 XX

PA (UYVA-) UNIV VANDERBILT.
 XX

PA (USGO) US DEPT VETERANS AFFAIRS.
 XX

PI Kernodle DS, Bochan MR;
 XX

DR WPI; 2002-643387/69.
 XX
 PT Modifying a bacterium to enhance immunogenicity, as vaccines for
 PT preventing bacterial infections, e.g. tuberculosis comprises reducing the

PT activity of an anti-apoptotic enzyme, e.g. superoxide dismutase produced
 PT by the bacterium.
 XX
 PS Example 13; Page 94; 164pp; English.
 XX
 CC The invention relates to modifying a bacterium to enhance immunogenicity
 CC of the bacterium comprising reducing the activity of an anti-apoptotic
 CC enzyme produced by the bacterium e.g. superoxide dismutase (SOD) where
 CC the bacterium has enhanced immunogenicity in a subject. Also included are
 CC the modified bacterium, an immunogenic composition comprising the
 CC modified bacterium, an attenuated intracellular bacterium (further
 CC modified to reduce the activity of an anti-apoptotic enzyme of the
 CC bacterium), modifying a bacterium so it retains or increases
 CC immunogenicity but loses or reduces pathogenicity in a subject.
 CC comprising reducing but not eliminating an activity of an enzyme produced
 CC by the bacterium, where reducing the activity of the enzyme attenuates
 CC the bacterium. The methods are useful for preventing bacterial
 CC infections, e.g. tuberculosis. The attenuated intracellular bacterium is
 CC useful as a vaccine for preventing bacterial infections. The present
 CC sequence is the active site of M. tuberculosis thioredoxin (TRX) which
 CC was eliminated by mutagenesis to create an attenuated bacterium of the
 CC invention
 CC
 XX
 SQ Sequence 4 AA;
 XX
 Query Match 100.0%; Score 31; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 1 CGPC 4
 XX
 RESULT 8
 ID AAU97916 standard; peptide; 4 AA.
 AC AAU97916;
 XX
 DT 14-AUG-2002 (first entry)
 XX
 DE Tetrapeptide antioxidant peptide composition CB.
 XX
 DE Antioxidant; oxidative stress; central nervous system; cancer; ageing;
 KM neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KM Creutzfeldt Jakob's disease; cerebral ischaemia; multiple sclerosis;
 KM motor neuron disease; scrapie; spongiform encephalopathy;
 KM acute respiratory distress syndrome; amyotrophic lateral sclerosis;
 KM atherosclerosis; acquired immunodeficiency syndrome; AIDS.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N terminal acetylation"
 FT Modified-site 4 /note= "C terminal amide"
 FT
 XX
 PN GB2368339-A.
 XX
 PD 01-MAY-2002.
 XX
 PF 26-OCT-2000; 2000GB-00026254.
 XX
 PR 26-OCT-2000; 2000GB-00026254.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 XX
 PI Atlas D;
 XX
 DR WPI; 2002-419127/45.
 XX

PT Antioxidant compound used for treating e.g. Alzheimer's disease and
 PT multiple sclerosis comprises peptide including cysteine residues having
 PT sulphydryl groups and hydrophobic or non charged groups attached to amino
 PT and carboxy terminal.
 XX
 PS Example 1; Page 32; 62pp; English.
 XX
 CC This invention relates to an antioxidant compound comprising a peptide
 CC including at least 3 amino acid residues of which at least 2 are cysteine
 CC residues each having a readily oxidisable sulphydryl group for effecting
 CC antioxidant, and a first hydrophobic or non charged group attached to
 CC an amino terminal of the peptide and a second hydrophobic or non charged
 CC group attached to a carboxy terminal. the antioxidant peptide compound
 CC may be used for preventing or reducing oxidative stress and for treating
 CC central nervous system neurodegenerative disorders, particularly
 CC Parkinson's disease, Alzheimer's disease, Creutzfeldt Jakob's disease,
 CC cerebral ischaemia, multiple sclerosis, basal ganglia degenerative
 CC disease, motor neuron diseases, scrapie, spongiform encephalopathy and
 CC loss or impaired memory, peripheral tissue disorders, particularly acute
 CC respiratory distress syndrome, amyotrophic lateral sclerosis,
 CC atherosclerotic cardiovascular disease, multiple lateral organ
 CC dysfunction, complication resulting from inflammatory processes, acquired
 CC immunodeficiency syndrome, AIDS, cancer and ageing. The antioxidant
 CC compound of the invention has the advantage that it may cross a blood
 CC barrier. The present sequence represents an antioxidant peptide of the
 CC invention
 CC
 XX
 SQ Sequence 4 AA;
 XX
 Query Match 100.0%; Score 31; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 1 CGPC 4
 XX
 RESULT 9
 ID ABB05573 standard; peptide; 4 AA.
 AC ABB05573;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Dithiol peptide #1.
 XX
 KM dithiol; disulfide bond; chemical reagent; sulphydryl group; SH group;
 KM trans-(Pt(ethylenediamine)2Cl2)2+.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 4 /note= "amidated"
 FT
 XX
 PN WO200192466-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015923.
 XX
 PR 26-MAY-2000; 2000US-00579883.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Rabenstein DA, Shi T;
 XX
 DR WPI; 2002-114335/15.
 XX

PT Forming an intramolecular disulfide bond in a peptide, comprises
 PT contacting a peptide comprising at least two sulfhydryl groups with an
 PT oxidizing agent that forms disulfide linkages in peptides.
 XX Example 1; Page 14; 40pp; English.
 XX
 XX The present invention describes a method of forming an intramolecular
 CC disulfide bond in a peptide, comprising contacting a peptide comprising
 CC at least two sulfhydryl (SH) groups with a compound (trans-
 CC (Pt(ethylenediamine)2Cl2)2+) (I). Also describes are: (1) a solution (II)
 CC comprising a peptide which comprises at least two sulfur groups, and (1);
 CC (2) a peptide synthesizer (III) for the synthesis of a peptide having an
 CC intramolecular disulfide linkage, comprises a number of vials containing
 CC amino acids derivatised for chemical peptide synthesis, where at least
 CC one of the vials comprises an amino acid that, when fully deprotected,
 CC bears a SH group, and a vial comprising (1); (3) chemically synthesising
 CC a peptide comprising a disulfide linkage, involving chemically coupling a
 CC number of amino acids to form a peptide comprising at least two SH
 CC groups, and contacting the peptide with (1); and (4) a kit for forming an
 CC intramolecular disulfide bond in a peptide, comprising a container
 CC containing (II). The method can be used for forming an intramolecular
 CC disulfide bond in a peptide. (II) is useful as a positive control when
 CC evaluating the efficacy of particular reagent species, and as a sample
 CC solution when optimising a purification protocol to clean up or to
 CC isolate the desired reaction product (e.g., when optimising a high
 CC pressure liquid chromatography (HPLC) protocol or evaluating a particular
 CC chromatography column). The present sequence represents a dithiol peptide
 CC which is used in an example from the present invention
 XX
 XX Sequence 4 AA;
 XX
 XX Query Match 100.0%; Score 31; DB 5; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 CGPC 5
 XX ||||
 XX 1 CGPC 4
 XX
 XX Db
 XX
 XX RESULT 10
 XX AAE37340
 XX ID AAE37340 standard; peptide; 4 AA.
 XX AC AAE37340;
 XX XX
 XX DT 27-AUG-2003 (first entry)
 XX XX
 XX DE E. coli thioredoxin active site peptide.
 XX XX
 XX KM Disulphide bond formation protein; Dsb protein; gene therapy; vaccine;
 XX HME; human monocytotropic ehrlichiosis; canine monocytic ehrlichiosis;
 XX CME; antibacterial; immunostimulant; thioredoxin.
 XX XX
 XX OS Escherichia coli.
 XX OS
 XX PN WO2003038061-A2.
 XX XX
 XX PD 08-MAY-2003.
 XX XX
 XX PF 01-NOV-2002; 2002WO-US035226.
 XX XX
 XX PR 01-NOV-2001; 2001US-0335611P.
 XX XX
 XX PA (RERE-) RES DEV FOUND.
 XX XX
 XX PI McBride JW, Walker DH;
 XX XX
 XX DR WPI; 2003-441356/41.
 XX XX
 XX PT New isolated DNA encoding a disulfide bond formation (Dsb) protein from
 PT bacteria of the genus Ehrlichia, useful for preventing human
 PT monocytotropic ehrlichiosis, or canine monocytic ehrlichiosis.

XX
 XX Example 10; Page 71; 73pp; English.
 XX
 XX The present invention relates to disulphide bond formation (Dsb) proteins
 CC and polynucleotides encoding such proteins from bacteria of the genus
 CC Ehrlichia. Sequences of the invention are useful for preventing human
 CC monocytotropic ehrlichiosis (HME) or canine monocytic ehrlichiosis (CME).
 CC The kits are useful for determining whether an animal or individual has
 CC been infected with a species of the bacteria of the Ehrlichia genus. Dsb
 CC sequences are also used in gene therapy and as vaccines. The present
 CC sequence is Escherichia coli thioredoxin protein active site peptide
 CC (conserved cysteine motif) used in the exemplification of the invention
 XX
 XX Sequence 4 AA;
 XX
 XX Query Match 100.0%; Score 31; DB 6; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 CGPC 5
 XX ||||
 XX 1 CGPC 4
 XX
 XX Db
 XX
 XX RESULT 11
 XX ADJ47607
 XX ID ADJ47607 standard; peptide; 4 AA.
 XX AC ADJ47607;
 XX XX
 XX DT 06-MAY-2004 (first entry)
 XX XX
 XX DE Trx catalytic site consensus sequence, SEQ ID 15.
 XX XX
 XX KM Antidiabetic; Antihypertensive; Neuroprotective; Nootropic;
 XX Antiparkinsonian; Anticonvulsant; Cardiac; Cardiovascular;
 XX Antithrombotic; Antithrombotic; Cytostatic; Antiproliferative; Gene Therapy;
 XX thioredoxin; Trx; atherosclerosis; diabetes; apoptotic disease;
 XX mitochondrial disease; cardiac dysfunction;
 XX angiogenesis dependent disease; neurodegenerative disease;
 XX rheumatoid arthritis; cancer; psoriasis; catalytic site.
 XX XX
 XX OS Unidentified.
 XX OS
 XX PN WO2004013283-A2.
 XX XX
 XX PD 12-FEB-2004.
 XX XX
 XX PF 22-JUL-2003; 2003WO-US022847.
 XX XX
 XX PR 02-AUG-2002; 2002US-0401073P.
 XX XX
 XX PA (UYRP) UNIV ROCHESTER.
 XX XX
 XX PI Min W, Yingmei L;
 XX XX
 XX DR WPI; 2004-157111/15.
 XX XX
 XX PT New mutant thioredoxin molecule which is resistant to oxidizing effects
 PT of cytokines or reactive oxygen species, useful for treating or
 PT diagnosing atherosclerosis, diabetes, Alzheimer's disease, myocardial
 PT infarction or cancer.
 XX
 XX PS Disclosure; SEQ ID NO 15; 145pp; English.
 XX
 XX The present invention relates to mutant thioredoxin (Trx) proteins and
 CC their coding sequences, where the thioredoxin molecule is resistant to
 CC the oxidizing effects of cytokines or reactive oxygen species or
 CC resistant to S-nitrosylation of a SH-group by nitrous oxide. The mutant
 CC Trx proteins are useful for treating or diagnosing atherosclerosis,
 CC diabetes, apoptotic disease, mitochondrial dysfunction disease or cardiac
 CC dysfunction. Mitochondrial dysfunction diseases include Kearns-Sayre
 CC syndrome or encephalomyopathy lactic acidosis and stroke-like episodes.

CC Apoptotic diseases include neurodegenerative diseases, e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral
 CC sclerosis, multiple sclerosis or peripheral neuropathy. Cardiac
 CC dysfunction includes myocardial infarction, cardiomyopathy, arterial
 CC hypertension or heart failure. The mutant Trx proteins are also useful
 CC for treating or diagnosing angiogenesis dependent diseases, e.g.
 CC rheumatoid arthritis, cancer or psoriasis. The present sequence is the
 CC consensus sequence for the catalytic site of the Trx protein (residues 32
 CC to 35).

XX Sequence 4 AA;

Query Match 100.0%; Score 31; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 12

ADM32927 standard; peptide; 4 AA.

AC ADM32927;

DT 17-JUN-2004 (first entry)

DE Amino acid sequence of the thioredoxin active site.

XX mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KM lung disease; cystic fibrosis.

OS Synthetic.

PN WO2004024868-A2.

PD 25-MAR-2004.

PF 10-SEP-2003; 2003WO-US028526.

PR 10-SEP-2002; 2002US-0409960P.

PR 11-APR-2003; 2003US-0462082P.

PA (NAJR-) NAT JEWISH MEDICAL & RES CENT.

PI White CW;

DR WPI; 2004-270016/25.

PT Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.

PS Disclosure; Page 15; 69pp; English.

XX The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive
 CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC statistically significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the

CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for
 CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
 CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
 CC cause of the disease. The present sequence represents an active site of a
 CC thioredoxin which is used in the method of the invention.

XX Sequence 4 AA;

Query Match 100.0%; Score 31; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 13

ADR46076 standard; peptide; 4 AA.

AC ADR46076;

DT 04-NOV-2004 (first entry)

DE Antioxidant CB4.

XX Antioxidant; CB4; L-DOPA amide; levodopa amide; antiparkinsonian;
 KM neuroleptic; cytostatic.

OS Synthetic.

PN Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 4 /note= "C-terminal amide"

PN WO2004069146-A2.

PD 19-AUG-2004.

PF 03-FEB-2004; 2004WO-11000103.

PR 07-FEB-2003; 2003US-0445439P.

PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

PI Aclae D;

DR WPI; 2004-625378/60.

PT New L-dihydroxy phenyl alanine derivatives useful for the treatment of
 PT e.g. Parkinson's disease, Tourette's syndrome, attention deficit
 PT hyperactive disorder and schizophrenia.

PS Disclosure; Page 18; 44pp; English.

XX The present sequence is that of the antioxidant peptide, CB4. This
 CC peptide is used in a claimed pharmaceutical composition of the invention
 CC also comprising an L-DOPA amide derivative. The pharmaceutical
 CC composition is useful for treatment of a condition associated with
 CC impaired dopaminergic signalling, such as Parkinson's disease, Tourette's
 CC syndrome, attention deficit hyperactive disorder, generation of pituitary
 CC tumours and schizophrenia. The inclusion of an antioxidant in the
 CC pharmaceutical composition provides for improved stability particularly
 CC in vivo, and also provides neuroprotection against oxidative stress,
 CC which is typically associated with L-DOPA treatment, and with the
 CC biosynthesis and degradation of dopamine and other catecholamines.

SQ Sequence 4 AA;
 Query Match 100.0%; Score 31; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 1 CGPC 4
 RESULT 14
 ADV11816
 XX ADV11816 standard; peptide; 4 AA.
 AC ADV11816;
 XX
 DT 24-MAR-2005 (revised)
 DT 24-FEB-2005 (first entry)
 XX
 DE Thioresoxin conserved active site motif, SEQ ID NO:149.
 XX
 XX Antisense therapy; thioresoxin inhibitor; cancer; neoplasm; carcinoma;
 XX melanoma; basal cell carcinoma; ovary tumor; breast tumor;
 XX non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
 XX stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
 XX uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
 XX sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;
 XX endocrine disease; gynecology and obstetrics; genitourinary disease;
 XX respiratory disease; musculoskeletal disease; dermatological disease;
 XX proliferative disease; atherosclerosis; psoriasis; antipsoriatic;
 XX cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
 XX immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
 XX cardiovascular disease; ocular disease; rheumatoid arthritis;
 XX antirhectic; antirheumatic; inflammation; asthma; antiasthmatic;
 XX skin allergy; anti-allergic; anti-inflammatory; dermatological;
 XX verruca vulgaris; vitiligo; metabolism; cell proliferation;
 XX apoptosis modulation; cell cycle; thioresoxin; cyclic.
 XX
 OS cellular organisms.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..4
 XX /note = Formation of this disulfide bond is reversible
 PN US2004241717-A1.
 XX
 PD 02-DEC-2004.
 XX
 PF 10-FEB-2004; 2004US-0076933.
 XX
 PR 10-FEB-2003; 2003US-0446374P.
 XX
 PA (SANT-) SANTARIS PHARMA AS.
 XX
 PI Hansen B, Thue CA, Westergaard M, Petersen KD, Wissenbach M;
 XX WPI; 2005-056301/06.
 DR
 XX
 PT Novel compound useful for modulating expression of gene involved in
 PT cancer disease, or for modulating red blood cell proliferation, cellular
 PT proliferation, ion metabolism or glucose and energy metabolism.
 XX
 PS Disclosure; SEQ ID NO 149; 92pp; English.
 XX
 CC The invention relates to antisense oligonucleotides consisting of 8-50
 CC nucleotides and/or nucleotide analogs which inhibit expression of the
 CC putative human oncogene thioresoxin (TRX). The antisense oligonucleotides
 CC comprise a subsequence of 8 or more nucleotides or nucleotide analogs,
 CC wherein the subsequence is located within a sequence selected from
 CC ADV11669-ADV11724. The oligonucleotides preferably contain at least
 CC nucleotide analog, especially a locked nucleic acid (LNA) or a modified
 CC nucleobase selected from 5-methylcytosine, isocytosine,

CC pseudoisocytosine, 5-bromouracil, 5-propynyluracil, 6-aminopurine, 2-
 CC aminopurine, inosine, diaminopurine and 2-chloro-6-aminopurine. The
 CC invention also relates to a conjugate comprising a TRX antisense
 CC oligonucleotide of the invention and one or more non-nucleotide or non-
 CC polynucleotide moieties covalently attached to the oligonucleotide; and a
 CC pharmaceutical composition comprising a TRX antisense oligonucleotide or
 CC conjugate of the invention, optionally further comprising a
 CC chemotherapeutic agent, an anti-inflammatory compound or an antiviral
 CC compound. The TRX antisense oligonucleotides, and conjugates and
 CC compositions containing them, are useful in the treatment of cancers such
 CC as carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
 CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
 CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
 CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
 CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
 CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma
 CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
 CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
 CC gliomas. The TRX antisense oligonucleotides are also useful in the
 CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
 CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
 CC dermatitis. They may additionally be used for inhibiting cellular
 CC proliferation and for modulating red blood cell proliferation, ion
 CC metabolism, glucose and energy metabolism, pH regulation, matrix
 CC metabolism, apoptosis, cytokinesis or the cell cycle. The TRX antisense
 CC oligonucleotides of the invention have increased specificity and affinity
 CC for TRX mRNA, and are resistant to degradation. The present sequence
 CC represents the reversibly disulfide-bonded conserved active site motif of
 CC thioresoxin which is referred to in the invention.
 CC
 CC Revised record issued on 24-MAR-2005 : Correction to comments field
 CC
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 31; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 1 CGPC 4
 RESULT 15
 ADW97624
 XX ADW97624 standard; peptide; 4 AA.
 AC ADW97624;
 XX
 DT 19-MAY-2005 (first entry)
 XX
 DE Human thioresoxin protein-related active center peptide #1.
 XX
 KW chronic obstructive pulmonary disease; thioresoxin; respiratory-Gen.;
 KW anti-inflammatory; cytokine antagonist; histamine antagonist;
 KW interleukin 2 antagonist; interleukin 4 antagonist;
 KW interleukin 6 antagonist; TNF alpha antagonist; emphysema;
 KW chronic bronchitis.
 XX
 OS Homo sapiens.
 XX
 PN JP2005060408-A.
 XX
 PD 10-MAR-2005.
 XX
 PF 30-NOV-2004; 2004JP-00346572.
 XX
 PR 13-FEB-2004; 2004JP-00071691.
 XX
 PA (JPCF-) JPC KK.
 XX
 DR WPI; 2005-200153/21.
 XX

PT Agent e.g. tablet or capsules, for preventing and treating chronic
PT obstructive pulmonary disease, contains polypeptide of thioredoxin super
PT family as active ingredient.
XX
PS Disclosure; SEQ ID NO 3; 10pp; Japanese.
XX
CC This invention relates to a novel prophylactic or therapeutic agent of
CC chronic obstructive pulmonary disease which contains a polypeptide of the
CC thioredoxin super family as active ingredient, preferably human
CC thioredoxin. The invention may be used for the production of compounds
CC with a respiratory-Gen. or antiinflammatory activity acting as cytokine-
CC antagonists, histamine-antagonists, interleukin-2-antagonists,
CC interleukin-4-antagonists, interleukin-6-antagonists or TNF-alpha
CC antagonists. The invention may be used for preventing and treating
CC chronic obstructive pulmonary disease (COPD), preferably pulmonary
CC emphysema or chronic bronchitis, caused by contaminants such as smoking
CC gas, waste gas, dust and soot, and COPD accompanied with inflammation of
CC cell or tissue, fibrosis and necrosis. The agent effectively prevents and
CC treats chronic obstructive pulmonary disease, with negligible side
CC effects. The present sequence is that of a peptide which represents the
CC active center of thioredoxin and which is related to the
CC prophylactic/therapeutic agent of the invention.
CC
XX
SQ Sequence 4 AA;
XX
Query Match 100.0%; Score 31; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 1 CGPC 4
XX
RESULT 16
ADY81685
ID ADY81685 standard; peptide; 4 AA.
XX
AC ADY81685;
XX
DT 02-JUN-2005 (first entry)
XX
DE Thioredoxin TrxA wild type redox active disulfide motif SEQ ID NO:2.
XX
KM genetic engineering; protein production; antimicrobial; antifungal;
KM antiparasitic; antiviral; immunostimulant; thioredoxin.
XX
OS Synthetic.
XX
PN US6872563-B1.
XX
PD 29-MAR-2005.
XX
PF 05-OCT-2000; 2000US-00679705.
XX
PR 05-OCT-1999; 99US-0157770P.
PR 08-NOV-1999; 99US-0163939P.
PR 17-NOV-1999; 99US-0166044P.
XX
PA (HARD) HARVARD COLLEGE.
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Beckwith J, Aslund F, Bessette PH, Georgiou G, Ritz D, Lim JB;
XX WPI; 2005-239572/25.
XX
DR New prokaryotic cell that is genetically modified to shift the redox
XX PT status of the cytoplasm to a more oxidative state, useful for producing
XX PT disulfide bond containing proteins.
XX
PS Example 6; SEQ ID NO 2; 44pp; English.
XX
CC The invention relates to a prokaryotic cell that is genetically modified

CC to shift the redox status of the cytoplasm to a more oxidative state that
CC favors disulfide bond formation, relative to a prokaryotic cell that is
CC not genetically modified. The cell further comprises a mutated Ahpc gene
CC comprising an insertion of three nucleotides in the TGT triplet rich
CC region located at codons 36-39 of an Ahpc gene. The insertion increases
CC the cell's ability to proliferate relative to a cell that is not further
CC genetically modified. Also described is a method for producing a protein
CC having at least one disulfide bond. The prokaryotic cell and method are
CC useful for producing disulfide bond containing proteins. The proteins,
CC polypeptides, and compositions are used for diagnostic, therapeutic, or
CC prophylactic purposes. They are useful for inhibiting the growth of
CC bacteria, viruses, fungi, or other parasites and for stimulating an
CC immune response. They may be used as food supplements, as well as
CC components of wash powders and creams. The present sequence represents a
CC thioredoxin TrxA redox active disulfide motif.
XX
SQ Sequence 4 AA;
XX
Query Match 100.0%; Score 31; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 1 CGPC 4
XX
RESULT 17
AA78911
ID AA78911 standard; peptide; 5 AA.
XX
AC AA78911;
XX
DT 05-JUN-2000 (first entry)
XX
DE Thioredoxin conserved active site amino acid sequence.
XX
KM Thioredoxin reductase; redox inhibitor; cellular proliferation; cancer;
KM apoptosis; reperfusion injury; hepatitis; amyotrophic lateral sclerosis;
KM Alzheimer's disease; autoimmune disease; Sjogren's syndrome; lupus;
KM rheumatoid arthritis; HIV; Heremansky-Pudlack syndrome; retinopathy;
KM wound healing; Crohn's disease; ulcerative colitis; angiogenesis;
KM adult respiratory distress syndrome; AIDS; infection;
KM inflammatory conditions; psoriasis; inflammatory bowel disease;
KM hyperproliferative disease; mycosis fungoides.
XX
OS Synthetic.
XX
PN WO200006088-A2.
XX
PD 10-FEB-2000.
XX
PF 02-AUG-1999; 99WO-US017496.
XX
PR 31-JUL-1998; 98US-00127219.
XX
PA (KIRK/) KIRKPATRICK D L.
PA (POMT/) POWIS G.
XX
PI Kirpatrick DL, Powis G;
XX
DR WPI; 2000-195158/17.
XX
PT New composition for preventing inhibition of apoptosis and for treating
XX PT e.g. cancer or reperfusion injuries comprises inhibitor of cellular redox
XX PT signaling.
XX
PS Disclosure; Page 12; 55pp; English.
XX
CC This sequence represents a conserved active site found in thioredoxins.
CC The thioredoxins are a class of low molecular weight redox proteins.
CC Thioredoxin exerts specific redox control over a number of transcription
CC factors to modulate their DNA binding and therefore regulates gene

transcription. Thioredoxin reductase catalyses the reduction of thioredoxin. The thioredoxin redox system plays an important role in a number of diseased states. The invention relates to a composition comprising an inhibitor of cellular redox signalling and a carrier. The composition can be used for inhibiting cellular proliferation or preventing inhibition of apoptosis and is therefore useful for treating cancer, reperfusion injury following ischaemia, hepatitis, amyotrophic lateral sclerosis, neurodegenerative diseases, Alzheimer's disease, autoimmune diseases, Sjogren's syndrome, lupus, rheumatoid arthritis, HIV, Herpesvirus-Putlak syndrome, retinal oxidative damage, retinopathy, skin hyperplasia, aging, ultraviolet damage, wound healing, Crohn's disease, ulcerative colitis, angiogenesis, uterine disorders, adult respiratory distress syndrome (ARDS), lung disorders, viral infections such as herpes virus, pox virus and adenovirus infections, inflammatory conditions, autoimmune diseases (such as systemic lupus erythematosus, rheumatoid arthritis, psoriasis, inflammatory bowel disease and autoimmune diabetes), immune mediated glomerular nephritis and hyperproliferative diseases (such as fibrosis) and mycosis fungoides

Sequence 5 AA;

Query Match 100.0%; Score 31; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
1 CGPC 4

RESULT 18

AAE05156
ID AAE05156 standard; peptide; 5 AA.

AAE05156;

12-SEP-2001 (first entry)

Human thioredoxin (ADF) active site.

T cell-derived colony stimulating factor; TC-CSF; immunostimulant;
acquired immune deficiency syndrome; AIDS; cancer; gene therapy;
haematopoietic growth factor; human; thioredoxin; ADF; active site.

Homo sapiens.

US6254861-B1.

03-JUL-2001.

24-JAN-1994; 94US-00180371.

23-MAY-1989; 89US-00356006.

12-JUL-1991; 91US-00729135.

19-AUG-1991; 91US-00747784.

01-NOV-1991; 91US-00788115.

01-JUL-1992; 92US-00906866.

(CHOI/) CHOUHURY C.

Choudhury C;

New T cell-derived colony stimulating factor for treating immune-compromised patients, including acquired immunodeficiency syndrome patients and certain types of cancer patients.

Example 33; Col 36; 38pp; English.

The invention relates to T-cell derived colony stimulating factors (TC-CSF) and nucleic acid molecules encoding them. TC-CSF which is a novel haematopoietic growth factor is useful for treating immune-compromised

patients, including acquired immune deficiency syndrome (AIDS) patients and certain types of cancer patients. TC-CSF DNA is used in gene therapy. The present sequence is human thioredoxin active site which is used in the exemplification of the invention

Sequence 5 AA;

Query Match 100.0%; Score 31; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
2 CGPC 5

AAO21523
ID AAO21523 standard; peptide; 5 AA.

AAO21523;

02-SEP-2002 (first entry)

wild type thioredoxin active site peptide sequence.

Cytostatic; thioredoxin; cell growth stimulator; modulating; apoptosis; tumour; wild type.

Unidentified.

US2002055131-A1.

09-MAY-2002.

06-JUN-2001; 2001US-00875578.

03-JUN-1999; 99US-00319292.

(POWI/) POWIS G.

Powis G;

WPI; 2002-470971/50.

Modulating thioredoxin-associated inhibition of apoptosis for the treatment of tumors.

Disclosure; Page 1; 59pp; English.

The invention relates to the use of thioredoxin as a cell growth stimulator, for modulating thioredoxin cell growth stimulator-associated inhibition of apoptosis, comprising controlling the expression and/or activity of the thioredoxin. The invention is useful for treating tumours associated with aberrant thioredoxin expression and activity. This sequence represents a wild type thioredoxin active site peptide sequence relating to the invention

Sequence 5 AA;

Query Match 100.0%; Score 31; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
1 CGPC 4

RESULT 20

ABG71301
ID ABG71301 standard; peptide; 5 AA.

XX

AC ABG71301;
 XX
 DT 16-DEC-2002 (first entry)
 XX
 DE Thioresoxin protein active site disulphide/dithiol conserved sequence.
 XX
 KM Thioresoxin; TRXP-2; cancer; actinic keratosis;
 KM cell proliferative disorder; arteriosclerosis; bursitis;
 KM cirrhosis; hepatitis; mixed connective tissue disease; AIDS; trauma;
 KM polythaemia vera; primary thrombocytopenia; psoriasis; anaemia;
 KM inflammatory disorder; acquired immunodeficiency syndrome; infection;
 KM adult respiratory distress syndrome; Addison's disease; allergy; asthma;
 KM atherosclerosis; gout; myocardial inflammation; scleroderma;
 KM pericardial inflammation; osteoporosis; rheumatoid arthritis;
 KM systemic lupus erythematosus; ulcerative colitis; Reiter's syndrome;
 KM haemodialysis; Crohn's disease; atopic dermatitis; viral disorder;
 KM autoimmune thyroiditis; diabetes mellitus; Graves' disease;
 KM glomerulonephritis; active site disulphide/dithiol conserved sequence.
 XX
 OS Unidentified.
 XX
 PN US2002102654-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 17-SEP-2001; 2001US-00954846.
 XX
 PR 30-JUN-1998; 98US-00107248.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Corley NC, Guegler KJ, Patterson C, Baughn MR;
 DR WPI; 2002-690612/74.
 XX
 PT Novel human thioresoxin protein and polynucleotide for diagnosing,
 PT preventing and treating cell proliferative, inflammatory and viral
 PT disorders.
 XX
 PS Disclosure; Page 1; 41pp; English.

The invention relates to isolated human thioresoxin polypeptide TRXP-2, a naturally occurring polypeptide comprising an amino acid sequence 90% identical to TRXP-2, a biologically active or immunogenic fragment of TRXP-2 and its encoding polynucleotide (TRXP-2 NA). Also included are a recombinant polynucleotide comprising a promoter sequence operably linked to TRXP-2 NA, a cell transformed with the recombinant sequence, a TRXP-2 transgenic organism, an anti-TRXP-2 antibody and a composition comprising TRXP-2, an agonist or antagonist compound identified using TRXP-2, or the above antibody. TRXP-2 is useful for screening a compound for effectiveness as an agonist or antagonist of TRXP-2. TRXP-2, the identified agonist and antagonist are useful for creating a disease or condition associated with decreased or overexpression of functional TRXP in a patient. TRXP-2 is useful for screening for a compound that modulates the activity of the polypeptide or that binds to the polypeptide. TRXP-2 is also useful as an immunogen for preparing polyclonal or monoclonal antibodies by hybridoma technology. TRXP-2 NA is useful for screening a compound for effectiveness in altering expression of a target polynucleotide comprising the sequence of TRXP-2 NA. The antibody is useful for detecting the presence of TRXP-2 and purifying TRXP-2 from a sample. The antibody, optionally labeled, is useful for diagnosing a condition or disease associated with expression of TRXP in a subject or in a biological sample. TRXP-2 and TRXP-2 NA and modulators of TRXP-2 are useful for diagnosis, treatment and prevention of cell proliferation (e.g. cancer, actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, polythaemia vera, primary thrombocytopenia and psoriasis), inflammatory (e.g. adult respiratory distress syndrome, Addison's disease, allergies, anaemia, asthma, atherosclerosis, gout, myocardial or pericardial inflammation, osteoporosis, rheumatoid arthritis, Reiter's syndrome, systemic lupus erythematosus, ulcerative colitis, autoimmune thyroiditis, diabetes mellitus, Graves' disease and glomerulonephritis),

CC infection (e.g. viral, bacterial, fungal, parasitic, protozoal and
 CC helminthic), viral disorders (e.g. acquired immunodeficiency syndrome
 CC (AIDS) and trauma. The present sequence represents a thioresoxin active
 CC site disulphide/dithiol conserved sequence as found in TRXP-2
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 31; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 2 CGPC 5
 RESULT 21
 AAP71087
 ID AAP71087 standard; peptide; 6 AA.
 XX
 AC AAP71087;
 XX
 DT 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 06-JUN-1991 (first entry)
 XX
 DE Sequence of thioresoxin analogue.
 XX
 KM Redox active peptide; antioxidant; stress; ischaemia; lipid peroxidation;
 KM food industry; cosmetics; antibiotic.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note="optional, and may optionally be joined to a
 FT terminal blocking gp."
 FT Misc-difference 6 /note="see above"
 FT
 XX
 PN BP237189-A.
 XX
 PD 16-SEP-1987.
 XX
 PF 10-FEB-1987; 87EP-00301150.
 XX
 PR 10-FEB-1986; 86US-00828112.
 PR 14-MAR-1986; 86US-00839857.
 PR 20-OCT-1986; 86US-00921287.
 XX
 PA (REPK) REPLIGEN CORP.
 XX
 PI Piglet VP, Millis CD;
 DR WPI; 1987-258442/37.
 XX
 PT New and known thioresoxin derivs. and analogues - useful for preventing
 PT metal catalysed oxidative damage in biological reactions and disease
 PT states.
 XX
 PS Claim 7; Page 7; 7pp; English.
 XX
 CC It is a redox active peptide which can be used in cpds. to treat stress
 CC and ischaemia, for inhibiting lipid peroxidn. due to drugs or toxic
 CC effects, as anti-inflammatory agents, to prevent DNA damage, and to
 CC maintain the biological activity of antibiotics or proteins. Thioresoxin
 CC can be used as a general antioxidant in the food and cosmetic industry.
 CC It may be used in prodn. processes for antibiotics, proteins or
 CC polypeptides. Therapeutic dose is 1 microgram/kg - 10mg/kg. (Updated on
 CC 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct
 CC PA field.)
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 2 CGPC 5

RESULT 22

ABP54936
 ID ABP54936 standard; peptide; 6 AA.

XX
 AC ABP54936;

DT 08-JAN-2003 (first entry)

DE Active site peptide of thioredoxin.

XX
 XX Thioredoxin; organoarsenical; arsenoxide; antiarthritic; antigout;
 KM osteopathic; antineumatic; arthritis; therapy.

OS Homo sapiens.

XX
 PN WO200274305-A1.

PD 26-SEP-2002.

XX
 PF 19-MAR-2002; 2002WO-AU000310.

XX
 PR 19-MAR-2001; 2001AU-00003798.

XX
 PA (UNIX) UNISEARCH LTD.

PI Hogg RJ, Donoghue N;

XX
 DR WPI; 2002-750519/81.

PT Use of an impermeable cell membrane compound for the treatment of
 PT arthritis in vertebrates.

XX
 PS Example 2 (b) ; Page 42; 91pp; English.

CC The present sequence is that of a hexapeptide comprising the active site
 CC sequence of thioredoxin. The hexapeptide was used in an example from the
 CC invention that examined the binding of 4-(N-(S-
 CC glutathionylacetyl)amino)phenylarsenoxide (GSAO) to peptide and protein
 CC containing closely spaced thiols. The invention provides a method for the
 CC treatment and/or prophylaxis of arthritis using a compound of formula A-
 CC (L-Y)P, where A is a cell-membrane impermeable pendant group, L is a
 CC linker and/or spacer, Y is an arsenoxide or arsenoxide equivalent, and P
 CC is an integer from 1 to 10. The compound, e.g. GSAO, is useful for the
 CC treatment of arthritic conditions such as calcific periarthritis,
 CC enteropathic, chronic, thumb, hip, peripheral, psoriatic, rheumatoid,
 CC septic or Jaccoud's arthritis, gout, hand or knee osteoarthritis,
 CC juvenile osteoarthritis, oligoarthritis, and polyarthritis (all claimed).
 CC The compound blocks angiogenesis in the synovial tissue and leucocyte
 CC ingress that triggers inflammation, with no signs or symptoms of toxicity
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 2 CGPC 5

RESULT 23

ADA08451
 ID ADA08451 standard; peptide; 6 AA.

XX
 AC ADA08451;

DT 06-NOV-2003 (first entry)

DE Mammalian peptide found in thioredoxin and protein disulphide isomerase.

XX
 XX Anti-angiogenesis plasmin fragment; plasminogen; plasminogen activator;
 KM plasmin reductase; reduced plasmin protein; anti-angiogenesis activity;
 KM urokinase-type plasminogen activator; A61; annexin II heterotetramer;
 KM annexin II p36 subunit; annexin II p11 subunit; thioredoxin;
 KM protein disulphide isomerase; modulating angiogenesis; mammalian;
 KM cleavage peptide.

XX
 OS Mammalia.

XX
 PN US2003083234-A1.

PD 01-MAY-2003.

XX
 PF 26-NOV-2002; 2002US-00304287.

XX
 PR 28-NOV-2001; 2001US-0333866P.

XX
 PA (WAIS/) WAISMAN D.

XX
 PA (KMON/) KMON M.

PI Waisman D, Kwon M;

XX
 DR WPI; 2003-596985/56.

PT Producing an anti-angiogenesis plasmin fragment, useful for modulating,
 PT e.g. promoting or inhibiting angiogenesis, comprises contacting a
 PT plasminogen polypeptide with a plasminogen activator and a plasmin
 PT reductase.

XX
 PS Example 2; Page 6; 29pp; English.

CC The present invention relates to a method for producing an anti-
 CC angiogenesis plasmin fragment. The method comprises contacting a
 CC plasminogen polypeptide with a plasminogen activator and a plasmin
 CC reductase, where a reduced plasmin protein is produced and the anti-
 CC angiogenesis plasmin fragment having anti-angiogenesis activity, is
 CC released from the reduced plasmin protein. The plasminogen activator is
 CC preferably a urokinase-type plasminogen activator. The angiogenesis
 CC plasmin fragment is A61. The plasmin reductase is selected from annexin
 CC II heterotetramer, annexin II p36 subunit, p11, thioredoxin, and protein
 CC disulphide isomerase. The annexin II heterotetramer is associated with a
 CC cell membrane. The method of the invention is useful for modulating (e.g.
 CC promoting or inhibiting) angiogenesis. The present sequence represents a
 CC mammalian cleavage peptide found in thioredoxin and protein disulphide
 CC isomerase.
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 6; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 2 CGPC 5

RESULT 24

ADH05024
 ID ADH05024 standard; peptide; 6 AA.

XX
 AC ADH05024;

DT 11-MAR-2004 (first entry)

XX Target peptide #5 of the invention.
 DE pendant phenylarsine moieties; labeling; target peptide.
 XX
 XX Synthetic.
 XX WO2003107010-A1.
 XX
 PD 24-DEC-2003.
 XX
 XX 13-JUN-2003; 2003WO-US018792.
 XX
 XX 14-JUN-2002; 2002US-038699P.
 XX
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Ebright RH, Ebright YW;
 XX
 DR WPI; 2004-156348/15.
 XX
 XX New bis-phenylarsine derivatives useful for labeling protein in living
 PT cells and for screening a library of peptides and identifying a cysteine
 PT containing peptides.
 XX
 PS Claim 23; SEQ ID NO 5; 82pp; English.
 XX
 CC The present invention relates to a molecule with two pendant phenylarsine
 CC moieties. The invention is useful for imparting detectable properties to
 CC target material, for detecting target material, for monitoring binding
 CC process, for isolating and immobilizing at least one target material, for
 CC screening a library of peptides and identifying a cysteine containing
 CC peptides and for labeling protein in living cells. The present sequence
 CC represents a target peptide of the invention.
 XX
 SQ Sequence 6 AA;
 QY
 Db 2 CGPC 5
 ||||
 2 CGPC 5
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
 RESULT 25
 ADM32929
 ID ADM32929 standard; peptide; 6 AA.
 XX
 AC ADM32929;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Amino acid sequence of the thioredoxin active site.
 XX
 KW mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KW lung disease; cystic fibrosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Active-site 1..6 /note= "active site of thioredoxin"
 FT Modified-site 2 /note= "this residue is in a reduced state"
 FT Modified-site 5 /note= "this residue is in a reduced state"
 FT
 FT
 PN WO2004024868-A2.
 XX
 PD 25-MAR-2004.
 XX

PF 10-SEP-2003; 2003WO-US028526.
 XX
 XX 10-SEP-2002; 2002US-0409960P.
 PR 11-APR-2003; 2003US-0462082P.
 XX
 XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
 XX
 XX White CW;
 XX
 DR WPI; 2004-270016/25.
 XX
 XX
 PT Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.
 XX
 PS Claim 13; Page 51; 69pp; English.
 XX
 CC The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive
 CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC statistically significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
 CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for
 CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
 CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or a
 CC cause of the disease. The present sequence represents an active site of a
 CC thioredoxin which is used in the method of the invention.
 XX
 SQ Sequence 6 AA;
 QY
 Db 2 CGPC 5
 ||||
 2 CGPC 5
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
 RESULT 26
 ADM32928
 ID ADM32928 standard; peptide; 6 AA.
 XX
 AC ADM32928;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Amino acid sequence of the thioredoxin active site.
 XX
 KW mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KW lung disease; cystic fibrosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Active-site 1..6 /note= "active site of thioredoxin"
 FT Misc-difference 1 /note= "any amino acid"
 FT

FT Modified-site 2 /note= "this residue is in a reduced state"
 FT Misc-difference 3 /note= "any amino acid"
 FT Misc-difference 4 /note= "any amino acid"
 FT Modified-site 5 /note= "this residue is in a reduced state"
 FT Misc-difference 6 /note= "any amino acid"
 PN WO2004024868-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 10-SEP-2003; 2003WO-US028526.
 XX
 PR 10-SEP-2002; 2002US-0409960P.
 PR 11-APR-2003; 2003US-0462082P.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI White CW;
 XX
 DR WPI; 2004-270016/25.
 XX
 PT Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.
 XX
 PS Claim 12; Page 51; 69pp; English.
 XX
 CC The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive
 CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC substantially significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
 CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for
 CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
 CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
 CC cause of the disease. The present sequence represents an active site of a
 CC thioredoxin which is used in the method of the invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 2 CGPC 5
 RESULT 27
 ID ADP87509
 AC ADP87509; standard; peptide; 6 AA.

XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Thioredoxin family conserved catalytic site peptide.
 XX
 KW 4-(1(Sulfonyl)-1H-indol-2-yl)-4(hydroxy)-cyclohexa-2,5-dienone;
 KW cytosstatic; thioredoxin reductase inhibitor; proliferative condition;
 KW colon cancer; renal cancer; thioredoxin; thioredoxin reductase;
 KW cell cycle progression; cell proliferation; apoptosis;
 KW catalytic site peptide.
 XX
 OS Synthetic.
 OS
 PN WO2004056361-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 20-DEC-2002; 2002WO-GB005842.
 XX
 PR 20-DEC-2002; 2002WO-GB005842.
 XX
 PA (CANC-) CANCER RES TECHNOLOGY LTD.
 XX
 PI Stevens MFG, Westwell AD, Poole TD, Wells G, Berry JM;
 XX
 DR WPI; 2004-517586/49.
 XX
 PT New 4-(1(Sulfonyl)-1H-indol-2-yl)-4(hydroxy)-cyclohexa-2,5-dienone
 PT derivatives are thioredoxin reductase inhibitors useful for treating e.g.
 PT colon or renal cancer.
 XX
 PS Disclosure; Page 82; 141pp; English.
 XX
 CC The present invention described 4-(1(Sulfonyl)-1H-indol-2-yl)-4(hydroxy)-
 CC cyclohexa-2,5-dienone derivatives (I) and their salts, esters, amides,
 CC solvates, hydrates or protected forms. (I) have cytosstatic activities,
 CC and can be used as thioredoxin reductase inhibitors. (I) can be used for
 CC treating a proliferative condition (especially colon or renal cancer) or
 CC a condition mediated by thioredoxin/thioredoxin reductase in the human or
 CC animal body. (I) are also useful for inhibiting thioredoxin/thioredoxin
 CC reductase and cell cycle progression, to regulate/inhibit cell
 CC proliferation and/or to promote apoptosis in a cell in vitro or in vivo.
 CC The present sequence represents a thioredoxin family conserved catalytic
 CC site peptide, which is given in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 2 CGPC 5
 RESULT 28
 ID ADP67423
 AC ADP67423; standard; peptide; 6 AA.
 AC ADP67423;
 DT 23-SEP-2004 (first entry)
 XX
 DE Thioredoxin and protein disulfide isomerase common sequence SEQ ID NO:4.
 XX
 KW p11; p11 activity modulator; plasminogen activation; cytosstatic;
 KW antisense therapy; cancer; tumour; tumour growth inhibition; thioredoxin;
 KW protein disulfide isomerase.
 XX
 OS Homo sapiens.
 OS Synthetic.

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XX WO2004054517-A2.
XX
XX
XX 01-JUL-2004.
XX
XX
XX 12-DEC-2003; 2003WO-US040029.
XX
XX 13-DEC-2002; 2002US-0433140P.
XX
XX (MEDI-) MEDIONICS LLC.
XX (WAIS/) WAISMAN D.
XX
XX Waismann D;
XX
XX WPI; 2004-487995/46.
XX
XX Composition useful for inhibiting growth of tumor in patient, modulates
XX activity of p11 protein and effects change in level of plasminogen
XX activation by a cell.
XX
XX Example 2; SEQ ID NO 4; 140pp; English.
XX
XX The present invention describes a composition (I) which modulates the
XX activity of a p11 protein and effects a change in the level of
XX plasminogen activation by a cell. Also described: (1) making (M1) a
XX clonal cell line, which involves isolating a cell, then characterizing
XX the activity of a protein produced by the cell or clonal progeny of the
XX cell, where the protein is involved in plasminogen activation; and (2) a
XX clonal cell line (II) useful in the identification of composition that
XX modulate p11 activity, where the clonal cell line is obtained by (M1).
XX (1) has cytostatic activity, and can be used in antisense therapy. (1) is
XX useful for modulating the activity of p11 which involves administering
XX (1) to a cell. The cell can be a human cancer cell, chosen from a HT1080
XX fibrosarcoma cell, a LNCaP prostate cancer cell and a CCL-22 colorectal
XX adenocarcinoma cell. (1) is also useful for reducing the development of
XX cancer in a patient e.g., mouse which involves administering (1) to a
XX cancer cell in the patient. (II) is useful for inhibiting the growth of
XX tumors or inhibiting tumour cell invasion in a patient, which involves
XX administering (II) to a cancer cell in the patient. (II) is useful for
XX identifying a composition that modulates p11 activity which involves
XX administering the composition to (II) obtained by (M1), determining the
XX change in p11 activity of a cell of the clonal cell line relative to a
XX cell of a clonal cell line that had not received the composition, and
XX identifying the composition that produces a change in p11 activity. The
XX change in p11 activity is a change in the level of plasminogen activation
XX activity. The present sequence represents a thioredoxin and protein
XX disulfide isomerase common sequence, which is used in the exemplification
XX of the present invention.
XX
XX SQ
XX
XX Sequence 6 AA:
XX
XX Query Match 100.0%; Score 31; DB 8; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
XX Matches 4; Conservative 0; Mismatches 0;
XX
XX QY 2 CGPC 5
XX ||||
XX Db 2 CGPC 5
XX
XX
XX RESULT 29
XX ADO97008
XX ID ADO97008 standard; peptide; 6 AA.
XX
XX ADO97008;
XX
XX 07-OCT-2004 (first entry)
XX
XX Thioredoxin and protein disulphide isomerase common sequence.
XX
XX p11 protein; plasminogen activation; tumour growth; metastasis; treating.
XX
XX Synthetic.
XX
XX OS

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XX US2004142897-A1.
XX
XX
XX 22-JUL-2004.
XX
XX
XX 12-DEC-2003; 2003US-00735577.
XX
XX 28-NOV-2001; 2001US-033866P.
XX 26-NOV-2002; 2002US-00304287.
XX 13-DEC-2002; 2002US-0433140P.
XX
XX (WAIS/) WAISMAN D M.
XX
XX Waismann DM;
XX
XX WPI; 2004-579971/56.
XX
XX New composition which modulates the activity of a p11 protein and effects
XX a change in the level of plasminogen activation by a cell useful for
XX treating cancer or reducing p11 protein activity in cancer cells.
XX
XX Example 2; SEQ ID NO 4; 66pp; English.
XX
XX The invention relates to a composition which modulates the activity of a
XX p11 protein and effects a change in the level of plasminogen activation
XX by a cell. The composition is useful for reducing p11 protein activity in
XX cancer cells. They are also useful for inhibiting tumour growth or
XX metastasis or treating cancer. The present sequence represents the amino
XX acid sequence of the thioredoxin and protein disulphide isomerase common
XX sequence involved with cleavage, formation and reshuffling of disulphide
XX bonds.
XX
XX SQ
XX
XX Sequence 6 AA:
XX
XX Query Match 100.0%; Score 31; DB 8; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
XX Matches 4; Conservative 0; Mismatches 0;
XX
XX QY 2 CGPC 5
XX ||||
XX Db 2 CGPC 5
XX
XX
XX RESULT 30
XX AAP50203
XX ID AAP50203 standard; peptide; 8 AA.
XX
XX AAP50203;
XX
XX 17-OCT-1991 (first entry)
XX
XX Sequence of oligopeptide 3 specific to the beta-subunit of luteinising
XX hormone (LH).
XX
XX Contraception; assay; pregnancy test; luteinising hormone;
XX human chorionic gonadotropin.
XX
XX Homo sapiens.
XX
XX EP142387-A.
XX
XX 22-MAY-1985.
XX
XX 23-AUG-1984; 84EP-00401710.
XX 26-AUG-1983; 83BP-00401714.
XX
XX (ANDA-) ANDA BIOLOGICALS.
XX
XX Maes RF.
XX
XX WPI; 1985-124152/21.
XX
XX DR

```

PT	Prepn. of anti-HCG and anti-LH vaccines - by use of oligo-peptide(s)
PT	specific to beta-sub-unit of LH and HCG.
XX	
PS	Claim 1, Page 17; 22pp; English.
XX	
CC	Oligopeptides AAP501398-P50205, specific to the beta-subunit of LH and of
CC	HCG, located near cysteine groups, are used in a claimed process for the
CC	preparation of anti-HCG and anti-LH vaccines. The vaccines are
CC	characterised in that these oligopeptides are complexed upon themselves
CC	and between themselves by disulphur bridges, upon their own beta-subunit
CC	of HCG and LH or upon oligopeptides containing cysteine whose AA chain is
CC	common to LH and HCG, namely the peptides in AAP50208-P50212. Through
CC	disulphur bridges the specific oligopeptides are administered by injection
CC	in vaccinees to cause prodn. of antibodies so that a contraceptive effect
CC	is achieved; and the antibodies are also useful in assays for HCG and LH
CC	in body fluids
XX	
SQ	Sequence 8 AA;
QY	2 CGPC 5
Db	4 CGPC 7
RESULT 31	
ADC81369	
ID	ADC81369 standard; peptide; 8 AA.
AC	ADC81369;
XX	
DT	01-JAN-2004 (first entry)
DE	Bovln THF-gamma2 analogue C3-C6-cyclicTHF gamma2.
XX	
KW	Cow; thymic humoral factor gamma2; THF-gamma2; concanavalin A;
KW	Con A-induced interleukin-2 production; mouse spleen cells;
KW	granulocyte-monocyte colony forming cell; GM-CFC; mouse bone marrow;
KW	immunomodulatory agent; congenital immune defect;
KW	primary T cell deficiency; thymic dysplasia; Down's syndrome;
KW	viral infection; herpes; adenovirus infection; HIV infection;
KW	subacute sclerosing pan-encephalitis; immune suppression; leukopaenia;
KW	cancer; chemotherapy; radiotherapy; autoimmune inflammatory disorder;
KW	rheumatoid arthritis; systemic lupus erythematosus; psoriasis;
KW	bone marrow transplantation; atopic condition; asthma; atopic dermatitis;
XX	mutant; mutein; cyclic.
OS	Synthetic.
OS	Bos taurus.
XX	
FH	Key Location/Qualifiers
FT	Disulfide-bond 3..6 /note= "This bond cyclises the molecule"
FT	Misc-difference 3 /note= "Wild-type Asp substituted by Cys"
FT	Misc-difference 6 /note= "Wild-type Lys substituted by Cys"
FT	
PN	WO9501182-A1.
XX	
PD	12-JAN-1995.
PF	28-JUN-1994; 94WO-US007304.
PR	01-JUL-1993; 93IL-00106214.
XX	
PA	(YEDA) YEDA RES & DEV CO LTD.
XX	
PI	Rycus A, Burestein Y, Trainin N;
XX	

DR	WT; 1995-060814/08.
PT	New thymic humoral factor gamma 2 analogues - used as immunomodulatory agents for treating e.g. immune defects, viral infections or auto-immune disease.
PS	Example 2; Page 17; 30pp; English.
XX	A peptide is claimed which is a thymic humoral factor (THF)-gamma2 analogue of at least 4 amino acid (AA) residues or a functional derivative or salt, capable of enhancing concanavalin A (Con A)-induced interleukin-2 (IL-2) production in mouse spleen cells and/or the number of granulocyte-macrophage colony forming cells (GM-CFC) of mouse bone marrow. The peptide comprises one or more sequences corresponding to the sequence of the wild-type THF-gamma2 but differing by (i) deletion of one or more AA residues, (ii) addition of one or more AA residues at the N-and/or C-terminus, (iii) substitution of one or more AA residues by a protein natural or non-natural AA residue, (iv) cyclisation through a free carboxyl group and a free amino group or through disulphide bonds of cysteine residues or (v) linkage of two or more sequences or modified sequences corresponding to (i)-(iv), either directly or through a peptide or non-peptide chain. The peptides are used as immunomodulatory agents. They can be used for treating e.g. congenital immune defects involving primary T cell deficiencies such as thymic dysplasia and Down's syndrome, primary and secondary viral infections (e.g. herpes virus, adenovirus and HIV), as well as subacute infections and leukopenia following pancreatic encephalitis, immune suppression and leukaemia following cancer treatment by chemotherapy and/or radiotherapy, autoimmune inflammatory disorders, e.g. rheumatoid arthritis, systemic lupus erythematosus and psoriasis, in bone marrow transplantation to prevent viral infections and in atopic conditions such as asthma and atopic dermatitis. The present sequence is a bovine THF-gamma2 analogue peptide of the invention.
XX	Sequence 8 AA;
SQ	
OY	Query Match 100.0%; Score 31; DB 2; Length 8; Best Local Similarity 100.0%; Pred. NO. 2e+06; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dd	2 CGPC 5 3 CGPC 6
RESULT 32	
AAW05002	ID AAW05002 standard; peptide; 8 AA.
AC	AAW05002;
DT	03-DEC-1996 (first entry)
DE	Thymic humoral factor gamma-2 cyclic analogue.
KM	Immunomodulation; immunomodulator; immune system; anxiety; deficiency; aberrant response; chronic bronchitis; atopic disease; AIDS;
KW	acquired immune deficiency syndrome; herpes virus infection; cyclic.
OS	Synthetic.
FH	Key Location/Qualifiers
FT	Disulfide-bond 3..6
PN	MO9611943-A1.
PD	25-APR-1996.
PF	06-OCT-1995; 95WO-SB001151.
PR	14-OCT-1994; 94SE-00003526.
PA	(ASTR) ASTRA AB.

PI Bergstrand H, Eriksson T, Karabelas K, Lindvall M, Saernstrand B;
 DR WPI; 1996-221938/22.
 XX
 PT Peptide(s) with immunomodulatory activity - useful for treating e.g.
 CC chronic bronchitis, malignancies, herpes, AIDS or atopic disease, as
 CC adjuvants in vaccines, or for inhibiting graft rejection.
 XX
 PS Claim 1; Page 50; 63pp; English.
 CC The present peptide is a known immunomodulatory agent. It is described as
 CC a cyclic analogue of thymic humoral factor gamma-2 and was disclosed in
 CC WO9501182. The peptide is one of 6 known peptides which concord with a
 CC highly genetic sequence covering immunomodulatory peptides of 4-15 amino
 CC acids being claimed in the present patent application; all 6 peptides are
 CC specifically excluded from the claim
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 31; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 XX
 RESULT 33
 AAM41664
 ID AAM41664 standard; peptide; 8 AA.
 XX
 AC AAM41664;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DB Immunomodulatory peptide.
 XX
 KW Immunomodulator; immunosuppressant; immunostimulator; treatment;
 KW transplant rejection; autoimmune disease; cancer; infection.
 XX
 OS Synthetic.
 OS
 PN WO9739023-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 04-APR-1997; 97WO-SE000574.
 XX
 PR 12-APR-1996; 96SE-00001422.
 PR 23-SEP-1996; 96SE-00003469.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX WPI; 1997-526397/48.
 DR
 XX
 PT Nucleic acids encoding cysteine- or methionine-containing peptide(s)
 PT which have immunostimulatory or immunosuppressive activity - can be used
 PT to treat, e.g. cancers, infection, autoimmune disease or transplant
 PT rejection.
 XX
 PS Disclosure; Page 19; 183pp; English.
 XX
 CC A novel immunosuppressing or immunostimulatory peptide conforms to the
 CC motifs represented by the formulae of the invention, with the proviso
 CC that the peptides described in AAM36999, AAM37000 and AAM41647 to
 CC AAM41682 are excluded. An immunosuppressant can be used to treat
 CC transplant rejection or autoimmune disease, e.g. rheumatoid arthritis,
 CC systemic lupus erythematosus, Sjogren's syndrome, scleroderma, mixed
 CC connective tissue disease, dermatomyositis, polymyositis, Reiter's
 CC syndrome, Behcet's disease, type I diabetes, Hashimoto's thyroiditis,

CC Graves' disease, multiple sclerosis, myasthenia gravis,
 CC encephalomyelitis, phemphigus vulgaris, vegetans or foliaceus, Senear-
 CC Usher syndrome or Brazilian phemphigus. An immunostimulator can be used
 CC to treat conditions such as cancer or infection
 XX
 SQ Sequence 8 AA;
 CC
 Query Match 100.0%; Score 31; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 XX
 RESULT 34
 ADH05029
 ID ADH05029 standard; peptide; 8 AA.
 XX
 AC ADH05029;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Target peptide #10 of the invention.
 XX
 KW pendant phenylarsine moieties; labeling; target peptide.
 XX
 OS Synthetic.
 OS
 PN WO2003107010-A1.
 XX
 PD 24-DEC-2003.
 XX
 PF 13-JUN-2003; 2003WO-US018792.
 XX
 PR 14-JUN-2002; 2002US-0388699P.
 XX
 PA (RUPF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Ebright RH, Ebright YW;
 XX
 DR WPI; 2004-156348/15.
 XX
 PT New bis-phenylarsine derivatives useful for labeling protein in living
 PT cells and for screening a library of peptides and identifying a cysteine
 PT containing peptides.
 XX
 PS Claim 25; SEQ ID NO 10; 82pp; English.
 XX
 CC The present invention relates to a molecule with two pendant phenylarsine
 CC moieties. The invention is useful for imparting detectable properties to
 CC target material, for detecting target material, for monitoring binding
 CC process, for isolating and immobilizing at least one target material, for
 CC screening a library of peptides and identifying a cysteine containing
 CC peptides and for labeling protein in living cells. The present sequence
 CC represents a target peptide of the invention.
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 31; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 1 CGPC 4
 XX
 RESULT 35
 ADV60194
 ID ADV60194 standard; peptide; 8 AA.
 XX

AC ADV60194;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE VEGF peptide SEQ ID NO 7699.
 XX
 DE diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
 KM food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
 XX
 OS unidentified.
 XX
 PN WO2004111636-A2.
 XX
 PD 23-DEC-2004.
 XX
 PF 17-JUN-2004; 2004WO-EP051158.
 XX
 PR 17-JUN-2003; 2003EP-00101775.
 PR 17-JUN-2003; 2003US-0479061P.
 XX
 PA (VIRB-) VIB VZM.
 PI (UYGE-) UNIV GENT.
 XX
 PI Kas K, Vandekerckhove J, Krols L;
 XX
 DR WPI; 2005-057893/06.
 XX
 PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 XX
 PS Example; SEQ ID NO 7699; 265pp; English.
 XX
 CC The invention relates to a method of identifying a peptide combo which
 CC corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a VEGF peptide combo.
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 31; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 2 CGPC 5
 XX
 RESULT 36
 ID ADZ28911 standard; protein; 8 AA.
 AC ADZ28911;
 XX

DT 30-JUN-2005 (first entry)
 XX
 DE Calmodulin Ortho C-terminus.
 XX
 DE cell culture; DNA detection; RNA detection; protein purification;
 KM calmodulin ortho; Cam.
 XX
 OS unidentified.
 XX
 PN WO2005033286-A2.
 XX
 PD 14-APR-2005.
 XX
 PF 01-OCT-2004; 2004WO-US032337.
 XX
 PR 01-OCT-2003; 2003US-0508142P.
 XX
 PA (INVI-) INWITROGEN CORP.
 PI Hanson G, Kudlicki WA, Keppertjola S;
 XX
 DR WPI; 2005-296136/30.
 XX
 PT New cellular extract from an organism comprises a SlyD gene,
 PT substantially free of a SlyD polypeptide that binds to a bi-
 PT reagent, useful for synthesizing, purifying, or detecting biomolecules,
 PT e.g. nucleic acids.
 XX
 PS Example 5; Page 4; 65pp; English.
 XX
 CC The invention relates to a cellular extract from an organism comprising a
 CC SlyD gene, substantially free of a SlyD polypeptide that binds to a bi-
 CC arsenical reagent. Also described are: (i) a kit for the in vitro
 CC production of proteins, the kit comprising a cellular extract above; (ii)
 CC a polypeptide comprising an amino acid sequence that binds specifically
 CC to EDR 2 [4,5'-bis(1,3,2-dithioarsolan-2-yl)fluorescein-(1,2-
 CC ethanedithiol)2; and (iii) a fusion protein comprising an amino acid
 CC sequence that binds specifically to EDR 2 [5'-bis(1,3,2-dithioarsolan-2-
 CC yl)fluorescein-(1,2-ethanedithiol)2. Preferably, the cellular extract is
 CC an Escherichia coli extract or from an E. coli comprising a SlyD mutant
 CC gene. The SlyD mutant gene encodes a SlyD that is mutated in an amino
 CC acid sequence that binds a bi-arsenical molecule. The SlyD mutant gene
 CC also encodes a truncated SlyD protein. The cellular extract further
 CC comprises a nuclease inhibitor, which is a Gam protein. The extract has
 CC reduced activity of at least one enzyme that catalyzes hydrolysis of high
 CC -energy phosphate bonds or hydrolysis or formation of phosphodiester
 CC bonds. It further comprises at least one inhibitor of at least one enzyme
 CC that catalyzes hydrolysis of high-energy phosphate bonds or hydrolysis or
 CC formation of phosphodiester bonds. The cellular extract further comprises
 CC at least two energy sources providing chemical energy for synthesis. It
 CC also comprises a nucleic acid encoding a fusion protein encoding an
 CC exogenous protein fused to a tag, where the tag binds a bi-arsenical
 CC reagent. The cellular extract is useful for synthesizing, purifying, and
 CC detecting biomolecules, e.g. nucleic acids and polypeptides. It is
 CC preferably useful for purifying and detecting recombinant polypeptides
 CC having polyhistidine or polycysteine tags. The present sequence
 CC represents calmodulin ortho C-terminus used as a control in measurement
 CC of real-time in vitro protein synthesis.
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 31; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 1 CGPC 4
 XX
 RESULT 37
 ID ADV60195 standard; peptide; 9 AA.
 AC ADV60195
 XX

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XX AC ADV60195;
XX XX 10-MAR-2005 (first entry)
XX DE VEGF peptide SEQ ID NO 7700.
XX KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX KM food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
XX OS Unidentified.
XX PN WO200411636-A2.
XX XX
XX PD 23-DEC-2004.
XX PF 17-JUN-2004; 2004WO-EP051158.
XX PR 17-JUN-2003; 2003EP-00101775.
XX PR 17-JUN-2003; 2003US-0479061P.
XX PA (VIBV-) VIB VZM.
XX PA (UYGE-) UNIV GENT.
XX PI Kas K, Vandekerckhove J, Krols L;
XX DR WPI; 2005-057893/06.
XX PT Identifying a peptide combo, which corresponds with a family of proteins,
XX PT useful for diagnosing a variety of diseases, drug development or in
XX PT agriculture, comprises generating peptides by applying a digest on the
XX PT family of protein.
XX PS Example; SEQ ID NO 7700; 265pp; English.
XX
XX CC The invention relates to a method of identifying a peptide combo which
XX CC corresponds with a family of proteins where each of the members of the
XX CC peptide combo is derived from a unique protein from the family. The
XX CC peptide combo is useful for quantifying specific known splice variants of
XX CC one or more particular proteins in a sample, for diagnosing complex
XX CC genetic diseases such as cancer, obesity, diabetes, asthma and
XX CC inflammation, neuropsychiatric disorders such as depression, for
XX CC quantifying one to several hundreds of protein disease markers
XX CC simultaneously leading to a more accurate diagnostic sub-classification,
XX CC for determining the extent of protein modification in a particular sample
XX CC of proteins, for tissue-typing analysis, for prenatal testing to detect
XX CC the presence of a congenital disease or for quantitating protein levels
XX CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX CC or neurological diseases, as biomarkers preclinical drug development,
XX CC development of improved animal models, biomarkers related with
XX CC toxicology, clinical drug development, guidance marketed drugs,
XX CC prognostic or diagnostic disease markers, drug target validation and
XX CC selection, monitoring protein splicing, drug lead profiling, pathway
XX CC analysis, answering basic disease biology questions, and in the fields of
XX CC food and feed, cosmetics, agriculture and animal breeding. The present
XX CC sequence represents a peptide from a VEGF peptide combo.
XX SQ Sequence 9 AA;
XX
XX Query Match 100.0%; Score 31; DB 9; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 CGPC 5
XX DB 2 CGPC 5
XX
XX RESULT 38
XX ID AAR50846 standard; peptide; 10 AA.
XX AC AAR50846;

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XX XX
XX DT 25-MAR-2003 (revised)
XX DT 27-SEP-1994 (first entry)
XX DE Cyclic peptide inhibitor of selectins and integrins.
XX KM Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;
XX KM inflammation; coagulation; ischemia; reperfusion injury;
XX KM bacterial sepsis; tumour metastasis;
XX KM disseminated intravascular coagulation; rheumatoid arthritis;
XX KM adult respiratory distress syndrome; atherosclerosis; treatment;
XX KM prevention; detection; tumour; leucocyte; imaging.
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue."
XX FT Misc-difference 2 /note= "D-form residue."
XX FT Disulfide-bond 3 . 6
XX FT Misc-difference 3 /note= "D-form residue."
XX FT Modified-site 5 /label= Other.
XX FT FT /note= "3,4-dehydro-D-Pro."
XX FT Misc-difference 6 /note= "D-form residue."
XX FT Misc-difference 7 /note= "D-form residue."
XX FT Misc-difference 8 /note= "D-form residue."
XX FT Misc-difference 9 /note= "D-form residue."
XX FT FT /note= "D-form residue."
XX FT Misc-difference 10 /note= "D-form residue."
XX PN WO9405310-A1.
XX PD 17-MAR-1994.
XX PF 08-SEP-1993; 93WO-US008504.
XX PR 08-SEP-1992; 92US-00941653.
XX PA (CENZ ) CENTOCOR INC.
XX PI Heavner GA;
XX DR WPI; 1994-100848/12.
XX PT New cyclic peptide(s) inhibiting selectins and integrins - prevent
XX PT cellular adhesion in treatment of inflammation, perfusion, injury,
XX PT metastasis, etc. also for diagnosis.
XX PS Claim 2; Page 25; 175pp; English.
XX
XX CC The peptide modifies the binding of P-, E- and L-selectin and of
XX CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It
XX CC inhibits cellular adhesion. It can be used to treat or prevent
XX CC inflammation, coagulation, ischemia, reperfusion injury, bacterial
XX CC sepsis, disseminated intravascular coagulation, adult respiratory
XX CC distress syndrome, tumour metastasis, rheumatoid arthritis and
XX CC atherosclerosis. When labelled it can be used to detect defective
XX CC selectin (or integrin) binding ligands or high (localised) concentrations
XX CC of selectin (or integrin) binding cells, especially leucocytes or tumour
XX CC cells. It can also be used for in vivo imaging. This is a specific
XX CC example of a degenerate sequence given in the specification. (Updated on
XX CC 25-MAR-2003 to correct PN field.)
XX SQ Sequence 10 AA;
XX
XX Query Match 100.0%; Score 31; DB 2; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
| | | |
DB 3 CGPC 6

RESULT 39

AAR50868
ID AAR50868 standard; peptide; 10 AA.

AC AAR50868;

XX 25-MAR-2003 (revised)

DT 27-SEP-1994 (first entry)

XX Cyclic peptide inhibitor of selectins and integrins.

XX Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;

KM inflammation; coagulation; ischaemia; reperfusion injury;

KM bacterial sepsis; tumour metastasis;

KM disseminated intravascular coagulation; rheumatoid arthritis;

KW adult respiratory distress syndrome; atherosclerosis; treatment;

XX prevention; detection; tumour; leucocyte; imaging.

OS Synthetic.

XX Key

FT Misc-difference 1 Location/Qualifiers

FT Misc-difference 2 /note= "D-form residue."

FT Disulfide-bond 3 .6 /note= "D-form residue."

FT Misc-difference 3 /note= "D-form residue."

FT Modified-site 5 /label= Other.

FT Misc-difference 6 /note= "D-thio-proline."

FT Misc-difference 7 /note= "D-form residue."

FT Misc-difference 8 /note= "D-form residue."

FT Misc-difference 9 /note= "D-form residue."

FT Misc-difference 10 /note= "D-form residue."

XX WO9405310-A1.

XX PD 17-MAR-1994.

XX PF 08-SEP-1993; 93WO-US008504.

XX PR 08-SEP-1992; 92US-00941653.

XX PA (CENZ) CENTOCOR INC.

XX PI Heavner GA;

XX WPI; 1994-100848/12.

XX New cyclic peptide(s) inhibiting selections and integrins - prevent

XX cellular adhesion in treatment of inflammation, pertusion, injury,

XX metaabasis, etc. also for diagnosis.

XX Claim 2; Page 26; 175pp; English.

CC The peptide modifies the binding of P-, E- and L-selectin and of

CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It

CC inhibits cellular adhesion. It can be used to treat or prevent

CC inflammation, coagulation, ischaemia, reperfusion injury, bacterial
CC sepsis, disseminated intravascular coagulation, adult respiratory
CC distress syndrome, tumour metastasis, rheumatoid arthritis and
CC atherosclerosis. When labelled it can be used to detect defective
CC selectin (or integrin) binding ligands or high (localised) concentrations
CC of selectin (or integrin) binding cells, especially leucocytes or tumour
CC cells. It can also be used for in vivo imaging. This is a specific
CC example of a degenerate sequence given in the specification. (Updated on
CC 25-MAR-2003 to correct PN field.)

XX SQ Sequence 10 AA;

XX Query Match 100.0%; Score 31; DB 2; Length 10;

XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 3 CGPC 6

XX RESULT 40

XX AAR50834

XX ID AAR50834 standard; peptide; 10 AA.

XX AC AAR50834;

XX 25-MAR-2003 (revised)

DT 27-SEP-1994 (first entry)

XX Cyclic peptide inhibitor of selectins and integrins.

XX Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;

KM inflammation; coagulation; ischaemia; reperfusion injury;

KM bacterial sepsis; tumour metastasis;

KM disseminated intravascular coagulation; rheumatoid arthritis;

KW adult respiratory distress syndrome; atherosclerosis; treatment;

KW prevention; detection; tumour; leucocyte; imaging.

XX Synthetic.

XX Key

FT Misc-difference 1 Location/Qualifiers

FT Misc-difference 2 /note= "D-form residue."

FT Disulfide-bond 3 .6 /note= "D-form residue."

FT Misc-difference 3 /note= "D-form residue."

FT Misc-difference 6 /note= "D-form residue."

FT Misc-difference 7 /note= "D-form residue."

FT Misc-difference 8 /note= "D-form residue."

FT Misc-difference 9 /note= "D-form residue."

FT Misc-difference 10 /note= "D-form residue."

XX WO9405310-A1.

XX PD 17-MAR-1994.

XX PF 08-SEP-1993; 93WO-US008504.

XX PR 08-SEP-1992; 92US-00941653.

XX PA (CENZ) CENTOCOR INC.

XX PI Heavner GA;

XX WPI; 1994-100848/12.

XX New cyclic peptide(s) inhibiting selections and integrins - prevent
 PT cellular adhesion in treatment of inflammation, perfusion, injury,
 PT metastasis, etc. also for diagnosis.
 XX
 PS Claim 2; Page 24; 175pp; English.
 XX
 CC The peptide modifies the binding of P-, E- and L-selectin and of
 CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It
 CC inhibits cellular adhesion. It can be used to treat or prevent
 CC inflammation, coagulation, ischaemia, reperfusion injury, bacterial
 CC sepsis, disseminated intravascular coagulation, adult respiratory
 CC distress syndrome, tumour metastasis, rheumatoid arthritis and
 CC atherosclerosis. When labelled it can be used to detect defective
 CC selectin (or integrin) binding ligands or high (localised) concentrations
 CC of selectin (or integrin) binding cells, especially leucocytes or tumour
 CC cells. It can also be used for in vivo imaging. This is a specific
 CC example of a degenerate sequence given in the specification. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 AA;
 SO
 Query Match 100.0%; Score 31; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 AC AAR50895;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1994 (first entry)
 XX
 DE Cyclic peptide inhibitor of selectins and integrins.
 XX
 KW Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;
 KW inflammation; coagulation; ischaemia; reperfusion injury;
 KW bacterial sepsis; tumour metastasis;
 KW disseminated intravascular coagulation; rheumatoid arthritis;
 KW adult respiratory distress syndrome; atherosclerosis; treatment;
 KW prevention; detection; tumour; leucocyte; imaging.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue."
 FT Misc-difference 2 /note= "D-form residue."
 FT Disulfide-bond 3 .6
 FT Misc-difference 3 /note= "D-form residue."
 FT Misc-difference 6 /note= "D-form residue."
 FT Misc-difference 7 /note= "D-form residue."
 FT Misc-difference 8 /note= "D-form residue."
 FT Misc-difference 9 /note= "D-form residue."
 FT Misc-difference 10 /note= "D-form residue."
 XX
 PN WO9405310-A1.
 XX
 PD 17-MAR-1994.

XX
 PF 08-SEP-1993; 93WO-US008504.
 XX
 PR 08-SEP-1992; 92US-00941653.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Hevner GA;
 XX
 DR WPI; 1994-100848/12.
 XX
 PT New cyclic peptide(s) inhibiting selections and integrins - prevent
 PT cellular adhesion in treatment of inflammation, perfusion, injury,
 PT metastasis, etc. also for diagnosis.
 XX
 PS Claim 2; Page 28; 175pp; English.
 XX
 CC The peptide modifies the binding of P-, E- and L-selectin and of
 CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It
 CC inhibits cellular adhesion. It can be used to treat or prevent
 CC inflammation, coagulation, ischaemia, reperfusion injury, bacterial
 CC sepsis, disseminated intravascular coagulation, adult respiratory
 CC distress syndrome, tumour metastasis, rheumatoid arthritis and
 CC atherosclerosis. When labelled it can be used to detect defective
 CC selectin (or integrin) binding ligands or high (localised) concentrations
 CC of selectin (or integrin) binding cells, especially leucocytes or tumour
 CC cells. It can also be used for in vivo imaging. This is a specific
 CC example of a degenerate sequence given in the specification. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 AA;
 SO
 Query Match 100.0%; Score 31; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 AC AAR50830;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1994 (first entry)
 XX
 DE Cyclic peptide inhibitor of selectins and integrins.
 XX
 KW Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;
 KW inflammation; coagulation; ischaemia; reperfusion injury;
 KW bacterial sepsis; tumour metastasis;
 KW disseminated intravascular coagulation; rheumatoid arthritis;
 KW adult respiratory distress syndrome; atherosclerosis; treatment;
 KW prevention; detection; tumour; leucocyte; imaging.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue."
 FT Misc-difference 2 /note= "D-form residue."
 FT Disulfide-bond 3 .6
 FT Misc-difference 3 /note= "D-form residue."
 FT Misc-difference 5 /note= "D-form residue."
 FT Misc-difference 6 /note= "D-form residue."
 FT

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PT Misc-difference 7 /note= "D-form residue."
PT Misc-difference 8 /note= "D-form residue."
PT Misc-difference 9 /note= "D-form residue."
PT Misc-difference 10 /note= "D-form residue."
PT Misc-difference 10 /note= "D-form residue."
XX WO9405310-A1.
XX 17-MAR-1994.
XX 08-SEP-1993; 93WO-US008504.
XX 08-SEP-1992; 92US-00941653.
XX (CENZ ) CENTOCOR INC.
XX Heavner GA;
XX WPI; 1994-100848/12.
XX New cyclic peptide(s) inhibiting selections and integrins - prevent
PT cellular adhesion in treatment of inflammation, pertusion, injury,
PT metastasis, etc. also for diagnosis.
XX Claim 2; Page 24; 175pp; English.
XX The peptide modifies the binding of P-, E- and I-selectin and of
CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It
CC inhibits cellular adhesion. It can be used to treat or prevent
CC inflammation, coagulation, ischaemia, reperfusion injury, bacterial
CC sepsis, disseminated intravascular coagulation, adult respiratory
CC distress syndrome, tumour metastasis, rheumatoid arthritis and
CC atherosclerosis. When labeled it can be used to detect defective
CC selectin (or integrin) binding ligands or high (localised) concentrations
CC of selectin (or integrin) binding cells, especially leucocytes or tumour
CC cells. It can also be used for in vivo imaging. This is a specific
CC example of a degenerate sequence given in the specification. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 31; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 3 CGPC 6
RESULT 43
AAG94724
ID AAG94724 standard; peptide; 10 AA.
XX AAG94724;
AC
XX 18-SEP-2001 (first entry)
DT
XX Human complementary peptide, SEQ ID NO: 918.
DB Human; complementary peptide; ligand; drug discovery; drug design.
XX Homo sapiens.
OS
XX WO200142277-A2.
XX 14-JUN-2001.
XX 13-DEC-2000; 2000WO-GB004776.
XX

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PR 13-DEC-1999; 99GB-00029464.
XX (PROT-) PROTEOM LTD.
XX Roberts GW, Heal JR;
XX WPI; 2001-408419/43.
XX A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.
XX Example 4; Page 171; 646pp; English.
XX The invention relates to a set of complementary peptide ligands generated
CC from the human genome. The complementary peptides interact with their
CC relevant target proteins encoded in the human genome. They can be used as
CC reagents in drug discovery and as lead ligands to facilitate drug design
CC and development. The present sequence is a complementary peptide provided
CC in the specification
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 31; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 6 CGPC 9
RESULT 44
AAG94776
ID AAG94776 standard; peptide; 10 AA.
XX AAG94776;
AC
XX 18-SEP-2001 (first entry)
DT
XX Human complementary peptide, SEQ ID NO: 970.
DE Human complementary peptide, ligand; drug discovery; drug design.
XX Human; complementary peptide; ligand; drug discovery; drug design.
XX Homo sapiens.
OS
XX WO200142277-A2.
XX 14-JUN-2001.
XX 13-DEC-2000; 2000WO-GB004776.
XX 13-DEC-1999; 99GB-00029464.
XX (PROT-) PROTEOM LTD.
XX Roberts GW, Heal JR;
XX WPI; 2001-408419/43.
XX A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.
XX Example 4; Page 178; 646pp; English.
XX The invention relates to a set of complementary peptide ligands generated
CC from the human genome. The complementary peptides interact with their
CC relevant target proteins encoded in the human genome. They can be used as
CC reagents in drug discovery and as lead ligands to facilitate drug design
CC and development. The present sequence is a complementary peptide provided
CC in the specification
XX

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CC in the specification
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 31; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 6 CGPC 9

RESULT 45
AAG86916
ID AAG86916 standard; peptide; 10 AA.

AC AAG86916;

DT 11-SEP-2001 (first entry)

DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1865.

KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.

OS Saccharomyces cerevisiae.

PN WO200142276-A1.

PD 14-JUN-2001.

PF 13-DEC-2000; 2000WO-GB004773.

PR 13-DEC-1999; 99GB-00029471.

PA (PROT-) PROTEOM LTD.

PI Roberts GW, Heal JR;

DR WPI; 2001-367863/38.

PT Identifying complementary peptides by analysis of protein and nucleotide
sequence databases, useful in drug design.

PS Example 3; Page 287; 488pp; English.

XX The invention relates to the identification of complementary peptides by
CC analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents and
CC drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae

SQ Sequence 10 AA;

Query Match 100.0%; Score 31; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 3 CGPC 6

RESULT 46
AAG86918
ID AAG86918 standard; peptide; 10 AA.
AC AAG86918;
XX

DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1867.

KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.

OS Saccharomyces cerevisiae.

PN WO200142276-A1.

PD 14-JUN-2001.

PF 13-DEC-2000; 2000WO-GB004773.

PR 13-DEC-1999; 99GB-00029471.

PA (PROT-) PROTEOM LTD.

PI Roberts GW, Heal JR;

DR WPI; 2001-367863/38.

PT Identifying complementary peptides by analysis of protein and nucleotide
sequence databases, useful in drug design.

PS Example 3; Page 287; 488pp; English.

XX The invention relates to the identification of complementary peptides by
CC analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents and
CC drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae

SQ Sequence 10 AA;

Query Match 100.0%; Score 31; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 47
ADV60196
ID ADV60196 standard; peptide; 10 AA.

AC ADV60196;

DT 10-MAR-2005 (first entry)

DE VEGF peptide SEQ ID NO 7701.

KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.

OS Unidentified.

PN WO2004111636-A2.

PD 23-DEC-2004.

PF 17-JUN-2004; 2004WO-EP051158.

PR 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

PA (VIBV-) VIB VZM.

PA (UYGE-) UNIV GENT.
 XX
 PI Kas K, Vandekerckhove J, Krols L;
 XX
 DR WPI; 2005-057893/06.
 XX
 PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 XX
 PS Example; SEQ ID NO 7701; 265pp; English.
 XX
 CC The invention relates to a method of identifying a peptide combo which
 CC corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a VEGF peptide combo.
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 100.0%; Score 31; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 4 CGPC 7
 XX
 RESULT 48
 AAW45003
 ID AAW45003 standard; peptide; 12 AA.
 XX
 AC AAW45003;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Immunomodulatory peptide D7233.
 XX
 KM Immunomodulator; immunosuppressant; immunostimulator; treatment;
 KM transplant rejection; autoimmune disease; cancer; infection.
 XX
 OS Synthetic.
 XX
 PN WO9739023-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 04-APR-1997; 97WO-SE000574.
 XX
 PR 12-APR-1996; 96SE-00001422.
 PR 23-SEP-1996; 96SE-00003469.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Bertrand H, Eriksson T, Lindvall M, Saernstrand B;

XX
 DR WPI; 1997-526397/48.
 XX
 PT Nucleic acids encoding cysteine- or methionine-containing peptide(s)
 PT which have immunostimulatory or immunosuppressive activity - can be used
 PT to treat, e.g. cancers, infection, auto-immune disease or transplant
 PT rejection.
 XX
 PS Claim 12; Page 155; 183pp; English.
 XX
 CC The present peptide is an immunosuppressant or immunostimulator. An
 CC immunosuppressant can be used to treat transplant rejection or autoimmune
 CC disease, e.g. rheumatoid arthritis, systemic lupus erythematosus,
 CC Sjogren's syndrome, scleroderma, mixed connective tissue disease,
 CC dermatomyositis, polymyositis, Reiter's syndrome, Behcet's disease, type
 CC I diabetes, Hashimoto's thyroiditis, Graves' disease, multiple sclerosis,
 CC myasthenia gravis, encephalomyelitis, pemphigus vulgaris, vegetans or
 CC folliculitis, Senechal-Usher syndrome or Brazilian pemphigus. An
 CC immunostimulator can be used to treat conditions such as cancer or
 CC infection.
 XX
 SQ Sequence 12 AA;
 XX
 Query Match 100.0%; Score 31; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 2 CGPC 5
 XX
 RESULT 49
 AAY09429
 ID AAY09429 standard; peptide; 12 AA.
 XX
 AC AAY09429;
 XX
 DT 14-JUL-1999 (first entry)
 XX
 DE Immunoactive peptide SEQ ID NO:54.
 XX
 KM Immunoactive; immunomodulation; immunosuppression; immunostimulation;
 KM immune response; immunoreactive; autoimmune disease.
 XX
 OS Synthetic.
 XX
 PN WO9919347-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 06-OCT-1998; 98WO-SE001801.
 XX
 PR 10-OCT-1997; 97US-00949024.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Bertrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX
 DR WPI; 1999-287953/24.
 XX
 PT Synthetic genes encoding immunoreactive peptides containing cysteine or
 PT methionine.
 XX
 PS Claim 32; Page 52; 104pp; English.
 XX
 CC The present invention describes nucleic acid molecules comprising a
 CC coding sequence encoding an immunoreactive peptide and further encoding a
 CC protein targeting sequence. The nucleic acid is administered to a patient
 CC so that its expression product, an immunoreactive peptide, modulates an
 CC immune response in a patient. The nucleic acid can also be used to treat
 CC cancer, either after surgery to remove a portion of the cancer or after
 CC ionizing radiation. A cytokine is also administered in conjunction with

CC the nucleic acid. Cells containing the nucleic acid molecule can also be
CC used for treatment. The immunoreactive peptide is immunosuppressive and can
CC be used in patients with autoimmune disease. The present sequence
CC represents a specifically claimed immunoreactive peptide from the present
CC invention
XX

XX Sequence 12 AA;

Query Match 100.0%; Score 31; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 2 CGPC 5

RESULT 50

ADV60191

ID ADV60191 standard; peptide; 12 AA.

XX ADV60191;

XX 10-MAR-2005 (first entry)

XX VEGF peptide SEQ ID NO 7696.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;

XX food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.

XX Unidentified.

XX MO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004MO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

XX 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

XX (UYGE-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.

XX Example; SEQ ID NO 7696; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital abnormality, for quantitating immune levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway

CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a VEGF peptide combo.
XX

XX Sequence 12 AA;

Query Match 100.0%; Score 31; DB 9; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 6 CGPC 9

RESULT 51

ADV60192

ID ADV60192 standard; peptide; 13 AA.

XX ADV60192;

XX 10-MAR-2005 (first entry)

XX VEGF peptide SEQ ID NO 7697.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;

XX food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.

XX Unidentified.

XX MO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004MO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

XX 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

XX (UYGE-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.

XX Example; SEQ ID NO 7697; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital abnormality, for quantitating immune levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present

CC sequence represents a peptide from a VEGF peptide combo.
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 31; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 6 CGPC 9

RESULT 52
ADV60193
ID ADV60193 standard; peptide; 14 AA.
XX
AC ADV60193;
XX
DT 10-MAR-2005 (first entry)
XX
DE VEGF peptide SEQ ID NO 7698.
XX
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003RP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
PA (UYGB-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 7698; 265pp; English.

CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a VEGF peptide combo.

SQ Sequence 14 AA;
Query Match 100.0%; Score 31; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 8 CGPC 11

RESULT 53
ADM28625
ID ADM28625 standard; peptide; 14 AA.
XX
AC ADM28625;
XX
DT 07-APR-2005 (first entry)
XX
DE VEGF165 epitope, SEQ ID 2.
XX
KW Cytostatic; Antineumatic; Antidiabetic; Cardiant; Nootropic;
KW Neuroprotective; antibody identification; antibody production;
KW antibody therapy; cancer; vascular endothelial cell growth factor; VEGF.
XX
OS Homo sapiens.
XX
PN US2005009110-A1.
XX
PD 13-JAN-2005.
XX
PF 08-JUL-2003; 2003US-00615343.
XX
PR 08-JUL-2003; 2003US-00615343.
XX
PA (CHAN/) CHANG X.
XX
PI Chang X;
XX
DR WPI; 2005-099971/11.
DR N-PSDB; ADM28624.
XX
PT Identifying antibody to protein, involves contacting solid surface coated
PT with antibodies with fusion protein having portion of target protein and
PT carrier protein and conducting assay to determine presence of carrier
PT protein.
XX
PS Claim 32; SEQ ID NO 2; 55pp; English.

CC The present invention relates to a method for identifying antibodies for
CC target proteins. The method comprises: (1) contacting an antibody-coated
CC solid surface with a fusion protein, where the antibodies bind
CC specifically to the fusion protein and the fusion protein comprises at
CC least a portion of the target protein linked to a carrier protein, and
CC (1) conducting an assay to determine the presence of the carrier
CC protein, where the presence of a carrier protein indicates the presence
CC of an antibody to the target protein. The target protein may be an
CC isoform of a protein that is associated with disease, e.g. Vascular
CC Endothelial Growth Factor (VEGF) isoforms VEGF165 (ADM28644) and VEGF121
CC (ADM28645), which are associated with cancer; Prostate Specific Antigen
CC (PSA; ADM28642), which is associated with prostate cancer and Her2
CC (ADM28640), which is associated with breast cancer. Also claimed are
CC methods for: generating (M2) monoclonal antibodies, where each monoclonal
CC antibody binds to a target protein, specifically at least one monoclonal
CC antibody that binds to an isoform of a protein that is associated with a
CC disease; isolating (M3) an antibody binding specifically to a target
CC protein from several antibodies that are associated with the nucleic
CC acid(s) encoding the antibody; determining (M4) the presence of an
CC antigen in a sample; and identifying (M5) an epitope on a target protein.
CC The antibodies identified by (M1) are useful for treating or preventing
CC diseases in which the presence of an antibody to a particular molecule is
CC beneficial. The antibodies are useful for targeting agents such as toxins
CC to particular cells e.g., cancer cell. (M1) is useful for identifying

CC epitopes on target protein which are used for preparing DNA vaccines
CC having nucleotide sequences encoding epitope of a disease associated
CC protein isoforms used for prevention or treatment of diseases such as
CC cancer, rheumatoid arthritis, diabetes, acute myeloid leukemia (AML),
CC chronic lymphocytic leukemia (CLL), ovarian cancer, prostate cancer,
CC cardiovascular disease, Alzheimer's disease, etc. The antibodies are
CC useful for detecting antigens e.g. in specific cells, tissue or bodily
CC fluids such as serum, or for affinity purification of antigen from
CC recombinant cell culture or natural sources. The present sequence is a
CC VEGF isoform epitope, which can be used to produce a VEGF isoform fusion
CC protein.
CC
XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 31; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 9 CGPC 12

RESULT 54

ADV54876
ID ADV54876 standard; peptide; 17 AA.

XX ADV54876;

XX 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 2373.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCK.

XX Unidentified.

XX MO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

PA (UYGE-) UNITV GENT.

PI Kas K, Vandekerckhove J, Krois L;

DR WPI, 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX

PS Example; SEQ ID NO 2373; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels

CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
CC
XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 31; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 8 CGPC 11

RESULT 55

ADV54992
ID ADV54992 standard; peptide; 17 AA.

XX ADV54992;

XX 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 2489.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCK.

XX Unidentified.

XX MO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

PA (UYGE-) UNITV GENT.

PI Kas K, Vandekerckhove J, Krois L;

DR WPI, 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX

PS Example; SEQ ID NO 2489; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases

CC or neurological diseases, as biomarkers preclinical drug development.
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 31; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 8 CGPC 11
XX
RESULT 56
ADV55097
ID ADV55097 standard; peptide; 17 AA.
XX
AC ADV55097;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 2594.
XX
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZM.
PA (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 2594; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,

CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 31; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 8 CGPC 11
XX
RESULT 57
AAE23038
ID AAE23038 standard; peptide; 19 AA.
XX
AC AAE23038;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human thiorodoxin, 47916 peptide.
XX
KW Human; thiorodoxin; 22108; 47916; haematopoietic disorder; leukaemia;
KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
KW cytotoxic; carcinoma; cardiac; neuroprotective; antiinflammatory;
KW gene therapy; nootropic.
XX
OS Homo sapiens.
XX
PN WO200226803-A2.
XX
PD 04-APR-2002.
XX
PF 25-SEP-2001; 2001WO-US023967.
PF 25-SEP-2001; 2001WO-US023967.
XX
PR 25-SEP-2000; 2000US-0235049P.
XX
PA (MILL-) MILLINUTUM PHARM INC.
XX
PI Bandaru R, Kapeller-Libermann R;
XX
DR WPI; 2002-416475/44.
XX
PT New human thiorodoxin nucleic acid and polypeptide molecules, designated
PT 22108 and 47916, useful for diagnosing, preventing or treating cancer
PT (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain
PT disorders.
XX
PS Disclosure; Page 11; 124pp; English.
XX
CC The invention relates to human thiorodoxin nucleic acid and polypeptide
CC molecules, designated 22108 and 47916. The compound that modulates the
CC activity or expression of 22108 and 47916 nucleic acid is useful for
CC treating or preventing a disorder characterized by aberrant activity of
CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the
CC lung, breast, thyroid, head neck, prostate or genito-urinary tract),
CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
CC diseases). The thiorodoxin DNA is also useful in gene therapy. The

CC present sequence is human thioredoxin, 47916 peptide
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 31; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 CGPC 5
DB 9 CGPC 12
RESULT 58
ADV60188
ID ADV60188 standard; peptide; 20 AA.
XX
AC ADV60188;
XX
DT 10-MAR-2005 (first entry)
XX
DE VEGF peptide SEQ ID NO 7693.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX
PT 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZM.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 7693; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a VEGF peptide combo.
XX

SQ Sequence 20 AA;
Query Match 100.0%; Score 31; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 CGPC 5
DB 14 CGPC 17
RESULT 59
ADV60189
ID ADV60189 standard; peptide; 21 AA.
XX
AC ADV60189;
XX
DT 10-MAR-2005 (first entry)
XX
DE VEGF peptide SEQ ID NO 7694.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX
PT 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZM.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 7694; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a VEGF peptide combo.
XX
SQ Sequence 21 AA;
XX


```
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
SQ Sequence 24 AA:
Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 15 CGPC 18

RESULT 62
ADV56216
ID ADV56216 standard; peptide; 24 AA.
XX
AC ADV56216;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 3718.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX
PT 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZM.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX
PS Example; SEQ ID NO 3718; 265dp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide
```

```
CC combo.
XX
SQ Sequence 24 AA:
Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 15 CGPC 18

RESULT 63
ADV53880
ID ADV53880 standard; peptide; 24 AA.
XX
AC ADV53880;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 1377.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX
PT 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZM.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX
PS Example; SEQ ID NO 1377; 265dp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide
```

```
XX SQ Sequence 24 AA;
Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 15 CGPC 18

RESULT 64
ADV54929
ID ADV54929 standard; peptide; 24 AA.
XX AC ADV54929;
XX DT 10-MAR-2005 (first entry)
XX DE G protein coupled receptor peptide SEQ ID NO 2426.
XX KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX OS Unidentified.
XX PN MO2004111636-A2.
XX PD 23-DEC-2004.
XX PF 17-JUN-2004; 2004MO-EP051158.
XX PR 17-JUN-2003; 2003EP-00101775.
XX PR 17-JUN-2003; 2003US-0479061P.
XX PA (VIBV-) VIB VZW.
XX PA (UYGE-) UNIV GENT.
XX PI Kas K, Vandekerckhove J, Krols L;
XX DR WPI; 2005-057893/06.
XX PT Identifying a peptide combo which corresponds with a family of proteins,
XX PT useful for diagnosing a variety of diseases, drug development or in
XX PT agriculture, comprises generating peptides by applying a digest on the
XX PT family of protein.
XX PS Example; SEQ ID NO 2426; 265pp; English.
XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide
XX combo.
```

```
SQ Sequence 24 AA;
Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 15 CGPC 18

RESULT 65
ADV55148
ID ADV55148 standard; peptide; 24 AA.
XX AC ADV55148;
XX DT 10-MAR-2005 (first entry)
XX DE G protein coupled receptor peptide SEQ ID NO 2645.
XX KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX OS Unidentified.
XX PN MO2004111636-A2.
XX PD 23-DEC-2004.
XX PF 17-JUN-2004; 2004MO-EP051158.
XX PR 17-JUN-2003; 2003EP-00101775.
XX PR 17-JUN-2003; 2003US-0479061P.
XX PA (VIBV-) VIB VZW.
XX PA (UYGE-) UNIV GENT.
XX PI Kas K, Vandekerckhove J, Krols L;
XX DR WPI; 2005-057893/06.
XX PT Identifying a peptide combo which corresponds with a family of proteins,
XX PT useful for diagnosing a variety of diseases, drug development or in
XX PT agriculture, comprises generating peptides by applying a digest on the
XX PT family of protein.
XX PS Example; SEQ ID NO 2645; 265pp; English.
XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide
XX combo.
```

Sequence 24 AA;

Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
15 CGPC 18

RESULT 66
AAB38027 standard; peptide; 25 AA.

AC AAB38027;
DT 31-JAN-2001 (first entry)

DE Fragment of human secreted protein encoded by gene 7 clone HMTLH15.

KM Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KM antiatherogenic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KM vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KM cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KM neurological disease; infection; human; secreted protein.

OS Homo sapiens.

PN MO200055371-A1.

PD 21-SEP-2000.

PP 16-MAR-2000; 2000MO-US006783.

PR 18-MAR-1999; 99US-0125055P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruden SM, Ni J, Ebner R, Rosen CA, Shi Y, Birse C, Florence K;
PI Komatsoulis G, Lafleur DM, Moore PA, Olsen HS, Young PE;

DR WPI; 2000-594448/56.

PT New nucleic acid molecules encoding 27 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.

PS Disclosure; Page 20; 453bp; English.

CC Sequences AAB37984-B38019 represent the amino acid sequences of 27 human
CC secreted proteins encoded by the genes AAC69084-C69119. The genes and
CC proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)
CC immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischemias; (d) wound healing
CC (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections

SQ Sequence 25 AA;

Query Match 100.0%; Score 31; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 19 CGPC 22

RESULT 67
ADV55146
ADV55146 standard; peptide; 25 AA.

AC ADV55146;

DT 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 2643.

KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KM food; feedstuff; cosmetics; agriculture; animal breeding; GPCK.

OS Unidentified.

PN MO2004111636-AZ.

PD 23-DEC-2004.

PP 17-JUN-2004; 2004MO-EP051158.

PR 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

PA (VIBV-) VIB VZM.
PA (UYGE-) UNIV GENT.

PI Kas K, Vandekerckhove J, Krole L;

DR WPI; 2005-057893/06.

PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.

PS Example; SEQ ID NO 2643; 265bp; English.

CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.

SQ Sequence 25 AA;

Query Match 100.0%; Score 31; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 8 CGPC 11

RESULT 68

ADV55040 ID ADV55040 standard; peptide; 25 AA.

ADV55040;

10-MAR-2005 (first entry)

G protein coupled receptor peptide SEQ ID NO 2537.

diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression; food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

Unidentified.

WO2004111636-A2.

23-DEC-2004.

17-JUN-2004; 2004WO-EP051158.

17-JUN-2003; 2003EP-00101775.

17-JUN-2003; 2003US-0479061P.

(VIBV-) VIB VZW.

(UYGE-) UNIV GENT.

Kas K, Vandekerckhove J, Krols L;

WPI; 2005-057893/06.

Identifying a peptide combo which corresponds with a family of proteins, useful for diagnosing a variety of diseases, drug development or in agriculture, comprises generating peptides by applying a digest on the family of protein.

Example; SEQ ID NO 2537; 265pp; English.

The invention relates to a method of identifying a peptide combo which corresponds with a family of proteins where each of the members of the peptide combo is derived from a unique protein from the family. The peptide combo is useful for quantifying specific known splice variants of one or more particular proteins in a sample, for diagnosing complex genetic diseases such as cancer, obesity, diabetes, asthma and inflammation, neuropsychiatric disorders such as depression, for quantifying one to several hundreds of protein disease markers simultaneously leading to a more accurate diagnostic sub-classification, for determining the extent of protein modification in a particular sample of proteins, for tissue-typing analysis, for prenatal testing to detect the presence of a congenital disease or for quantitating protein levels diagnostic of a chromosomal abnormality, for diagnosing immune diseases or neurological diseases, as biomarkers preclinical drug development, development of improved animal models, biomarkers related with toxicology, clinical drug development, guidance marketed drugs, prognostic or diagnostic disease markers, drug target validation and selection, monitoring protein splicing, drug lead profiling, pathway analysis, answering basic disease biology questions, and in the fields of food and feed, cosmetics, agriculture and animal breeding. The present sequence represents a peptide from a G-protein coupled receptor peptide combo.

Sequence 25 AA;

Query Match 100.0%; Score 31; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CGPC 5

CGPC 11

RESULT 69

ADV54928 ID ADV54928 standard; peptide; 25 AA.

ADV54928;

10-MAR-2005 (first entry)

G protein coupled receptor peptide SEQ ID NO 2425.

diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression; food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

Unidentified.

WO2004111636-A2.

23-DEC-2004.

17-JUN-2004; 2004WO-EP051158.

17-JUN-2003; 2003EP-00101775.

17-JUN-2003; 2003US-0479061P.

(VIBV-) VIB VZW.

(UYGE-) UNIV GENT.

Kas K, Vandekerckhove J, Krols L;

WPI; 2005-057893/06.

Identifying a peptide combo which corresponds with a family of proteins, useful for diagnosing a variety of diseases, drug development or in agriculture, comprises generating peptides by applying a digest on the family of protein.

Example; SEQ ID NO 2425; 265pp; English.

The invention relates to a method of identifying a peptide combo which corresponds with a family of proteins where each of the members of the peptide combo is derived from a unique protein from the family. The peptide combo is useful for quantifying specific known splice variants of one or more particular proteins in a sample, for diagnosing complex genetic diseases such as cancer, obesity, diabetes, asthma and inflammation, neuropsychiatric disorders such as depression, for quantifying one to several hundreds of protein disease markers simultaneously leading to a more accurate diagnostic sub-classification, for determining the extent of protein modification in a particular sample of proteins, for tissue-typing analysis, for prenatal testing to detect the presence of a congenital disease or for quantitating protein levels diagnostic of a chromosomal abnormality, for diagnosing immune diseases or neurological diseases, as biomarkers preclinical drug development, development of improved animal models, biomarkers related with toxicology, clinical drug development, guidance marketed drugs, prognostic or diagnostic disease markers, drug target validation and selection, monitoring protein splicing, drug lead profiling, pathway analysis, answering basic disease biology questions, and in the fields of food and feed, cosmetics, agriculture and animal breeding. The present sequence represents a peptide from a G-protein coupled receptor peptide combo.

Sequence 25 AA;

Query Match 100.0%; Score 31; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CGPC 5

CGPC 11

RESULT 70
ADC89744

ID ADC89744 standard; peptide; 28 AA.

AC ADC89744;

DT 01-JAN-2004 (first entry)

DE Cyclic VEGF-165-derived peptide (residues 111-138), 3286.

KW Vascular endothelial growth factor; VEGF; VEGF-165 splice variant;
 KW neuropilin-1; NP-1; antagonist; competitive inhibitor; nerve growth;
 KW nerve repair; neurodegeneration; cancer; angiogenic condition;
 KW eye disease; rheumatoid arthritis; immunosuppressant; transplantation;
 KW antiangiogenic; neuroprotective; cytostatic; cerebroprotective;
 KW ophthalmological; antirheumatic; antineumatic; immunosuppressive;
 KW cyclic.

OS Synthetic.
 OS Unidentified.

Key Location/Qualifiers
 FT Disulfide-bond 7..25
 FT Disulfide-bond 10..27

PN WO2003082918-A1.

PD 09-OCT-2003.

PF 28-MAR-2003; 2003WO-GB001375.

PR 02-APR-2002; 2002GB-00007644.

PA (ARKT-) ARK THERAPEUTICS LTD.

PI Selwood D, Loefer M, Zachary I;

DR WPI; 2003-804028/75.

PT New cyclic peptide derived from vascular endothelial growth factor,
 PT useful for treating e.g. neurodegeneration and cancer, antagonizes
 PT neuropilin-1.

PS Disclosure; Fig 1; 21pp; English.

CC The invention relates to a cyclic VEGF (vascular endothelial growth
 CC factor) peptide (ADC89740) with NP-1 (neuropilin-1) antagonist activity.
 CC The peptide corresponds to residues 138-165 of the VEGF-165 splice
 CC variant, but contains 2 disulfide bonds. It acts as a competitive
 CC inhibitor of NP-1, which plays an important role in angiogenesis
 CC (including VEGF-mediated tumour angiogenesis), neurodegeneration
 CC (involving interaction with semaphorin 3) and in immunosuppression. NP-1
 CC is a non-tyrosine kinase receptor for the VEGF-165 splice variant.
 CC Additionally, VEGF is known to promote the survival of tumour cells that
 CC express NP-1, including some breast carcinoma cells. The cyclic VEGF
 CC peptide of the invention can be used to stimulate nerve growth and
 CC repair, to treat neurodegeneration, and for anti-cancer therapy. It can
 CC also be used for treating other angiogenic conditions such as eye
 CC diseases and rheumatoid arthritis, and as an immunosuppressant for use in
 CC transplantation. The present sequence represents a cyclic VEGF-165
 CC derived peptide which was used in a study of VEGF-165 binding to NP-1
 CC expressing cells. The present sequence had no inhibitory effect on the
 CC binding of VEGF-165 to NP-1, unlike the cyclic peptide of the invention
 CC (ADC89740).

SQ Sequence 28 AA;

Query Match 100.0%; Score 31; DB 7; Length 28;

Best Local Similarity 100.0%; Pred.No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 7 CGPC 10

Search completed: February 23, 2006, 00:36:51
 Job time : 179 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:38:49 / Search time 23.5 Seconds
(without alignments)
24.566 Million cell updates/sec

Title: US-10-660-118a-2
Perfect score: 31
Sequence: 1 XCGPCX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	31	100.0	35	1 NTSPRM	neurotoxin P2 - sc
2	31	100.0	35	2 A59356	neurotoxin Bmk 41-
3	31	100.0	55	2 S25774	testis-specific pr
4	31	100.0	56	1 WTRF	testis-specific pr
5	31	100.0	56	2 H81133	rubredoxin NMB0993
6	31	100.0	62	2 S15676	chorionic gonadotr
7	31	100.0	63	2 S25772	testis-specific pr
8	31	100.0	68	2 S25775	testis-specific pr
9	31	100.0	73	2 A60136	keratin, scale (cl
10	31	100.0	74	2 S25773	testis-specific pr
11	31	100.0	80	2 I65235	testicular luteini
12	31	100.0	88	2 B46264	chlorodoxin 2 - al
13	31	100.0	89	2 E84409	chlorodoxin [impor
14	31	100.0	98	1 KRGLBS	keratin, feather -
15	31	100.0	102	1 G64213	chlorodoxin - Myco
16	31	100.0	102	2 H86572	chlorodoxin [impor
17	31	100.0	102	2 S73896	chlorodoxin - Myco
18	31	100.0	102	2 B71503	probable chlorodox
19	31	100.0	102	2 D72052	chlorodoxin CP0088
20	31	100.0	102	2 C81660	chlorodoxin TC0826
21	31	100.0	103	1 TXBY2	chlorodoxin II - y
22	31	100.0	103	2 T39085	chlorodoxin II - f
23	31	100.0	103	2 A11228	chlorodoxin [impor
24	31	100.0	103	2 AC1582	chlorodoxin [impor
25	31	100.0	104	1 A28086	chlorodoxin - rabb
26	31	100.0	104	1 A28215	chlorodoxin - Rhod
27	31	100.0	104	1 B37192	chlorodoxin - Baci
28	31	100.0	104	1 TXBY1	chlorodoxin I - ye
29	31	100.0	104	2 S77780	chlorodoxin - Myco

30	31	100.0	104	2 H95206	chlorodoxin [impor
31	31	100.0	104	2 H98071	chlorodoxin-disulf
32	31	100.0	104	2 A59394	chlorodoxin - Clos
33	31	100.0	104	2 C46264	chlorodoxin 3 - al
34	31	100.0	104	2 B84037	chlorodoxin trxa l
35	31	100.0	104	2 B89885	chlorodoxin [impor
36	31	100.0	104	2 D66830	chlorodoxin [impor
37	31	100.0	104	2 C81432	chlorodoxin Cj0147
38	31	100.0	105	1 A30006	chlorodoxin - chic
39	31	100.0	105	1 A46264	chlorodoxin 1 - al
40	31	100.0	105	1 JH0568	chlorodoxin [valid
41	31	100.0	105	1 J60667	chlorodoxin - rhes
42	31	100.0	105	1 S04107	chlorodoxin - mous
43	31	100.0	105	1 S04352	chlorodoxin - rat
44	31	100.0	105	1 TXRX	chlorodoxin - cory
45	31	100.0	105	2 S76386	chlorodoxin M-1 -
46	31	100.0	105	2 B97700	chlorodoxin [impor
47	31	100.0	105	2 AG2042	chlorodoxin [impor
48	31	100.0	105	2 D97279	chlorodoxin [impor
49	31	100.0	106	1 A35135	chlorodoxin - Rhod
50	31	100.0	106	2 S33357	chlorodoxin - Stre
51	31	100.0	106	2 H64622	chlorodoxin - Heli
52	31	100.0	106	2 A49888	chlorodoxin - Peni
53	31	100.0	106	2 AG2579	chlorodoxin C-1 tr
54	31	100.0	107	1 A32956	chlorodoxin m - Sy
55	31	100.0	107	1 TXAI	chlorodoxin 1 - An
56	31	100.0	107	1 A26622	chlorodoxin - Chro
57	31	100.0	107	1 S31915	chlorodoxin - red
58	31	100.0	107	1 S47867	chlorodoxin-like p
59	31	100.0	107	2 S73146	chlorodoxin A - re
60	31	100.0	107	2 S46521	chlorodoxin - Porp
61	31	100.0	107	2 T33843	hypothetical prote
62	31	100.0	107	2 S46958	chlorodoxin A - Sy
63	31	100.0	107	2 T02814	chlorodoxin TRXp1
64	31	100.0	107	2 B53307	chlorodoxin - Stre
65	31	100.0	107	2 AD1813	chlorodoxin [impor
66	31	100.0	107	2 AH3504	chlorodoxin C-1 f1
67	31	100.0	107	2 B64047	chlorodoxin - Haem
68	31	100.0	108	2 G82991	chlorodoxin PA5240
69	31	100.0	108	2 B55124	chlorodoxin - Ch10
70	31	100.0	108	2 AD0471	chlorodoxin 1 [imp
71	31	100.0	108	2 AH2101	chlorodoxin [impor
72	31	100.0	108	2 D82338	chlorodoxin VC0306
73	31	100.0	109	1 A55124	chlorodoxin - Ch10
74	31	100.0	109	1 S35497	chlorodoxin - Salm
75	31	100.0	109	1 TXEC	chlorodoxin [valid
76	31	100.0	109	2 S27053	chlorodoxin - Emer
77	31	100.0	109	2 S77444	hypothetical prote
78	31	100.0	109	2 S46522	chlorodoxin A - Gr
79	31	100.0	109	2 AF0922	chlorodoxin [impor
80	31	100.0	110	2 T36576	chlorodoxin - Stre
81	31	100.0	110	2 T42061	chlorodoxin - Stre
82	31	100.0	110	2 AD2039	chlorodoxin [impor
83	31	100.0	110	2 A87688	chlorodoxin [impor
84	31	100.0	110	2 C81090	chlorodoxin NMB136
85	31	100.0	110	2 B81850	chlorodoxin I NMA1
86	31	100.0	111	1 A32233	chlorodoxin 2 [val
87	31	100.0	111	1 S57775	chlorodoxin h, cyt
88	31	100.0	114	1 JQ2242	chlorodoxin h - Ar
89	31	100.0	114	1 B64423	ychn protein homol
90	31	100.0	114	1 D75422	hypothetical prote
91	31	100.0	115	2 T29044	hypothetical prote
92	31	100.0	115	2 AF2098	chlorodoxin 2 [imp
93	31	100.0	116	2 T10739	chlorodoxin - comm
94	31	100.0	116	2 B70851	probable trxc prot
95	31	100.0	116	2 S09845	hypothetical prote
96	31	100.0	117	2 E70107	chlorodoxin (trxa)
97	31	100.0	118	2 S34812	chlorodoxin h2 - c
98	31	100.0	118	2 T10170	chlorodoxin - cast
99	31	100.0	118	2 PNO141	lutropin beta chai
100	31	100.0	118	2 PNO139	hypothetical prote
101	31	100.0	119	2 T18644	
102	31	100.0	119	2 T08271	probable chlorodox

103	31	100.0	119	2	T50867	176	31	100.0	194	2	T00482	probable thioredox
104	31	100.0	119	2	A61465	177	31	100.0	201	2	S16897	alanine-cRNA ligas
105	31	100.0	121	2	T93987	178	31	100.0	201	2	S16899	alanine-cRNA ligas
106	31	100.0	122	2	T04090	179	31	100.0	202	2	T50635	hypothetical prote
107	31	100.0	123	2	B70873	180	31	100.0	205	2	F71491	probable UDP-gluc
108	31	100.0	124	2	T13559	181	31	100.0	216	2	S72901	hypothetical prote
109	31	100.0	124	2	A83707	182	31	100.0	216	2	A70545	hypothetical prote
110	31	100.0	125	2	T50866	183	31	100.0	216	2	PT0375	natural killer cel
111	31	100.0	126	1	S16590	184	31	100.0	218	2	F81650	UDP-N-acetylglucos
112	31	100.0	127	1	S19498	185	31	100.0	220	2	T30688	hypothetical prote
113	31	100.0	127	2	B91218	186	31	100.0	220	2	G86164	protein F15K9.8 [i
114	31	100.0	127	2	C86064	187	31	100.0	222	2	A53263	tetraspas TSPAN-2
115	31	100.0	128	2	JQ1002	188	31	100.0	222	2	H87210	conserved hypothet
116	31	100.0	129	2	B96621	189	31	100.0	232	2	A41551	vascular endotheli
117	31	100.0	129	2	T08084	190	31	100.0	232	2	D96663	unknown protein, 5
118	31	100.0	130	2	D71707	191	31	100.0	233	2	D84797	hypothetical prote
119	31	100.0	131	2	T50862	192	31	100.0	241	2	C82852	competence protei
120	31	100.0	131	2	T50863	193	31	100.0	242	2	A96499	hypothetical prote
121	31	100.0	131	2	T50864	194	31	100.0	245	2	A43905	sperm outer dense
122	31	100.0	131	2	T50865	195	31	100.0	247	2	I48699	outer dense fiber
123	31	100.0	133	2	S58123	196	31	100.0	250	2	E87921	protein F56G4.5 [i
124	31	100.0	133	2	F97361	197	31	100.0	265	2	B48151	sperm tail protein
125	31	100.0	138	2	S00512	198	31	100.0	268	2	C38095	T-cell-specific tr
126	31	100.0	139	2	G70464	199	31	100.0	273	2	B31479	env polyprotein pr
127	31	100.0	139	2	H91059	200	31	100.0	277	2	I52825	gene M625 protein
128	31	100.0	139	2	G85904	201	31	100.0	281	2	S49353	protein S2 - phala
129	31	100.0	139	2	AB0831	202	31	100.0	282	2	S50031	proteacyclin-stimu
130	31	100.0	139	2	E65036	203	31	100.0	282	2	S49352	protein S1 - phala
131	31	100.0	139	2	I52320	204	31	100.0	289	2	TC5938	thioredoxin-like p
132	31	100.0	140	1	S57774	205	31	100.0	290	2	T40552	thioredoxin-like p
133	31	100.0	140	1	G87183	206	31	100.0	296	2	T07367	thioredoxin-like p
134	31	100.0	141	1	UTBOB	207	31	100.0	299	2	E87262	thioredoxin [impor
135	31	100.0	141	1	UTHNB	208	31	100.0	302	2	A96789	protein T23E18.2 [
136	31	100.0	141	1	UTPCB	209	31	100.0	309	2	AB0838	virulence protein
137	31	100.0	141	1	UTRMB	210	31	100.0	321	2	AD0580	lipidic acid synthe
138	31	100.0	141	1	UTSHB	211	31	100.0	322	2	AH3011	thioredoxin trxA [
139	31	100.0	141	1	G75455	212	31	100.0	323	2	I48667	Mha3 [keratin acid
140	31	100.0	142	2	JC4527	213	31	100.0	329	2	AH3559	thioredoxin [impor
141	31	100.0	142	2	G75612	214	31	100.0	331	2	G98272	probable thioredox
142	31	100.0	145	2	S70356	215	31	100.0	332	2	I48691	regulatory protein
143	31	100.0	145	2	AD0397	216	31	100.0	334	2	A48151	sperm tail protein
144	31	100.0	148	2	B96721	217	31	100.0	340	1	C70538	probable 6-phospho
145	31	100.0	151	2	B96796	218	31	100.0	340	2	T33313	hypothetical prote
146	31	100.0	155	1	KRCHS	219	31	100.0	356	1	A35253	2-dehydro-3-deoxy-
147	31	100.0	156	2	T08086	220	31	100.0	356	1	ADECHY	2-dehydro-3-deoxy-
148	31	100.0	157	2	S16728	221	31	100.0	356	2	AB0833	2-dehydro-3-deoxy-
149	31	100.0	158	1	ZBBE11	222	31	100.0	356	2	H91061	hypothetical prote
150	31	100.0	160	2	A82020	223	31	100.0	356	2	D85906	hypothetical prote
151	31	100.0	160	2	D81247	224	31	100.0	356	2	AC0399	2-dehydro-3-deoxy-
152	31	100.0	161	2	T48767	225	31	100.0	357	2	S23526	cinnamyl-alcohol d
153	31	100.0	162	2	T49420	226	31	100.0	357	2	S23525	cinnamyl-alcohol d
154	31	100.0	167	2	T03957	227	31	100.0	357	2	D82292	phospho-2-dehydro-
155	31	100.0	169	1	KTHOB	228	31	100.0	362	2	I37459	keratin Ha3-II, cy
156	31	100.0	172	1	S38909	229	31	100.0	363	2	B97199	uncharacterized co
157	31	100.0	173	2	F84530	230	31	100.0	366	2	S61796	T-cell-specific tr
158	31	100.0	174	2	T29491	231	31	100.0	373	2	T33145	hypothetical prote
159	31	100.0	177	2	T09495	232	31	100.0	380	2	A71181	probable isomerase
160	31	100.0	179	2	T00893	233	31	100.0	380	2	H75159	3-isopropylmalate
161	31	100.0	179	2	A87654	234	31	100.0	380	2	G01639	transmembrane prot
162	31	100.0	181	1	TXSPM	235	31	100.0	381	2	A33477	protein-glutamine
163	31	100.0	182	2	T07837	236	31	100.0	386	2	T51171	homoaconitate hydr
164	31	100.0	182	2	S20929	237	31	100.0	392	2	A60777	keratin 2, type I,
165	31	100.0	182	2	B96539	238	31	100.0	395	1	J00396	nodulation protein
166	31	100.0	185	2	P75549	239	31	100.0	396	2	C84797	hypothetical prote
167	31	100.0	185	2	D95115	240	31	100.0	397	2	G97335	subtilisin-like se
168	31	100.0	186	2	F85044	241	31	100.0	398	1	S24802	subliferredoxin 6x2
169	31	100.0	186	2	T03808	242	31	100.0	399	2	F82657	beta-ketocacyl- (ACP
170	31	100.0	186	2	S04661	243	31	100.0	404	2	J50073	keratin, 47.6K tYP
171	31	100.0	190	2	S52130	244	31	100.0	412	1	KRSHTL	keratin, 48K type
172	31	100.0	190	2	B40080	245	31	100.0	413	1	S34305	nodulation protein
173	31	100.0	191	2	T12261	246	31	100.0	415	1	S51977	FUN9 protein - yea
174	31	100.0	191	2	H97984	247	31	100.0	416	2	A61404	keratin A, type I
175	31	100.0	192	2	A72646	248	31	100.0	416	2	S60034	keratin Ha1, type

249	31	100.0	416	2	A46559	keratin, type I, h	322	31	100.0	835	2	T26086	hypothetical prote
250	31	100.0	416	2	A99419	hypothetical prote	323	31	100.0	836	2	A54269	protein-glutamine
251	31	100.0	416	2	G69524	3-isopropylmalate	324	31	100.0	837	2	T02761	outer arm dynein I
252	31	100.0	417	2	H72362	3-isopropylmalate	325	31	100.0	842	2	C81396	alanine-tRNA ligas
253	31	100.0	418	2	C72394	hypothetical prote	326	31	100.0	847	2	A64675	alanine-tRNA ligas
254	31	100.0	419	2	D69051	3-isopropylmalate	327	31	100.0	847	2	F71842	alanine-tRNA ligas
255	31	100.0	420	2	B64425	homoaconitate hydr	328	31	100.0	860	2	G82310	alanyl-tRNA synth
256	31	100.0	422	2	C97290	3-isopropylmalate	329	31	100.0	873	2	H96503	protein Pg16.17 I
257	31	100.0	423	2	B75045	probable 3-isoprop	330	31	100.0	874	2	H83533	alanyl-tRNA synth
258	31	100.0	424	1	S12793	nodulation protein	331	31	100.0	874	2	F81063	alanyl-tRNA synth
259	31	100.0	424	1	ZZZKCL	nodulation protein	332	31	100.0	874	2	C81804	alanine-tRNA ligas
260	31	100.0	426	1	ZZZRC4	nodulation protein	333	31	100.0	875	2	I64095	alanine-tRNA ligas
261	31	100.0	426	2	A95321	NodC N-ACETYLGLUCO	334	31	100.0	875	2	AE0401	alanine-tRNA ligas
262	31	100.0	428	2	A69085	3-isopropylmalate	335	31	100.0	876	1	SYECAT	alanine-tRNA ligas
263	31	100.0	432	2	C70381	large subunit of i	336	31	100.0	876	2	AF0843	alanine-tRNA ligas
264	31	100.0	433	2	B69495	aconitase (acn) ho	337	31	100.0	876	2	B91073	alanyl-tRNA synth
265	31	100.0	434	2	D75373	3-isopropylmalate	338	31	100.0	877	2	S76394	hypothetical prote
266	31	100.0	452	2	T36042	probable plasmid r	339	31	100.0	877	2	H71647	alanine-tRNA ligas
267	31	100.0	454	2	T21358	hypothetical prote	340	31	100.0	878	2	B84977	alanine-tRNA ligas
268	31	100.0	455	2	A55050	enigma - human	341	31	100.0	878	2	E85917	alanyl-tRNA synth
269	31	100.0	458	1	S77662	thioredoxin-disulf	342	31	100.0	878	2	G97865	alanine-tRNA ligas
270	31	100.0	458	2	D70325	hypothetical prote	343	31	100.0	880	2	AC3108	alanyl-tRNA synth
271	31	100.0	463	2	T49460	hypothetical prote	344	31	100.0	880	2	H87562	alanyl-tRNA synth
272	31	100.0	464	2	H90140	transcription regu	345	31	100.0	881	2	A97107	alanyl-tRNA synth
273	31	100.0	464	2	T46333	hypothetical prote	346	31	100.0	885	2	AG3350	alanine-tRNA ligas
274	31	100.0	483	2	AG1898	thioredoxin reduct	347	31	100.0	887	2	AC2806	alanyl-tRNA synth
275	31	100.0	486	2	T39456	zinc finger protei	348	31	100.0	890	2	F75289	alanyl-tRNA synth
276	31	100.0	508	1	KRSHL2	keratin type II, m	349	31	100.0	900	2	F97585	alanyl-tRNA synth
277	31	100.0	525	2	T21357	hypothetical prote	350	31	100.0	900	2	C64232	alanyl-tRNA synth
278	31	100.0	534	1	VCWSP	env polypeptide -	351	31	100.0	900	2	S73748	alanyl-tRNA ligas
279	31	100.0	535	2	T00824	probable thioredox	352	31	100.0	906	2	D82899	alanyl-tRNA synth
280	31	100.0	574	1	HOCCLP	hydrogenase (BC 1,	353	31	100.0	916	2	C82844	alanyl-tRNA synth
281	31	100.0	584	2	T02392	hypothetical prote	354	31	100.0	955	2	D96538	cytosolic tRNA-Ala
282	31	100.0	584	1	C8HUA	complement C8 alfa	355	31	100.0	955	2	A45441	thrombospondin 4 -
283	31	100.0	585	2	I46686	complement compo	356	31	100.0	956	1	A46016	thrombospondin 3 -
284	31	100.0	597	2	S72468	probable transcrip	357	31	100.0	956	2	A57121	thrombospondin 3 p
285	31	100.0	604	2	T36966	hypothetical prote	358	31	100.0	958	2	S62065	alanine-tRNA ligas
286	31	100.0	606	2	T31557	hypothetical prote	359	31	100.0	959	2	T38247	probable alanyl-cr
287	31	100.0	633	2	A75069	dipeptide transpor	360	31	100.0	961	1	TSHUP4	thrombospondin 4 p
288	31	100.0	642	2	H97019	aconitase A [impor	361	31	100.0	965	2	S62935	hypothetical prote
289	31	100.0	654	2	B56011	transcription fact	362	31	100.0	967	1	SYMTAT	alanine-tRNA ligas
290	31	100.0	659	2	F70453	aconitase - Aquife	363	31	100.0	968	2	I60107	alanine-tRNA ligas
291	31	100.0	662	1	VCWTLB	env polypeptide -	364	31	100.0	968	2	T29466	hypothetical prote
292	31	100.0	662	1	VCWGF	env polypeptide -	365	31	100.0	975	2	I48974	receptor-protein t
293	31	100.0	662	2	A25982	env polypeptide -	366	31	100.0	976	2	A36355	protein-tyrosine k
294	31	100.0	668	1	VCWTF	env polypeptide pr	367	31	100.0	977	2	S49004	tyrosine kinase Mp
295	31	100.0	670	2	T33304	hypothetical prote	368	31	100.0	989	2	S32671	alanine-tRNA ligas
296	31	100.0	680	2	JC5133	protein-glutamine	369	31	100.0	1172	2	F96503	protein Pg16.13 I
297	31	100.0	687	2	T39638	hypothetical prote	370	31	100.0	1178	1	A39804	thrombospondin pre
298	31	100.0	693	1	S61067	homoaconitate hydr	371	31	100.0	1196	1	DNBEHF	DNA-binding protei
299	31	100.0	695	2	S66662	protein-glutamine	372	31	100.0	1196	1	DNBEKS	DNA-binding protei
300	31	100.0	712	2	A45638	immunodominant mlt	373	31	100.0	1196	1	DNBEV1	major DNA-binding
301	31	100.0	721	2	T38665	probable homoacon	374	31	100.0	1197	1	A48350	DNA-binding protei
302	31	100.0	724	2	A48569	antigen Emi100 - B1	375	31	100.0	1364	2	T00250	MEG2 protein - hu
303	31	100.0	744	2	A45622	surface antigen GP	376	31	100.0	1743	2	T15893	hypothetical prote
304	31	100.0	755	2	A44315	cartilage oligomer	377	31	100.0	1786	1	MMMSB1	laminin beta-1 cha
305	31	100.0	761	2	C64813	YbhJ protein - Bsc	378	31	100.0	2109	2	I38414	transcription fact
306	31	100.0	761	2	G90728	probable enzyme I1	379	31	100.0	2148	2	AS6011	transcription fact
307	31	100.0	761	2	H85579	RNA-directed RNA p	380	31	100.0	2228	2	T14029	variant-specific s
308	31	100.0	774	1	P31V50	basic polymerase 2	381	31	100.0	2282	2	T42717	DNA-binding protei
309	31	100.0	774	2	S13670	aconitase hydratase	382	31	100.0	2630	2	T08868	polypeptide PI - A
310	31	100.0	778	2	S50387	aconitase hydratase	383	31	100.0	3034	2	T14119	seven-pass transme
311	31	100.0	778	2	T38347	aconitase hydratase	384	31	100.0	4302	2	A38971	polycyclic kidney
312	31	100.0	779	2	S57805	aconitase hydratase	385	31	100.0	4957	2	T03455	ALR protein - huma
313	31	100.0	780	2	T52543	aconitase hydratase	386	31	100.0	5262	2	T03455	ALR protein - huma
314	31	100.0	781	2	A35544	aconitase hydratase	387	31	100.0	58	2	C61233	conceptus protein
315	31	100.0	781	2	S57528	aconitase hydratase	388	31	100.0	58	1	SMKD18	metallothionein 1
316	31	100.0	788	2	S44831	FS4H2.1 protein -	389	31	100.0	58	2	A37039	metallothionein 1
317	31	100.0	788	2	T26967	hypothetical prote	390	31	100.0	80.6	2	S59072	metallothionein 1
318	31	100.0	789	2	S46631	hypothetical prote	391	31	100.0	80.6	2	S15137	thioredoxin h2 - s
319	31	100.0	817	1	TGRUM1	protein-glutamine	392	31	100.0	80.6	2	SMBH1	metallothionein - I
320	31	100.0	824	2	B38423	protein-glutamine	393	31	100.0	80.6	2	S57768	metallothionein - I
321	31	100.0	832	2	A40205	Na+/H+-exchanging	394	31	100.0	80.6	2	JQ2358	neutral aluminum ind

395	25	80.6	77	2	S47158	metallochionein II	468	25	80.6	201	2	AC0255	probable phage pro
396	25	80.6	77	2	S57862	metallochionein 2b	469	25	80.6	208	2	E97094	ncharacterized con
397	25	80.6	77	2	S52636	metallochionein -	470	25	80.6	209	2	E71647	hypothetical prote
398	25	80.6	77	2	S31660	voltage-dependent	471	25	80.6	209	2	H97864	hypothetical prote
399	25	80.6	79	2	T17014	metallochionein-11	472	25	80.6	210	2	A87523	thiol-disulfide in
400	25	80.6	79	2	JQ2128	metallochionein -	473	25	80.6	212	2	H75148	hypothetical prote
401	25	80.6	80	2	T12928	thioredoxin - Bact	474	25	80.6	220	2	S48781	Li protein - human
402	25	80.6	80	2	T10087	metallochionein -	475	25	80.6	221	2	T29509	hypothetical prote
403	25	80.6	81	2	S27366	metallochionein B(476	25	80.6	222	2	S48786	Li protein - human
404	25	80.6	81	2	S27369	metallochionein F(477	25	80.6	222	2	D70866	hypothetical prote
405	25	80.6	82	2	T07114	metallochionein-11	478	25	80.6	224	2	S48779	Li protein - human
406	25	80.6	82	2	T07076	metallochionein Iy	479	25	80.6	225	2	S19428	SKD1 protein - yea
407	25	80.6	82	2	T07327	metallochionein-11	480	25	80.6	227	2	B70790	hypothetical prote
408	25	80.6	84	2	C69499	virulence associat	481	25	80.6	228	2	S48783	Li protein - human
409	25	80.6	85	2	T00508	metallochionein-II	482	25	80.6	229	1	B43685	nonstructural prot
410	25	80.6	85	2	T07090	metallochionein-II	483	25	80.6	229	1	D43685	nonstructural prot
411	25	80.6	85	2	T05719	metallochionein II	484	25	80.6	230	2	C84606	probable Ras type
412	25	80.6	87	2	A39439	small cysteine-ric	485	25	80.6	232	2	T16258	hypothetical prote
413	25	80.6	88	2	JC5203	outer membrane pro	486	25	80.6	233	2	H69611	phosphoadenylyl-su
414	25	80.6	88	2	JQ0514	cysteine-rich 9K P	487	25	80.6	236	2	G82578	conserved hypotet
415	25	80.6	88	2	S12126	cysteine-rich oute	488	25	80.6	240	2	H90064	conserved hypotet
416	25	80.6	88	2	S12125	cysteine-rich oute	489	25	80.6	241	2	F81835	hypothetical prote
417	25	80.6	88	2	E71513	probable ykda-cyst	490	25	80.6	241	2	B81129	conserved hypotet
418	25	80.6	88	2	D81671	cysteine rich oute	491	25	80.6	242	2	G86795	hypothetical prote
419	25	80.6	90	2	B86560	9 kDa-Cysteine-ric	492	25	80.6	242	2	T22915	hypothetical prote
420	25	80.6	90	2	A72064	cysteine rich oute	493	25	80.6	245	2	E64015	hypothetical prote
421	25	80.6	91	2	JN0140	InsA protein - Esc	494	25	80.6	247	2	T31509	hypothetical prote
422	25	80.6	91	2	E90800	InsA protein of in	495	25	80.6	247	2	T17311	hypothetical prote
423	25	80.6	98	2	S62346	I71-5 protein - fr	496	25	80.6	248	2	AD0394	hypothetical prote
424	25	80.6	101	2	S33514	I3K prolamin - ric	497	25	80.6	250	2	S71522	outer dense fiber
425	25	80.6	106	2	AE1428	thioredoxin homolo	498	25	80.6	251	2	G84957	di-trans,poly-cis-
426	25	80.6	106	2	AD1802	thioredoxin homolo	499	25	80.6	254	2	C70682	probable cybH - My
427	25	80.6	108	1	S02802	thioredoxin C-2 -	500	25	80.6	255	2	I38426	lymphocyte activat
428	25	80.6	108	2	B84999	thioredoxin [impor	501	25	80.6	257	2	I38025	keratin-like prote
429	25	80.6	113	2	F82526	thioredoxin XF2698	502	25	80.6	259	1	IC0H11	insulin-like growt
430	25	80.6	113	2	F65188	hypothetical 12.1	503	25	80.6	260	2	B71353	probable D,D-carbo
431	25	80.6	115	2	G84848	metallochionein-11	504	25	80.6	262	2	S56100	outer dense fiber
432	25	80.6	119	2	T17930	thioredoxin-like p	505	25	80.6	263	1	S56101	insulin-like growt
433	25	80.6	124	2	A706873	probable trxa prot	506	25	80.6	263	2	S23009	insulin-like growt
434	25	80.6	124	2	S25113	insulin-like growt	507	25	80.6	265	2	C70332	sulfate adenylate
435	25	80.6	132	2	AI0543	probable secreted	508	25	80.6	266	2	C96913	hypothetical prote
436	25	80.6	133	2	C90180	thioredoxin (trxa-	509	25	80.6	267	2	T15595	hypothetical prote
437	25	80.6	133	2	T37311	hypothetical prote	510	25	80.6	268	2	T20379	hypothetical prote
438	25	80.6	133	2	F72479	hypothetical prote	511	25	80.6	269	2	A89208	protein K10D6.2b [
439	25	80.6	134	2	AD2592	cytidine deaminase	512	25	80.6	270	2	T19207	hypothetical prote
440	25	80.6	134	2	G72678	hypothetical prote	513	25	80.6	272	1	A36082	insulin-like growt
441	25	80.6	135	2	C90393	thioredoxin (trxa-	514	25	80.6	272	2	I48600	insulin-like growt
442	25	80.6	140	2	H70809	probable thix prot	515	25	80.6	277	2	I37552	OX40 homolog - hum
443	25	80.6	141	2	T08790	hypothetical prote	516	25	80.6	279	1	B40731	alcohol dehydrogen
444	25	80.6	143	2	A72602	hypothetical prote	517	25	80.6	282	2	E83283	hypothetical prote
445	25	80.6	144	2	B82423	thioredoxin 2 VCA0	518	25	80.6	283	2	T26448	hypothetical prote
446	25	80.6	145	2	F97374	cytidine deaminase	519	25	80.6	286	2	C69100	conserved hypotet
447	25	80.6	145	2	S77736	probable zinc fing	520	25	80.6	286	2	S07533	puff II/9A-2 prote
448	25	80.6	150	2	A69551	conserved hypotet	521	25	80.6	286	2	S07532	puff II/9-1 proteI
449	25	80.6	150	2	A95388	thiol:disulfide in	522	25	80.6	287	2	T23579	hypothetical prote
450	25	80.6	151	2	AB3263	protein [impor	523	25	80.6	289	2	E83138	probable thioredox
451	25	80.6	154	2	H83526	hypothetical prote	524	25	80.6	290	1	D47468	cytochrome-c oxida
452	25	80.6	155	2	F87696	hypothetical prote	525	25	80.6	290	2	T23268	hypothetical prote
453	25	80.6	155	2	T30489	apoptosis inhibito	526	25	80.6	290	2	B88638	protein F58F6.2 [l
454	25	80.6	158	2	T25654	hypothetical prote	527	25	80.6	292	1	D55582	cytochrome-c oxida
455	25	80.6	161	2	T18498	hypothetical prote	528	25	80.6	294	2	E88640	protein F55A8.1 [l
456	25	80.6	170	2	H87704	thiol-disulfide in	529	25	80.6	297	2	T23909	hypothetical prote
457	25	80.6	176	1	A47384	cytochrome c bioge	530	25	80.6	304	2	T02125	chlorophyll a/b-bi
458	25	80.6	179	2	A13424	transcription regu	531	25	80.6	304	2	S04853	galactose 1-dehydr
459	25	80.6	180	2	S65026	finger protein XfG	532	25	80.6	307	2	F71294	hypothetical prote
460	25	80.6	185	2	A12991	conserved hypotet	533	25	80.6	310	2	T17980	hypothetical prote
461	25	80.6	185	2	A99292	hypothetical prote	534	25	80.6	314	2	AH3435	protein yicc [impo
462	25	80.6	186	2	A45910	ultra-high-sulfur	535	25	80.6	317	2	G70313	lipopolysaccharide
463	25	80.6	187	2	G87521	HNH endonuclease f	536	25	80.6	319	2	T02454	hypothetical prote
464	25	80.6	189	2	T19559	hypothetical prote	537	25	80.6	321	2	A82070	transcription regu
465	25	80.6	190	2	A13289	5-methylcytosine-s	538	25	80.6	322	2	PS0019	Ig gamma-2a chain
466	25	80.6	197	2	S22501	coat protein - And	539	25	80.6	322	2	T23580	hypothetical prote
467	25	80.6	199	2	S73702	hypothetical prote	540	25	80.6	325	2	B43692	t2 protein - rabbl

541	25	80.6	326	1	GOVZML	T2 protein - myxom	614	25	80.6	490	2	I48189	cytochrome P450 11
542	25	80.6	327	2	A46484	apoptosis-mediati	615	25	80.6	490	2	I49610	cytochrome P450 -
543	25	80.6	329	2	S32582	structural protein	616	25	80.6	490	2	A25954	cytochrome P450 2C
544	25	80.6	336	2	S61299	lipopolysaccharide	617	25	80.6	490	2	A32140	steroid 15beta-mon
545	25	80.6	336	2	C81073	ADP-hepoxe-LPS he	618	25	80.6	490	2	B28516	cytochrome P450 2C
546	25	80.6	336	2	B81869	lipopolysaccharide	619	25	80.6	490	2	F38462	S-mephenytoin 4'-h
547	25	80.6	337	2	S70125	PAS4 protein - yea	620	25	80.6	491	2	S05408	keratin, type II,
548	25	80.6	338	2	C82590	chlorodioxin XP2174	621	25	80.6	491	2	T10930	3C3.21 protein - S
549	25	80.6	345	2	H83020	hepoxyltransferase	622	25	80.6	493	2	A31949	cytochrome P450 2E
550	25	80.6	346	2	S34165	keratin, type II -	623	25	80.6	493	2	A47350	cytochrome P450 11
551	25	80.6	348	2	T28623	hypothetical prote	624	25	80.6	493	2	A21231	cytochrome P450 2B
552	25	80.6	349	2	D36858	gene G4K protein -	625	25	80.6	493	2	A25341	cytochrome P450 2E
553	25	80.6	349	2	D72175	G2R protein - vari	626	25	80.6	494	2	S13101	cytochrome P450 c1
554	25	80.6	349	2	E71847	lipopolysaccharide	627	25	80.6	494	2	A46588	cytochrome P450 ar
555	25	80.6	349	2	G64668	lipopolysaccharide	628	25	80.6	494	2	G97496	integral membrane
556	25	80.6	351	2	I55601	Na/taurocholate co	629	25	80.6	495	2	I57463	keratin type II -
557	25	80.6	351	2	F81959	site-specific DNA-	630	25	80.6	496	2	S55665	hypothetical prote
558	25	80.6	354	2	S60242	cinamyl-alcohol d	631	25	80.6	498	2	A47286	3',5'-cyclic-AMP p
559	25	80.6	354	2	JT0594	site-specific DNA-	632	25	80.6	500	2	A26685	cytochrome P450 2C
560	25	80.6	355	2	G83020	hepoxyltransferase	633	25	80.6	500	2	S62785	cytochrome P450 2C
561	25	80.6	356	2	S21423	cytochrome P450 2C	634	25	80.6	502	2	A83029	conserved hypotet
562	25	80.6	357	2	T05413	cinamyl-alcohol d	635	25	80.6	506	2	S13720	coat protein - ara
563	25	80.6	357	2	T49690	hypothetical prote	636	25	80.6	513	2	A44150	structural protein
564	25	80.6	367	2	T02767	cinamyl-alcohol d	637	25	80.6	514	2	S48730	Cry j II protein -
565	25	80.6	367	2	T02990	cinamyl-alcohol d	638	25	80.6	514	2	JC2498	second major aller
566	25	80.6	368	2	T38901	probable dimeric d	639	25	80.6	517	2	S36496	L1 protein - human
567	25	80.6	369	2	T20505	hypothetical prote	640	25	80.6	518	2	S36472	hypothetical prote
568	25	80.6	370	2	G34462	cytochrome P450 2C	641	25	80.6	518	2	T00398	hypothetical prote
569	25	80.6	374	1	A53142	alcohol dehydrogen	642	25	80.6	519	2	T48498	hypothetical prote
570	25	80.6	378	2	B27718	cytochrome P450 2C	643	25	80.6	521	2	H69317	conserved hypotet
571	25	80.6	382	2	AB0945	alcohol dehydrogen	644	25	80.6	522	1	T42234	structural polypro
572	25	80.6	382	2	AI0040	probable methanol	645	25	80.6	530	2	T42234	fork head-related
573	25	80.6	396	2	T06102	heat shock protein	646	25	80.6	534	2	T15405	hypothetical prote
574	25	80.6	407	2	I48739	Mha2(keratin acid	647	25	80.6	538	2	G69317	conserved hypotet
575	25	80.6	411	2	S41648	translation elonga	648	25	80.6	546	2	S36490	L1 protein - human
576	25	80.6	417	2	JC8000	N-acetylglactosam	649	25	80.6	550	2	JH0711	genome polyprotein
577	25	80.6	420	2	T00629	hypothetical prote	650	25	80.6	552	2	A33616	heterogeneous ribo
578	25	80.6	423	2	G71315	probable DNA polym	651	25	80.6	565	2	E91268	thiol disulfide in
579	25	80.6	429	2	T26192	hypothetical prote	652	25	80.6	565	2	C86109	thiol disulfide in
580	25	80.6	431	2	E96671	hypothetical prote	653	25	80.6	565	2	S56364	inner membrane cop
581	25	80.6	432	2	T28931	hypothetical prote	654	25	80.6	567	2	AE1044	thiol,disulfide in
582	25	80.6	434	2	C86331	P6F9.14 protein -	655	25	80.6	590	2	I46687	complement compone
583	25	80.6	435	2	E82753	D-amino acid deha	656	25	80.6	591	1	C8HUB	dreiprin - chicken
584	25	80.6	439	2	B81701	phospholipase D fa	657	25	80.6	593	2	I51213	thiol,disulfide in
585	25	80.6	445	4	A28516	probable cytochrom	658	25	80.6	595	2	AI0042	inner membrane cop
586	25	80.6	448	2	F81703	phospholipase D fa	659	25	80.6	607	2	A82043	dreiprin E2 - chick
587	25	80.6	449	2	S28167	cytochrome P450 2B	660	25	80.6	609	2	A43776	hypothetical prote
588	25	80.6	449	2	T16259	hypothetical prote	661	25	80.6	616	2	T32131	hypothetical prote
589	25	80.6	450	2	JC7266	3',5'-cyclic-nucle	662	25	80.6	618	2	T26935	hypothetical prote
590	25	80.6	454	1	GOMST1	tumor necrosis fac	663	25	80.6	622	2	T37204	hypothetical prote
591	25	80.6	457	2	A37222	cytochrome P450 2C	664	25	80.6	627	2	T02610	probable YME1 ATP-
592	25	80.6	461	1	GQRTT1	tumor necrosis fac	665	25	80.6	629	2	T14776	hypothetical prote
593	25	80.6	466	2	JH0197	muscarinic acetyl	666	25	80.6	640	2	T08179	LK63 protein - Chl
594	25	80.6	466	2	S10126	muscarinic acetyl	667	25	80.6	640	2	T26820	hypothetical prote
595	25	80.6	466	2	A27386	muscarinic acetyl	668	25	80.6	645	2	T22178	hypothetical prote
596	25	80.6	466	2	S10856	muscarinic acetyl	669	25	80.6	647	2	T43952	hypothetical prote
597	25	80.6	466	2	F69331	conserved hypotet	670	25	80.6	647	2	T23814	hypothetical prote
598	25	80.6	468	2	I52418	cytochrome P450 -	671	25	80.6	651	2	JC7705	death receptor-6 -
599	25	80.6	468	2	T33857	hypothetical prote	672	25	80.6	658	2	F85024	probable GTP-rich
600	25	80.6	475	2	T24900	hypothetical prote	673	25	80.6	659	2	T01520	hypothetical prote
601	25	80.6	479	2	A61368	keratin type II, h	674	25	80.6	663	2	S21912	BrCore-Q1-21 prote
602	25	80.6	483	2	T47974	hypothetical prote	675	25	80.6	667	2	A48579	crophosolite surfac
603	25	80.6	485	2	C86143	hypothetical prote	676	25	80.6	670	2	F88297	protein M28.1 lim
604	25	80.6	487	1	O4RBC6	cytochrome P450 2C	677	25	80.6	698	1	TFRUP	transferrin precur
605	25	80.6	487	1	O4RBP4	progestosterone mono	678	25	80.6	700	2	A86690	hypothetical prote
606	25	80.6	487	1	A26731	cytochrome P450 2C	679	25	80.6	709	2	C86648	ferrous ion transp
607	25	80.6	490	2	S28166	cytochrome P450 2C	680	25	80.6	713	2	A35502	major surfac-labe
608	25	80.6	490	2	A29782	unspecific monooxy	681	25	80.6	723	2	E87706	prolyl oligopeptid
609	25	80.6	490	2	D28951	cytochrome P450 2C	682	25	80.6	726	2	H96689	hypothetical prote
610	25	80.6	490	2	A61269	cytochrome P450 2C	683	25	80.6	728	2	S21913	BrCore-TM1-Q1-21
611	25	80.6	490	2	B38462	S-mephenytoin 4-hy	684	25	80.6	737	2	P00219	RNA-2 polyprotein
612	25	80.6	490	2	I48162	cytochrome P450 -	685	25	80.6	755	2	S42462	structural polypro
613	25	80.6	490	2	I48163	cytochrome P450 -	686	25	80.6	759	2	T44142	DRI protein [impor

687	25	80.6	772	2	H84605	hypotheical prote	760	25	80.6	3704	2	T37316	probable laminin a
688	25	80.6	794	1	KXHP	furin (EC 3.4.21.7	761	25	80.6	3712	2	S18253	laminin alpha-1 ch
689	25	80.6	797	2	A71267	hypotheical prote	762	25	80.6	3766	2	T29165	hypotheical prote
690	25	80.6	800	2	T01843	chloride channel p	763	24	77.4	45	2	T12318	metallochionein -
691	25	80.6	802	2	T24293	hypotheical prote	764	24	77.4	45	2	T12322	metallochionein -
692	25	80.6	835	2	A88238	protein T13H5.4 [l	765	24	77.4	68	2	AD2481	hypotheical prote
693	25	80.6	838	2	I45557	eyeless, long form	766	24	77.4	71	2	T09587	metallochionein-11
694	25	80.6	889	2	A35679	rep protein - slim	767	24	77.4	72	2	T07073	metallochionein cy
695	25	80.6	917	2	B85057	hypotheical prote	768	24	77.4	72	2	T07105	metallochionein-11
696	25	80.6	934	1	A34372	complement C6 prec	769	24	77.4	72	2	A34131	metallochionein I
697	25	80.6	939	2	T24294	hypotheical prote	770	24	77.4	73	2	T07109	metallochionein-11
698	25	80.6	975	2	T16073	hypotheical prote	771	24	77.4	74	2	T16979	metallochionein-11
699	25	80.6	983	2	F86160	receptor tyrosine	772	24	77.4	75	2	S09098	metallochionein -
700	25	80.6	985	2	I51549	protein-tyrosine k	773	24	77.4	75	2	S37240	metallochionein-11
701	25	80.6	987	2	A54092	protein-tyrosine k	774	24	77.4	75	2	T12188	metallochionein -
702	25	80.6	988	2	I50611	hypotheical prote	775	24	77.4	76	2	S17560	metallochionein-11
703	25	80.6	989	2	T01519	hypotheical prote	776	24	77.4	77	2	S37239	metallochionein-11
704	25	80.6	991	1	P1BVCV	RNA 1 protein - cu	777	24	77.4	77	2	T12187	metallochionein, t
705	25	80.6	993	1	P1VXCM	RNA 1 protein - cu	778	24	77.4	78	2	S48038	metallochionein-11
706	25	80.6	993	1	P1VXTA	ATP-dependent RNA	779	24	77.4	80	2	T12326	metallochionein-11
707	25	80.6	993	2	E71392	RNA 1 protein - cu	780	24	77.4	80	2	T14387	metallochionein-11
708	25	80.6	993	2	JQ2169	RNA 1 protein - cu	781	24	77.4	81	1	SMWUL	metallochionein-11
709	25	80.6	993	2	JA0074	RNA 1 protein - cu	782	24	77.4	81	2	S57861	metallochionein 2a
710	25	80.6	1005	1	P1VXBJ	RNA 1 protein - pe	783	24	77.4	84	2	T07115	transcription acti
711	25	80.6	1006	2	JC5526	kinase-defective E	784	24	77.4	119	2	S14292	keratin high-sulfu
712	25	80.6	1021	2	I39207	leukocyte surface	785	24	77.4	130	1	KRSH3A	keratin high-sulfu
713	25	80.6	1021	2	T42626	secreted leucine-r	786	24	77.4	131	1	KRGR3M	keratin high-sulfu
714	25	80.6	1025	2	A53121	peroxisome assembl	787	24	77.4	131	1	KRSHA3	pigment deposition
715	25	80.6	1058	2	S08436	pol polyprotein -	788	24	77.4	131	2	A46298	keratin high-sulfu
716	25	80.6	1119	2	A88481	protein C16A3.6 [l	789	24	77.4	132	1	KRGR3J	agouti protein
717	25	80.6	1145	2	S37136	structural polypro	790	24	77.4	132	2	T17143	agouti allergen pre
718	25	80.6	1164	2	T24806	hypotheical prote	791	24	77.4	134	2	A54002	hypotheical prote
719	25	80.6	1221	2	T23472	hypotheical prote	792	24	77.4	135	2	F82551	hypotheical prote
720	25	80.6	1223	2	T10365	helicase - Oryzia	793	24	77.4	137	2	T22308	hypotheical prote
721	25	80.6	1247	1	VHMVN2	structural polypro	794	24	77.4	140	2	I38232	gene SMA3 protein
722	25	80.6	1257	1	A41060	neural cell adhesi	795	24	77.4	140	2	I38233	gene SMA4 protein
723	25	80.6	1257	2	S28764	neurocan precursor	796	24	77.4	140	2	I38234	hypotheical prote
724	25	80.6	1259	2	S36126	neural cell adhesi	797	24	77.4	205	2	T31489	probable phosphad
725	25	80.6	1260	1	S05479	neural cell adhesi	798	24	77.4	244	2	H81905	phosphodensome p
726	25	80.6	1268	2	S52781	neurocan - mouse	799	24	77.4	246	2	C81111	CD27 antigen precu
727	25	80.6	1291	2	T21694	hypotheical prote	800	24	77.4	250	1	A49053	hypotheical prote
728	25	80.6	1347	2	T02214	ubiquitous TPR mot	801	24	77.4	250	2	T30502	hypotheical prote
729	25	80.6	1357	2	B96696	protein FIN21.4 [l	802	24	77.4	260	1	A46517	CD27 antigen precu
730	25	80.6	1401	2	T02255	probable ubiquitou	803	24	77.4	265	2	T47537	pollen allergen ho
731	25	80.6	1408	2	S16148	gene serrate prote	804	24	77.4	265	2	T05668	hypotheical prote
732	25	80.6	1531	2	T42218	slit-1 protein hom	805	24	77.4	293	2	T51522	hypotheical prote
733	25	80.6	1541	2	T02851	RNA protein L4171.	806	24	77.4	314	2	I37383	FAS soluble protei
734	25	80.6	1573	2	S01845	DNA (cytosine-5-)	807	24	77.4	335	2	A40036	apoptosis-mediati
735	25	80.6	1607	1	MMMSB2	laminin gamma-1 ch	808	24	77.4	363	3	S42386	major outer membra
736	25	80.6	1646	2	MMTMS2	186K protein - cuc	809	24	77.4	372	2	S11009	major outer membra
737	25	80.6	1680	2	A43434	furin (EC 3.4.21.7	810	24	77.4	372	2	B60756	major outer membra
738	25	80.6	1681	2	A55138	sodium channel mna	811	24	77.4	374	2	S11006	major outer membra
739	25	80.6	1682	2	A45380	sodium channel pro	812	24	77.4	375	2	S11007	major outer membra
740	25	80.6	1790	1	MMFEB1	laminin beta-1 cha	813	24	77.4	377	2	B64628	formate hydrogonly
741	25	80.6	1808	2	T15099	hypotheical prote	814	24	77.4	381	2	D69032	major outer membra
742	25	80.6	1820	2	A55494	latent transformin	815	24	77.4	387	2	C81747	mouse pneumonitis
743	25	80.6	1846	2	T10670	hypotheical prote	816	24	77.4	387	2	JT0947	phage-related inte
744	25	80.6	2049	2	T43161	sodium channel pro	817	24	77.4	387	2	E82777	major outer membra
745	25	80.6	2052	2	T37711	probable n-end-rec	818	24	77.4	387	2	S16034	major outer membra
746	25	80.6	2109	1	ZLVN	genome polyprotein	819	24	77.4	389	1	MMCMP3	major outer membra
747	25	80.6	2175	1	GNNYBE	myosin VIIa - mous	820	24	77.4	389	2	I40864	major outer membra
748	25	80.6	2215	2	T30870	adenomacous polypro	821	24	77.4	389	2	A60109	major outer membra
749	25	80.6	2274	2	T30258	von Willebrand fac	822	24	77.4	389	2	A43587	major outer membra
750	25	80.6	2813	1	VWVHU	protein T22A3.8 [l	823	24	77.4	389	2	D86577	major outer membra
751	25	80.6	2823	2	F87908	hypotheical prote	824	24	77.4	392	2	I40739	alcohol dehydrogen
752	25	80.6	2823	2	T23064	hypotheical prote	825	24	77.4	392	2	A75593	major outer membra
753	25	80.6	2824	2	T22759	ocogelin - mouse	826	24	77.4	392	1	MMCW71	major outer membra
754	25	80.6	2910	2	T42214	laminin alpha-1 ch	827	24	77.4	393	2	H71484	probable major out
755	25	80.6	3084	1	MMMSA	laminin alpha-1 ch	828	24	77.4	393	2	JC1432	major outer membra
756	25	80.6	3084	1	MMMSA	laminin alpha-1 ch	829	24	77.4	393	2	S06259	major outer membra
757	25	80.6	3102	2	T43291	laminin alpha 5 ch	830	24	77.4	393	2	T01645	major outer membra
758	25	80.6	3635	2	T10053	hypotheical prote	831	24	77.4	394	1	MMCW7B	major outer membra
759	25	80.6	3672	2	T23433		832	24	77.4				

833	24	77.4	394	2	S11012	major outer membra	906	23	74.2	55	2	S36791	ferredoxin 2[4Fe-4
834	24	77.4	395	1	MMCWTF	major outer membra	907	23	74.2	55	2	A24932	ferredoxin 2[4Fe-4
835	24	77.4	396	2	S12799	major outer membra	908	23	74.2	56	1	FECLCP	zinc finger proteol
836	24	77.4	397	1	MMCWTC	major outer membra	909	23	74.2	56	2	I37970	metallothionein -
837	24	77.4	397	1	MMCWTH	major outer membra	910	23	74.2	56	2	S31198	metallothionein -
838	24	77.4	397	1	JEO413	major outer membra	911	23	74.2	56	2	F90059	hypothetical prote
839	24	77.4	402	1	MMCWPM	major outer membra	912	23	74.2	56	2	E64366	ferredoxin 2[4Fe-4
840	24	77.4	402	2	I40740	major outer membra	913	23	74.2	56	2	B69517	ferredoxin (fdx-8)
841	24	77.4	402	2	B60109	major outer membra	914	23	74.2	56	2	B69135	ferredoxin - Metha
842	24	77.4	402	2	A60341	major outer membra	915	23	74.2	56	2	A69337	ferredoxin [import
843	24	77.4	404	2	I40741	major outer membra	916	23	74.2	57	1	SMKD25	metallothionein 2
844	24	77.4	403	2	S33683	site-specific DNA-	917	23	74.2	57	2	S59073	metallothionein 1s
845	24	77.4	438	2	C82713	polyaccharide bio	918	23	74.2	58	2	S43367	zinc finger proteol
846	24	77.4	455	2	AH2055	hypothetical prote	919	23	74.2	58	2	A43284	RNA polymerase II
847	24	77.4	463	2	S75889	hypothetical prote	920	23	74.2	58	2	I37558	ferredoxin [import
848	24	77.4	469	2	A90166	conserved hypotet	921	23	74.2	58	2	B97333	hypothetical prote
849	24	77.4	481	2	UC7812	BCL6 homologous z1	922	23	74.2	58	2	G36953	ferredoxin 2[4Fe-4
850	24	77.4	511	2	UC7682	spermatogenesis as	923	23	74.2	58	2	B42960	ferredoxin (fdx-5)
851	24	77.4	524	2	A29677	complement C9 prec	924	23	74.2	58	2	C69365	ferredoxin 2[4Fe-4
852	24	77.4	537	2	B84772	probable DnaJ prot	925	23	74.2	59	1	FEDV2N	ferredoxin 2[4Fe-4
853	24	77.4	539	2	S58287	J-domain protein D	926	23	74.2	59	1	FEKZB	conserved hypotet
854	24	77.4	559	1	C9HU	complement C9 prec	927	23	74.2	59	2	F69315	metallothionein-1l
855	24	77.4	633	2	C98321	C4-dicarboxylate t	928	23	74.2	59	2	T08149	ferredoxin 2[4Fe-4
856	24	77.4	709	2	T28712	hypothetical prote	929	23	74.2	59	2	A54516	ribosomal protein
857	24	77.4	712	2	JC4935	peroxidase (EC 1.1	930	23	74.2	60	1	A64349	ferredoxin 2[4Fe-4
858	24	77.4	730	2	G84605	hypothetical prote	931	23	74.2	60	1	FRCI	metallothionein-1l
859	24	77.4	930	2	B84505	probable retroelem	932	23	74.2	60	2	T09258	hypothetical prote
860	24	77.4	1008	2	T18832	probable RNA helic	933	23	74.2	60	2	S42374	hypothetical prote
861	24	77.4	1040	2	E71412	hypothetical prote	934	23	74.2	60	2	S42375	ferredoxin 2[4Fe-4
862	24	77.4	1188	2	D86236	protein F1AN23.5 l	935	23	74.2	60	2	A42960	ferredoxin (fdx-4)
863	24	77.4	1296	2	T16859	hypothetical prote	936	23	74.2	61	1	F69270	ferredoxin 2[4Fe-4
864	24	77.4	1403	2	S64142	hypothetical prote	937	23	74.2	61	2	FRCP	metallothionein pr
865	24	77.4	1441	2	T39636	probable cleavage	938	23	74.2	61	2	S14049	hypothetical prote
866	24	77.4	1530	2	B82085	glutamate synthase	939	23	74.2	62	2	B86577	hypothetical prote
867	24	77.4	1786	1	MMHUB1	laminin beta-1 cha	940	23	74.2	62	2	T21305	bacterioferritin-a
868	24	77.4	1955	1	AGCH	agrin precursor -	941	23	74.2	62	2	F82332	ORF MSY185 hypotet
869	24	77.4	1959	1	AGRT	agrin - rat	942	23	74.2	62	2	T28346	ferredoxin [import
870	24	77.4	2182	2	T28634	erythrocyte membra	943	23	74.2	62	2	B97344	ferredoxin [4Fe-4S
871	24	77.4	2212	2	T28157	polymerase - Berne	944	23	74.2	63	1	FECLCP	ferredoxin 2[4Fe-4
872	24	77.4	2291	2	S11238	hypothetical prote	945	23	74.2	63	1	FERFIP	ferredoxin (fdx-4)
873	24	77.4	2647	2	T28161	variant-specific s	946	23	74.2	64	1	C69303	Yhea protein - Bac
874	24	77.4	3078	2	T28432	arylsulfatase A -	947	23	74.2	64	1	QOECB7	ferredoxin 2[4Fe-4
875	23	74.2	20	2	I54283	neurotoxin Bt-II -	948	23	74.2	64	1	FERMN	bacterioferritin-a
876	23	74.2	24	2	A53357	alpha-conotoxin p	949	23	74.2	64	2	ARI005	hypothetical prote
877	23	74.2	25	2	A58647	CAPS protein - ant	950	23	74.2	64	2	A85998	probable bacteriof
878	23	74.2	27	2	S55030	erythrocyte chemok	951	23	74.2	64	2	AG0025	FdxN ferredoxin (l
879	23	74.2	28	2	I52627	toxin-like protein	952	23	74.2	64	2	A95317	ferredoxin 2[4Fe-4
880	23	74.2	35	2	S06667	hypothetical prote	953	23	74.2	65	1	S09280	FERFIC
881	23	74.2	36	2	S33435	ribosomal protein	954	23	74.2	65	2	A38739	metallothionein -
882	23	74.2	37	2	T07519	spike protein - po	955	23	74.2	65	2	A13251	conserved hypotet
883	23	74.2	37	2	A49591	metallothionein -	956	23	74.2	65	2	B25103	ferredoxin 2[4Fe-4
884	23	74.2	38	2	T12331	hypothetical prote	957	23	74.2	65	2	B35405	protein YB056w-a
885	23	74.2	40	2	B69408	hypothetical prote	958	23	74.2	65	2	S78705	metallothionein -
886	23	74.2	42	2	A71265	ribosomal protein	959	23	74.2	66	2	T11547	riboseomal protein
887	23	74.2	44	1	S27036	hypothetical prote	960	23	74.2	68	1	A41608	phosphoprotein p2
888	23	74.2	44	2	F82363	hypothetical prote	961	23	74.2	68	2	A31490	ferredoxin (fdx-3)
889	23	74.2	47	2	T05661	Ig gamma heavy cha	962	23	74.2	69	2	C69294	50S ribosomeal prot
890	23	74.2	48	2	A30504	DNA-directed RNA p	963	23	74.2	70	2	AEO014	50S ribosomeal prot
891	23	74.2	48	2	C90189	cysteine proteinin	964	23	74.2	71	2	C53306	k1eB protein - pia
892	23	74.2	51	2	G69133	ferredoxin 2[4Fe-4	965	23	74.2	71	2	AE0014	conserved hypotet
893	23	74.2	53	2	F32946	ferredoxin 2[4Fe-4	966	23	74.2	73	2	H83204	salivary glue prot
894	23	74.2	54	1	FEMF	ferredoxin 2[4Fe-4	967	23	74.2	74	1	GSRF7	BiliB3 high-sulfur
895	23	74.2	55	1	FECLCB	ferredoxin 2[4Fe-4	968	23	74.2	74	2	I47084	hypothetical prote
896	23	74.2	55	1	FECLCB	ferredoxin 2[4Fe-4	969	23	74.2	74	2	C82919	hypothetical prote
897	23	74.2	55	1	FECLCT	ferredoxin 2[4Fe-4	970	23	74.2	74	2	G82810	ferredoxin - Metha
898	23	74.2	55	1	FECLCT	ferredoxin 2[4Fe-4	971	23	74.2	74	2	A69097	ferredoxin [import
899	23	74.2	55	1	FEPR	ferredoxin 2[4Fe-4	972	23	74.2	74	2	AH1317	ferredoxin homolo
900	23	74.2	55	1	FEORF	SSU ribosomeal prot	973	23	74.2	74	2	AH1689	ferredoxin homolo
901	23	74.2	55	2	A82464	hypothetical prote	974	23	74.2	75	2	H90187	hypothetical prote
902	23	74.2	55	2	A82464	hypothetical prote	975	23	74.2	76	1	S76753	FSH beta-subunit -
903	23	74.2	55	2	S17805	ferredoxin 2[4Fe-4	976	23	74.2	76	2	I83048	hypothetical prote
904	23	74.2	55	2	JU0126	ferredoxin - Clost	977	23	74.2	76	2	AB1970	
905	23	74.2	55	2	JX0144		978	23	74.2	76	2		

979 23 74.2 76 2 F83930
 980 23 74.2 77 2 T09815
 981 23 74.2 77 2 D69432
 982 23 74.2 77 2 C89878
 983 23 74.2 78 2 JC2496
 984 23 74.2 78 2 A70026
 985 23 74.2 79 2 P84076
 986 23 74.2 79 2 C84077
 987 23 74.2 79 2 C82740
 988 23 74.2 80 2 T43368
 989 23 74.2 80 2 T43625
 990 23 74.2 80 2 T02063
 991 23 74.2 80 2 A89860
 992 23 74.2 80 2 E64307
 993 23 74.2 81 1 A55790
 994 23 74.2 81 1 PEB8PF
 995 23 74.2 81 2 I48749
 996 23 74.2 81 2 T30482
 997 23 74.2 82 1 CCP85M
 998 23 74.2 82 2 D69621
 999 23 74.2 82 2 E83944
 1000 23 74.2 82 2 A83676

ALIGNMENTS

RESULT 1

NTSRPM
 neurotoxin P2 - scorpion (Androctonus mauretanicus)

C/Species: Androctonus mauretanicus mauretanicus

C/Date: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 09-Jul-2004

C/Accession: A01758

R/Rosao, J.P.; Rochat, H.

Toxicol 23, 113-125, 1985

A/Title: Characterization of ten proteins from the venom of the Moroccan scorpion Androctonus mauretanicus

A/Reference number: A94318; MUID:85193276; PMID:3992595

A/Accession: A01758

A/Molecule type: protein

A/Residues: 1-35 <ROS>

A/Cross-references: UNIPROT:P01498; UNIPARC:UPI0000036305

C/Superfamily: scorpion neurotoxin

C/Keywords: neurotoxin; venom

F/1-18,4-25,15-30,19-32/Diulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 35;

Best Local Similarity 100.0%; Pred. No. 59;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 1 CGPC 4

RESULT 2

A53356
 neurotoxin Bmk 41-2 - scorpion (Butkus Martensii Karsch)

C/Species: Butkus Martensii Karsch

C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 19-Apr-2002

C/Accession: A59356

R/Xu, C.

submitted to the Protein Sequence Database, October 2000

A/Description: Purification and Sequence determination of a new neurotoxin from Scorpion

A/Reference number: A59356

A/Accession: A59356

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-35 <XUC>

A/Cross-references: UNIPARC:UPI00001766C6

C/Superfamily: scorpion neurotoxin

C/Keywords: venom

F/1-35/Product: neurotoxin Bmk 41-2 #status experimental <Mat>

F/1-18,4-25,15-30,19-32/Diulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 1 CGPC 4

RESULT 3

S25774
 testis-specific protein Mat84dc - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: S25774; C56565

R/Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.

Mech. Dev. 35, 143-151, 1991

A/Title: A cluster of four genes selectively expressed in the male germ line of Drosophila

A/Reference number: A56565; MUID:92102953; PMID:1684716

A/Molecule type: DNA

A/Residues: 1-55 <KUH>

A/Cross-references: UNIPROT:Q01644; UNIPARC:UPI00001246FE; EMBL:X67703; NID:911072; PID

A/Note: the authors translated the codon TGC for residue 55 as Thr

A/Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBIR:74222)

C/Genetics:

A/Gene: Mat84dc

A/Cross-references: FlyBase:FBgn0004174

A/Map position: 3

C/Superfamily: fruit fly testis-specific protein

C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 55;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 3 CGPC 6

RESULT 4

WTFP
 testis-specific protein (clone mast(3)gl-9) - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C/Accession: S00340

R/Kuhn, R.; Schaefer, U.; Schaefer, M.

EMBO J. 7, 447-454, 1988

A/Title: Cis-acting regions sufficient for spermatocyte-specific transcriptional and sp

A/Reference number: S00340; MUID:88211557; PMID:2835228

A/Accession: S00340

A/Molecule type: DNA

A/Residues: 1-56 <KUH>

A/Cross-references: UNIPROT:P08175; UNIPARC:UPI0000124701; EMBL:Y00831; NID:98650; PID

C/Genetics:

A/Gene: FlyBase:Mat87F

A/Cross-references: FlyBase:FBgn0002862

C/Superfamily: fruit fly testis-specific protein

C/Keywords: sex-specific protein; testis

Query Match 100.0%; Score 31; DB 1; Length 56;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 3 CGPC 6

RESULT 5

H81133

rubredoxin NMB0993 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain C/Species: Neisseria meningitidis
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C/Accession: H81133; B81888
 R/Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M. Mech. Dev. 35, 143-151, 1991
 A/Title: A cluster of four genes selectively expressed in the male germ line of Drosophila
 A/Reference number: A56565; MUID:92102953; PMID:1684716
 A/Accession: S25772
 A/Molecule type: DNA
 A/Residues: 1-63 <KUH>
 A/Cross-references: UNIPROT:Q01642; UNIPARC:UP100001246FP; EMBL:X67703; NID:911072; PIDN: A/Note: sequence extracted from NCBI backbone (NCBIN:74219, NCBIPI:74224)
 C/Genetics:
 A/Genes: Met84Da
 A/Map position: 3
 A/Intons: 13/3
 C/Superfamily: fruit fly testis-specific protein
 C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 17 CGPC 20

RESULT 8
 S25775
 testis-specific protein Met84d - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S25772; A56565
 R/Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M. Mech. Dev. 35, 143-151, 1991
 A/Title: A cluster of four genes selectively expressed in the male germ line of Drosophila
 A/Reference number: A56565; MUID:92102953; PMID:1684716
 A/Accession: S25772
 A/Molecule type: DNA
 A/Residues: 1-63 <KUH>
 A/Cross-references: UNIPROT:Q01642; UNIPARC:UP100001246FP; EMBL:X67703; NID:911072; PIDN: A/Note: sequence extracted from NCBI backbone (NCBIN:74219, NCBIPI:74224)
 C/Genetics:
 A/Genes: Met84Da
 A/Map position: 3
 A/Intons: 13/3
 C/Superfamily: fruit fly testis-specific protein
 C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 17 CGPC 20

RESULT 9
 A60136
 keratin, scale (clone CSK9) - chicken (fragment)
 C/Species: Gallus gallus (chicken)
 C/Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
 C/Accession: A60136
 R/Wilton, S.D.; Crocker, L.A.; Rogers, G.E. Biochim. Biophys. Acta 824, 201-208, 1985
 A/Title: Isolation and characterization of keratin mRNA from the scale epidermis of the
 A/Reference number: A60136; MUID:85122780; PMID:2578618
 A/Accession: A60136
 A/Molecule type: mRNA
 A/Residues: 1-73 <WIL>

Query Match 100.0%; Score 31; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 10 CGPC 13

RESULT 6
 S15676
 chorionic gonadotropin beta chain - donkey (fragment)
 C/Species: Equus asinus (donkey)
 C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S15676
 R/Leigh, S.E.A.; Stewart, F. J. Mol. Endocrinol. 4, 143-150, 1990
 A/Title: Partial cDNA sequence for the donkey chorionic gonadotropin-beta subunit sugge
 A/Reference number: S15676; MUID:90262634; PMID:2344391
 A/Accession: S15676
 A/Status: Preliminary
 A/Molecule type: mRNA
 A/Residues: 1-62 <LEI>
 A/Cross-references: UNIPROT:P19794; UNIPARC:UP100001765CA; EMBL:X53669
 C/Superfamily: pituitary glycoprotein hormone beta chain

Query Match 100.0%; Score 31; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 6 CGPC 9

RESULT 7
 S25772
 testis-specific protein Met84da - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S25772; A56565
 R/Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M. Mech. Dev. 35, 143-151, 1991
 A/Title: A cluster of four genes selectively expressed in the male germ line of Drosophila
 A/Reference number: A56565; MUID:92102953; PMID:1684716
 A/Accession: S25772
 A/Molecule type: DNA
 A/Residues: 1-63 <KUH>
 A/Cross-references: UNIPROT:Q01642; UNIPARC:UP100001246FP; EMBL:X67703; NID:911072; PIDN: A/Note: sequence extracted from NCBI backbone (NCBIN:74219, NCBIPI:74224)
 C/Genetics:
 A/Genes: Met84Da
 A/Map position: 3
 A/Intons: 13/3
 C/Superfamily: fruit fly testis-specific protein
 C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 17 CGPC 20

RESULT 8
 S25775
 testis-specific protein Met84d - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S25772; D56565
 R/Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M. Mech. Dev. 35, 143-151, 1991
 A/Title: A cluster of four genes selectively expressed in the male germ line of Drosophila
 A/Reference number: A56565; MUID:92102953; PMID:1684716
 A/Accession: S25775
 A/Molecule type: DNA
 A/Residues: 1-68 <KUH>
 A/Cross-references: UNIPROT:Q01645; UNIPARC:UP1000012EA57; EMBL:X67703; NID:911072; PIDN: A/Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBIPI:74223)
 C/Genetics:
 A/Genes: Met84d
 A/Cross-references: FlyBase:FBgn0004175
 A/Map position: 3
 C/Superfamily: fruit fly testis-specific protein
 C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 10 CGPC 13

RESULT 9
 A60136
 keratin, scale (clone CSK9) - chicken (fragment)
 C/Species: Gallus gallus (chicken)
 C/Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
 C/Accession: A60136
 R/Wilton, S.D.; Crocker, L.A.; Rogers, G.E. Biochim. Biophys. Acta 824, 201-208, 1985
 A/Title: Isolation and characterization of keratin mRNA from the scale epidermis of the
 A/Reference number: A60136; MUID:85122780; PMID:2578618
 A/Accession: A60136
 A/Molecule type: mRNA
 A/Residues: 1-73 <WIL>

Query Match 100.0%; Score 31; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 10 CGPC 13

A;Cross-references: UNIPROT:Q9YH54; UNIPARC:UPI00000FB20A; GB:M25641; NID:g212233; PIDD:
C;Superfamily: feather keratin
C;Keywords: tandem repeat
F;1-49/Region: 13-residue repeats (G-G-S-S-L-G-Y-G-G-L-Y-G-Y)

Query Match 100.0%; Score 31; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 70 CGPC 73

RESULT 10
S25773
testis-specific protein Mat84Db - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S25773; B56565

R;Kuhn, R.; Kuhn, C.; Boersch, D.; Glaeser, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991

A;Title: A cluster of four genes selectively expressed in the male germ line of *Drosophi*
A;Reference number: A56565; MUID:92102953; PMID:1684716

A;Accession: S25773
A;Molecule type: DNA
A;Residues: 1-74 <KDH>
A;Cross-references: UNIPROT:Q01643; UNIPARC:UPI000012BAE6; EMBL:X67703; NID:g11072; PIDD:
A;Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBI:P:74220)

C;Genetics:
A;Gene: Mat84Db
A;Cross-references: FlyBase:FBgn0004173

A;Map position: 3
C;Superfamily: fruit fly testis-specific protein
C;Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 9 CGPC 12

RESULT 11

I65235
testicular luteinizing hormone beta subunit - rat
C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I65235

R;Zhang, P.P.; Rannikko, A.; Huhtaniemi, I.
Biochem. Biophys. Res. Commun. 210, 858-865, 1995

A;Title: Isolation and characterization of testis-specific cDNAs for luteinizing hormone

A;Reference number: I52320; MUID:95283549; PMID:7763258

A;Accession: I65235

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-80 <RES>

A;Cross-references: UNIPROT:Q63013; UNIPARC:UPI00000E74EB; EMBL:U25803; NID:g904025; PII

C;Genetics:
A;Gene: TLRB3

C;Superfamily: pituitary glycoprotein hormone beta chain

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 49 CGPC 52

RESULT 12
B46264
thioredoxin 2 - slime mold (*Dictyostelium discoideum*) (fragment)

C;Species: *Dictyostelium discoideum*
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Oct-2004
C;Accession: B46264

R;Wetterauer, B.; Jacquot, J.P.; Veron, M.
J. Biol. Chem. 267, 9895-9904, 1992

A;Title: Thioredoxin from *Dictyostelium discoideum* as a developmentally regulated mult

A;Reference number: A46264; MUID:92250653; PMID:1577820

A;Accession: B46264

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-88 <MET>

A;Cross-references: UNIPROT:P29446; UNIPARC:UPI0000136D74; GB:M91382; NID:g167930; PIDD

C;Superfamily: thioredoxin; thioredoxin homology
F;8-88/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 31 CGPC 34

RESULT 13

B84409
thioredoxin [imported] - *Halobacterium* sp. NRC-1

C;Species: *Halobacterium* sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 05-Oct-2004
C;Accession: B84409

R;Ng, W.V.; Kennedy, S.P.; Mahapatra, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laesky, E.
; Leithauer, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; L

A;Title: Genome sequence of *Halobacterium* species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: B84409

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-89 <STO>

A;Cross-references: UNIPROT:Q9HMD0; UNIPARC:UPI0000063B9A; GB:AE004437; NID:g10581982; I

C;Genetics:
A;Gene: trxA2

C;Superfamily: thioredoxin

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 13 CGPC 16

RESULT 14

KRG4BS
keratin, feather - silver gull

C;Species: *Larus novaehollandiae* (silver gull)

C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A02850

R;O'Donnell, I.U.; Inglis, A.S.
Aust. J. Biol. Sci. 27, 369-382, 1974

A;Title: Amino acid sequence of a feather keratin from silver gull (*Larus novaeholland*

A;Reference number: A02850; MUID:75054009; PMID:4429491

A;Accession: A02850

A;Molecule type: protein

A;Residues: 1-98 <ODO>

A;Cross-references: UNIPROT:P02451; UNIPARC:UPI000012B06F
A;Experimental source: calamus of wing feathers from a single bird

A>Note: the sequence of the region 75-83 is tentative due to carry-over of residues from
A>Note: 4-Asp and 27-Glu may be amidated in the original feather
A>Note: the alternatives 39-Gln, 48-Thr, 55-Val, 56-Ala, 62-Ala, 63-Ala, 76-Ile, 78-Ser,
C:Superfamily: feather keratin
C:Keywords: blocked amino end; epidermis; feather; fibrous protein; horn; integument
F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental

Query Match 100.0%; Score 31; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 6 CGPC 9

RESULT 15
G64213
thioredoxin - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revision 16-Aug-1996 #text_change 05-Oct-2004
C:Accession: G64213
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A>Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: G64213
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <TR>
A:Cross-references: UNIPROT:P47370; UNIPARC:UPI0000136E89; GB:U39691; GB:U43967; NID:910

A:Experimental source: strain G-37
A:Genetics:
A:Genetic code: SGC3
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-90/Domain: thioredoxin homology <THR>
F:30-33/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 30 CGPC 33

RESULT 16
H6572
thioredoxin [imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H6572
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: H6572
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <STO>
A:Cross-references: UNIPROT:Q9Z7P5; UNIPARC:UPI00004461A; GB:BA000008; NID:98979031; PI
A:Experimental source: strain J138
A:Genetics:
A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 28 CGPC 31

RESULT 17
S73896
thioredoxin - Mycoplasma pneumoniae (strain ATCC 29342)
N:Alternate names: hypothetical protein A65_orf102
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C>Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S73896
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A>Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73896
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <HIM>
A:Cross-references: UNIPROT:P75512; UNIPARC:UPI0000136E8A; EMBL:AE000056; GB:U00089; NID
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: thioredoxin; thioredoxin homology
F:9-90/Domain: thioredoxin homology <TXN>

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 30 CGPC 33

RESULT 18
B71503
probable thioredoxin - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 05-Oct-2004
C:Accession: B71503
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A>Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A:Reference number: A71570; MUID:99008089; PMID:9784136
A:Accession: B71503
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <ARN>
A:Cross-references: UNIPROT:O84544; UNIPARC:UPI0000136E75; GB:AE001344; GB:AE001273; NID
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 28 CGPC 31

RESULT 19
D72052
thioredoxin CP0088 [imported] - Chlamydia pneumoniae (strains CWI029 and AR39)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C:Accession: D72052; E81614

R;Kalan, S.; Mitchell, W.; Marathe, R.; Lammell, C.; Fan, Y.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
 A;Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.
 A;Reference number: A72000; MUID:99206606; PMID:10192388
 A;Accession: D72052
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-102 <RNA>
 A;Cross-references: UNIPROT:Q927P5; UNIPARC:UPI000004461A; GB:AE001648; GB:AE001363; NID:97189018; PIDN:CAA97572.1; PDB:1J82
 A;Experimental source: strain CWL029
 R;Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of *Chlamydia trachomatis* Mopn and *Chlamydia pneumoniae* AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: E81614
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-102 <REA>
 A;Cross-references: UNIPARC:UPI000004461A; GB:AE002172; GB:AE002161; NID:97189018; PIDN:CAA97572.1; PDB:1J82
 A;Experimental source: strain AR39, HL cells
 C;Genetics: trxA; CP0088
 C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 28 CGPC 31

RESULT 20
 C81660
 thioredoxin TC0826 [imported] - *Chlamydia muridarum* (strain N195)
 C;Species: *Chlamydia muridarum*, *Chlamydia trachomatis* Mopn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
 C;Accession: C81660
 R;Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of *Chlamydia trachomatis* Mopn and *Chlamydia pneumoniae* AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: C81660
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-102 <TET>
 A;Cross-references: UNIPROT:Q9FJK3; UNIPARC:UPI0000057A90; GB:AE002349; GB:AE002160; NID:97189018; PIDN:CAA97572.1; PDB:1J82
 A;Experimental source: strain N195 (MOPn)
 C;Genetics: trxA; CP0088
 C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 28 CGPC 31

RESULT 21
 TXB2
 thioredoxin II - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: protein L1933; protein YLR043C
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
 C;Accession: S15048; A39847; S15360; S64870; B38669
 R;Gen, Z.R.
 J. Biol. Chem. 266, 1692-1696, 1991

A;Title: Yeast thioredoxin genes.
 A;Reference number: A38669; MUID:91107668; PMID:1988444
 A;Accession: S15048
 A;Molecule type: DNA
 A;Residues: 1-103 <GAN>
 A;Cross-references: UNIPROT:P22217; UNIPARC:UPI000004F943; EMBL:M59169; NID:9173027; PDB:1J82
 R;Miller, E.G.D.
 J. Biol. Chem. 266, 9194-9202, 1991
 A;Title: Thioredoxin deficiency in yeast prolongs S phase and shortens the G1 interval
 A;Reference number: A39847; MUID:91225027; PMID:2026519
 A;Accession: A39847
 A;Molecule type: DNA
 A;Residues: 1-103 <MUL>
 A;Cross-references: UNIPARC:UPI000004F943; GB:M62647; NID:9173047; PIDN:AAA35177.1; PID:9173047
 R;Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.
 Eur. J. Biochem. 23, 328-335, 1971
 A;Title: Yeast thioredoxin. Amino-acid sequence around the active-center disulfide of thioredoxin.
 A;Reference number: S05793; MUID:72100583; PMID:4945270
 A;Accession: S15360
 A;Molecule type: protein
 A;Residues: 26-34 <HAL>
 A;Cross-references: UNIPARC:UPI0000171E21
 R;Koetter, P.; Rose, M.; Entian, K.D.
 submitted to the Protein Sequence Database, May 1996
 A;Reference number: S64863
 A;Accession: S64870
 A;Molecule type: DNA
 A;Residues: 1-103 <NOE>
 A;Cross-references: UNIPARC:UPI000004F943; EMBL:Z73215; NID:91360372; PIDN:CAA97572.1; PDB:1J82
 A;Note: experimental_source strain S288C
 C;Genetics: SGD:TRX1; TR-II; MIPS:YLR043C
 A;Gene: SGD:TRX1; TR-II; MIPS:YLR043C
 A;Cross-references: SGD:S0004033; MIPS:YLR043C
 A;Map position: 12R
 C;Superfamily: thioredoxin; thioredoxin homology
 C;Keywords: redox-active disulfide
 F;2-103/Product: thioredoxin II #status predicted <MAT>
 F;9-90/Domain: thioredoxin homology <THR>
 F;30-33/Disulfide bond: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 30 CGPC 33

RESULT 22
 T39085
 thioredoxin II - fission yeast (*Schizosaccharomyces pombe*)
 N;Alternate names: thioredoxine 2
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T39085; T46567
 R;Gentles, S.; Churcher, C.M.; Wood, V.; Barrett, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, September 1997
 A;Reference number: Z21826
 A;Accession: T39085
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-103 <GEN>
 A;Cross-references: UNIPROT:O14463; UNIPARC:UPI000016205F; EMBL:Z99532; PIDN:CAB16724.1
 R;Lemaers, G.; Perret, B.; Bonin, O.; Picard, A.; Caput, D.
 submitted to the EMBL Data Library, October 1997
 A;Description: TRX2, a fission yeast stress protein.
 A;Reference number: Z23075
 A;Accession: T46567
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-103 <LEN>

A:Cross-references: UNIPARC:UPI000016205F; EMBL:AJ003819; PIDN:CAA06033.1
 A:Experimental source: strain 972(-)
 C:Genetics:
 A:Gene: trx2: SPAC7D4.07C
 A:Map position: 1
 C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 30 CGPC 33

RESULT 23
 A11228
 thioredoxin [imported] - *Listeria monocytogenes* (strain EGD-e)
 C:Species: *Listeria monocytogenes*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
 C:Accession: A11228
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltounnam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tlerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: A11228
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-103 <GLA>
 A:Cross-references: UNIPROT:Q9S36; UNIPARC:UPI00005509E; GB:NC_003210; PIDN:CAC9311.1
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: trxA
 C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 28 CGPC 31

RESULT 24
 AC1582
 thioredoxin [imported] - *Listeria innocua* (strain C1p11262)
 C:Species: *Listeria innocua*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AC1582
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltounnam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tlerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AC1582
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-103 <GLA>
 A:Cross-references: UNIPROT:Q9S36; UNIPARC:UPI00005509E; GB:AL592022; PIDN:CAC96427.1;
 A:Experimental source: strain C1p11262
 C:Genetics:
 A:Gene: trxA
 C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 28 CGPC 31

RESULT 25
 A28086
 thioredoxin - rabbit
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C>Date: 30-Jun-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: A28086
 R:Johnson, R.S.; Mathews, W.R.; Biemann, K.; Hopper, S. J. Biol. Chem. 263, 9589-9597, 1988
 A:Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined
 A:Reference number: A28086; MUID:88257078; PMID:3164311
 A:Accession: A28086
 A:Molecule type: protein
 A:Residues: 1-104 <JOH>
 A:Cross-references: UNIPROT:P08628; UNIPARC:UPI000013696
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:8-91/Domain: thioredoxin homology <THR>
 F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 31 CGPC 34

RESULT 26
 A28215
 thioredoxin - *Rhodospirillum rubrum*
 C:Species: *Rhodospirillum rubrum*
 C>Date: 28-Aug-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: A28215
 R:Johnson, T.C.; Yee, B.C.; Carlson, D.E.; Buchanan, B.B.; Johnson, R.S.; Mathews, W.R. J. Bacteriol. 170, 2406-2408, 1988
 A:Title: Thioredoxin from *Rhodospirillum rubrum*: primary structure and relation to chlorophyll
 A:Reference number: A28215; MUID:88198045; PMID:3129411
 A:Accession: A28215
 A:Molecule type: protein
 A:Residues: 1-104 <JOH>
 A:Cross-references: UNIPROT:P10473; UNIPARC:UPI0000171E24
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:7-90/Domain: thioredoxin homology <THR>
 F:29-32/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 29 CGPC 32

RESULT 27
 B37192
 thioredoxin - *Bacillus subtilis*
 C:Species: *Bacillus subtilis*
 C>Date: 31-Jan-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: B37192; H69726
 R:Chen, N.Y.; Zhang, J.J.; Paulus, H. J. Gen. Microbiol. 135, 2931-2940, 1989

A>Title: Chromosomal location of the *Bacillus subtilis* aspartokinase II gene and nucleoid
A:Reference number: A37192; MUID:9012525; PMID:2559145
A:Accession: B37192
A:Molecule type: DNA
A:Residues: 1-104 <CHE>
A:Cross-references: UNIPROT:P14949; UNIPARC:UPI000006087B; GB:U03294; GB:M26384; NID:g14
R:Kunet, S.; Ogaawara, N.; Moszer, I.; Albertini, A.M.; Allioni, G.; Azevedo, V.; Berth
C.; Bron, F.; Bouillier, S.; Busch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Frlitz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall
A.; Itoh, J.; Harwood, C.R.; Hanaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningsreth, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y.M.; Ogawa, K.; Ogiwara, A.; Oudeg, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schreier, R.; Scollone, F.; Sekiguchi, J.; Sekowska, A.; Serch
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:9804403; PMID:9384377
A:Accession: H69726
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-104 <KUN>
A:Cross-references: UNIPARC:UPI000006087B; GB:Z91118; GB:AL009126; NID:g2635200; PIDN:CM
A:Experimental source: strain 168
A:Gene: trxA
C:Genetics:
A:Map position: 70 min
A:Superfamily: thioresdoxin; thioresdoxin homology
C:Keywords: redox-active disulfide
F:9-90/Domain: thioresdoxin homology <THR>
F:29-32/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
|||||
Db 29 CGPC 32

RESULT 28
TXB1
thioresdoxin I - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: protein G7746; protein YGR209C; thioresdoxin 2
C/Species: *Saccharomyces cerevisiae*
C/Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 05-Oct-2004
C/Accession: S15049; B39847; S05793; S53932; S61947; S63858; A38669
R:Gan, Z.R.
J. Biol. Chem. 266, 1692-1696, 1991
A>Title: Yeast thioresdoxin genes.
A:Reference number: A38669; MUID:91107668; PMID:1988444
A:Accession: S15049
A:Molecule type: DNA
A:Residues: 1-104 <GAN>
A:Cross-references: UNIPROT:P22803; UNIPARC:UPI000004F91C; GB:M59169; NID:g173025; PIDN:
R:Mueller, E.G.D.
J. Biol. Chem. 266, 9194-9202, 1991
A>Title: Thioresdoxin deficiency in yeast prolongs S phase and shortens the G1 interval
A:Reference number: A39847; MUID:91225027; PMID:2026619
A:Accession: B39847
A:Molecule type: DNA
A:Residues: 1-104 <MUI>
A:Cross-references: UNIPARC:UPI000004F91C; GB:M62648; NID:g173049; PIDN:AAA5178.1; PID:
R:Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.
Eur. J. Biochem. 23, 328-335, 1971
A>Title: Yeast thioresdoxin. Amino-acid sequence around the active-center disulfide of th
A:Reference number: S05793; MUID:72100583; PMID:14945270
A:Accession: S05793

A:Molecule type: protein
A:Residues: 2;27-43;98-104 <HAL>
A:Cross-references: UNIPARC:UPI000011EC95; UNIPARC:UPI0000171E1F; UNIPARC:UPI0000171E20
A>Note: the sequence from the summary and from Fig. 5 is inconsistent with that from pag
R:Guerrero, P.; Barreiro, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pousa
submitted to the EMBL Data Library, April 1995
A:Description: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII
es, of the human.
A:Reference number: S53922
A:Accession: S53932
A:Molecule type: DNA
A:Residues: 1-104 <GUS>
A:Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:g790489; PIDN:CAA89002.1; PT
A:Experimental source: strain S288C
A:Experimental source: strain S288C
R:Song, J.M.; Cheung, E.; Rabinowitz, J.C.
submitted to the EMBL Data Library, November 1995
A:Description: Analysis of the 15.6-kb fragment encompassing the ADE3 gene.
A:Reference number: S61947
A:Accession: S61947
A:Molecule type: DNA
A:Residues: 1-104 <SON>
A:Cross-references: UNIPARC:UPI000004F91C; EMBL:U40843; NID:g1165213; PIDN:AAA85584.1;
A:Experimental source: strain GRF88
R:Guerrero, P.; Barreiro, T.; Cyrne, L.; Soares, H.; Maia e Silva, A.; Rodrigues-Pous
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64517
A:Accession: S64531
A:Molecule type: DNA
A:Residues: 1-104 <GUM>
A:Cross-references: UNIPARC:UPI000004F91C; EMBL:Z72994; NID:g1323374; PIDN:CAA97236.1; I
A:Experimental source: strain S288C
R:Guerrero, P.; Barreiro, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pous
Yeast 12, 273-280, 1996
A>Title: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII reveal
terial electron-transferring flavoproteins (beta-chain) and of the *Escherichia coli* pho
A:Reference number: S63848; MUID:97060019; PMID:8504340
A:Accession: S63858
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-104 <GUF>
A:Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:g790489; PIDN:CAA89002.1; P
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C:Genetics:
A:Gene: SGD:TRX2; TR-1; MIPS:YGR209C
A:Map position: 7R
A:Superfamily: thioresdoxin; thioresdoxin homology
C:Keywords: redox-active disulfide
F:2-104/Product: thioresdoxin I #status experimental <MAT>
F:9-91/Domain: thioresdoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 29
S77780
thioresdoxin - *Mycoplasma capricolum* (fragment)
N/Alternate names: protein MC064
C/Species: *Mycoplasma capricolum*
C/Date: 09-Oct-1997 #sequence revision 24-Oct-1997 #text change 09-Jul-2004
C/Accession: S77780; S46921
R:Bork, P.; Ozonius, C.; Casati, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.
Mol. Microbiol. 16, 955-967, 1995
A>Title: Exploring the *Mycoplasma capricolum* genome: a minimal cell reveals its physiol
A:Reference number: S77739; MUID:96059641; PMID:7476192
A:Accession: S77780

A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-104 <BOR>
A:Cross-references: UNIPROT:Q48985; UNIPARC:UPI0000083213; EMBL:Z33053; NID:G514449; PID
A:Experimental source: ATCC 27343
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGCG
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:13-93/Domain: thioredoxin homology <THR>
F:33-36/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 36

RESULT 30
H95206
thioredoxin [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Jul-2004
C:Accession: H95206
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umeyam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:2157209; PMID:11463916
A:Accession: H95206
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <KUR>
A:Cross-references: UNIPROT:Q97P88; UNIPARC:UPI00000519A5; GB:AE005672; PIDN:AAK75849.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1776
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 28 CGPC 31

RESULT 31
H98071
thioredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Streptococcus pneumoniae (stra
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: H98071
R:Hoshino, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; Dehoff, B.S.; H
e, R.; LeBlanc, D.J.; Lee, L.N.; Lektowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5703-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H98071
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <KUR>
A:Cross-references: UNIPROT:Q8DNP9; UNIPARC:UPI00000836A4; GB:AE007317; PIDN:AAL00405.1;
C:Genetics:

A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: oxidoreductase

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 28 CGPC 31

RESULT 32
A59394
thioredoxin - Clostridium pasteurianum
C:Species: Clostridium pasteurianum
C>Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 05-Oct-2004
C:Accession: B59394; A59394
R:Reynolds, C.M.; Meyer, J.; Poole, L.B.
Biochemistry 41, 1990-2001, 2002
A:Title: NADH-dependent bacterial thioredoxin reductase-like protein, in conjunction wit
A:Reference number: B59394
A:Accession: B59394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <RE1>
A:Cross-references: UNIPARC:UPI0000174DEF
R:Reynolds, C.M.; Poole, L.B.; Hammel, K.E.; Wada, K.; Buchanan, B.B.
submitted to the Protein Sequence Database, September 2001
A:Reference number: A59394
A:Accession: A59394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <RE2>
A:Cross-references: UNIPARC:UPI0000174DEF
R:Hammel, K.E.; Cornwell, K.L.; Buchanan, B.B.
Proc. Natl. Acad. Sci. USA 80, 3681-3685, 1983
A:Title: Ferredoxin/flavoprotein-linked pathway for the reduction of thioredoxin.
A:Reference number: A59432
A:Contents: annotation; purification and characterization of the protein
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 28 CGPC 31

RESULT 33
C46264
thioredoxin 3 - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Oct-2004
C:Accession: C46264
R:Welterauer, B.; Jacquot, J.P.; Veron, M.
J. Biol. Chem. 267, 9895-9904, 1992
A:Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated mul
A:Reference number: A46264; MUID:92250653; PMID:1577820
A:Accession: C46264
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-104 <MEN>
A:Cross-references: UNIPROT:P29447; UNIPARC:UPI0000136D7B; GB:M91383; NID:G167932; PIDN:
F:8-91/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 31 CGPC 34

RESULT 34

B84037
 thioredoxin trxa [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004

C/Accession: B84037

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; PMID:20512582; PMID:11058132

A/Accession: B84037

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <STO>

A/Cross-references: UNIPROT:Q9X8A8; UNIPARC:UPI00000C40CD; GB:AE001517; GB:BA000004; NIT

A/Experimental source: strain C-125

C/Genetics:

A/Gene: trxa

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 29 CGPC 32

RESULT 35

B89885

thioredoxin [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004

C/Accession: B89885

R/Kuroda, M.; Ohwa, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; PMID:21311952; PMID:11418146

A/Accession: B89885

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <KUR>

A/Cross-references: UNIPROT:Q9ZE4; UNIPARC:UPI00000D78B6; GB:BA000018; PID:g13700945; F

A/Experimental source: strain N315

C/Genetics:

A/Gene: trxa

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 29 CGPC 32

RESULT 36

D86830

thioredoxin [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C/Species: Lactococcus lactis subsp. lactis

C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004

C/Accession: D86830

R/Bolotin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A/Reference number: A86625; PMID:21235186; PMID:11337471

A/Accession: D86830

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <STO>

A/Cross-references: UNIPROT:Q9CF37; UNIPARC:UPI00000C6AAD; GB:AE005176; PID:g12724655; F

A/Experimental source: strain IL1403

C/Genetics:

A/Gene: trxa

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 28 CGPC 31

RESULT 37

C81432

thioredoxin Cj0147c [imported] - Campylobacter jejuni (strain NCTC 11168)

C/Species: Campylobacter jejuni

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004

C/Accession: C81432

R/Perkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

Nature 403, 665-668, 2000

A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy

A/Reference number: A81250; PMID:20150912; PMID:10688204

A/Accession: C81432

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <PAR>

A/Cross-references: UNIPROT:Q9PIY0; UNIPARC:UPI00000C205F; GB:AL139074; GB:AL111168; NI

A/Experimental source: serotype O2, strain NCTC 11168

C/Genetics:

A/Gene: trxa; Cj0147c

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 29 CGPC 32

RESULT 38

A30006

thioredoxin - chicken

C/Species: Gallus gallus (chicken)

C/Date: 31-Mar-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C/Accession: A30006

R/Jones, S.W.; Luk, K.C.

J. Biol. Chem. 263, 9607-9611, 1988

A/Title: Isolation of a chicken thioredoxin cDNA clone: thioredoxin mRNA is diferencia

A/Reference number: A30006; PMID:88257080; PMID:2838473

A/Accession: A30006

A/Molecule type: mRNA

A/Residues: 1-105 <JON>

A/Cross-references: UNIPROT:P08629; UNIPARC:UPI00001713BC; GB:J03882; NID:g212765; PIDN

C/Superfamily: thioredoxin; thioredoxin homology

C/Keywords: redox-active disulfide

F;32-35/Domain: thioredoxin homology <THR>

F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 39

A46264

thioredoxin 1 - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C:Date: 10-Sep-1999 #sequence_rev: 10-Sep-1999 #text_change 05-Oct-2004

C:Accession: A46264

R:Wetterauer, B.; Jacquot, J.P.; Veron, M.

J. Biol. Chem. 267, 9895-9904, 1992

A:Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated mult

A:Reference number: A46264; MUID:92250553; PMID:1577820

A:Accession: A46264

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Cross-references: UNIPROT:P29445; UNIPARC:UPI0000136DA; GB:M91384; NID:g167928; PIDN:

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F:9-92/Domain: thioredoxin homology <THR>

F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 40

JH0568

thioredoxin [validated] - human

N:Alternate names: ATL-derived factor (ADF); eosinophil cytotoxicity-enhancing factor; C

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_rev: 10-Sep-1999 #text_change 05-Oct-2004

C:Accession: JH0568; S04106; S44375; A31993; P00709; A60749; A38922; S53453; A60870

R:Jonassen, K.F.; Wells, J.R.E.

Gene 102, 221-228, 1991

A:Title: Isolation and characterization of human thioredoxin-encoding genes.

A:Reference number: JH0568; MUID:91340156; PMID:1874447

A:Accession: JH0568

A:Molecule type: DNA

A:Cross-references: UNIPROT:P10599; UNIPARC:UPI000011065C; EMBL:X54539; NID:g37455; PIDN:

R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,

EMBO J. 8, 757-764, 1989

A:Title: ATL-derived factor (ADF), an IL-2 receptor/IL-2 inducer homologous to thioredoxin

A:Reference number: S04106; MUID:89251607; PMID:2785919

A:Accession: S04106

A:Molecule type: mRNA

A:Residues: 1-105 <TAG1>

A:Cross-references: UNIPARC:UPI000011065C; GB:X77584; NID:g453963; PIDN:CAA54687.1; PID:

A:Note: this sequence has been revised in reference S44375

R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,

EMBO J. 13, 2244, 1994

A:Reference number: S44375; MUID:94244626; PMID:8187776

A:Contents: erratum

A:Accession: S44375

A:Molecule type: mRNA

A:Residues: 1-105 <TAG2>

A:Cross-references: UNIPARC:UPI000011065C; EMBL:X77584; NID:g453963; PIDN:CAA54687.1; PI

R:Wollman, B.E.; d'Aurion, L.; Rimsky, L.; Shaw, A.; Jacquot, J.P.; Wingfield, P.; Grabe

J. Biol. Chem. 263, 15506-15512, 1988

A:Title: Cloning and expression of a cDNA for human thioredoxin.

A:Reference number: A31993; MUID:89008454; PMID:3170595

A:Accession: A31993

A:Molecule type: mRNA
 A:Residues: 1-78, 'N', '40-73', 'T', '75-105 <MOU>
 A:Cross-references: UNIPARC:UPI000003066B; GB:J04026; NID:g339648; PIDN:AAV74596.1; PID

R:Martin, H.; Dean, M.

Biochem. Biophys. Res. Commun. 175, 123-128, 1991

A:Title: Identification of a thioredoxin-related protein associated with plasma membran

A:Reference number: P00709; MUID:91151337; PMID:1998498

A:Accession: P00709

A:Molecule type: protein

A:Residues: 2-13, 'X', '15 <MAR>

A:Cross-references: UNIPARC:UPI0000171E19

R:Silberstein, D.S.; Ali, M.H.; Baker, S.L.; David, J.R.

J. Immunol. 143, 979-983, 1989

A:Title: Human eosinophil cytotoxicity-enhancing factor. Purification, physical charac

A:Reference number: A60749; MUID:89309777; PMID:2745979

A:Accession: A60749

A:Molecule type: protein

A:Residues: 2-12, 'K', '14-15, 'XX', '18-19, 'X', '21-22 <STL>

A:Cross-references: UNIPARC:UPI0000171E1A

A:Note: the abstract is inconsistent with figure 4 in having one undetermined residue a

R:Rimsky, L.; Makasugi, H.; Ferrara, P.; Robin, P.; Capdevielle, J.; Turcz, T.; Friedell

J. Immunol. 136, 3304-3310, 1986

A:Title: Purification to homogeneity and NH-2-terminal amino acid sequence of a novel i

A:Reference number: A38922; MUID:86169684; PMID:3485686

A:Accession: A38922

A:Molecule type: protein

A:Residues: 2-16 <MAX>

A:Cross-references: UNIPARC:UPI0000171E1B

R:Dean, M.F.; Martin, H.; Sansom, P.A.

Biochem. M.F. 304, 861-867, 1994

A:Title: Characterization of a thioredoxin-related surface protein.

A:Reference number: S53453; MUID:95118305; PMID:7818492

A:Accession: S53453

A:Molecule type: protein

A:Residues: 1-21, '38-57 <DEA>

A:Cross-references: UNIPARC:UPI00000353C5; UNIPARC:UPI0000171E1C

A:Note: described to be a surface-associated thioredoxin

R:Makasugi, H.; Rimsky, L.; Mahe, Y.; Kamel, A.M.; Fradelizi, D.; Turcz, T.; Bertoglio,

Proc. Natl. Acad. Sci. U.S.A. 84, 804-808, 1987

A:Title: Epstein-Barr virus-containing B-cell line produces an interleukin 1 that it use

A:Reference number: A60870; MUID:87118252; PMID:3027706

A:Accession: A60870

A:Contents: annotation

A:Reference number: A65533; PDB:1ERT

A:Contents: annotation; X-ray crystallography, 1.7 angstroms, reduced form, residues 1-1

R:Weichsel, A.; Gadsdask, J.R.; Powis, G.; Montfort, W.R.

submitted to the Brookhaven Protein Data Bank, February 1996

A:Reference number: A65534; PDB:1ERT

A:Contents: annotation; X-ray crystallography, 2.1 angstroms, oxidized form, residues 1-

R:Forman-Kay, J.D.; Clore, G.M.; Gronenborn, A.M.

submitted to the Brookhaven Protein Data Bank, December 1990

A:Reference number: A50924; PDB:4TRX

A:Contents: annotation; conformation by (1)H-NMR, residues 1-73, 'T', '75-105

R:Forman-Kay, J.D.; Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.

Biochemistry 30, 2685-2698, 1991

A:Title: High-resolution three-dimensional structure of reduced recombinant human thior

A:Reference number: A38953; MUID:91159399; PMID:2001356

A:Contents: annotation; conformation by (1)H- and (15)N-NMR

C:Comment: This small ubiquitous protein functions in many intracellular biological path

A:Gene: GDB:TXN

A:Cross-references: GDB:120475; OMIM:187700

A:Map position: 9q31-9q31

A:Introns: 8/3; 43/3; 63/3; 85/3

C:Superfamily: thioredoxin; thioredoxin homology

F:2-105/Product: thioredoxin #status experimental <MAT>

F:9-92/Domain: thioredoxin homology <THR>

F:32-35/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 41

thioredoxin - rhesus macaque
 C/Species: Macaca mulatta (rhesus macaque)
 C/Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C/Accession: J50667
 R/An, G.; Wu, R.
 Biochem. Biophys. Res. Commun. 183, 170-175, 1992
 A/Title: Thioredoxin gene expression is transcriptionally up-regulated by retinol in monocytes
 A/Reference number: J50667; MUID:92181438; PMID:1543467
 A/Accession: J50667
 A/Molecule type: mRNA
 A/Residues: 1-105 <ANG>
 A/Cross-references: UNIPROT:P29451; UNIPARC:UPI000016C493; GB:M64643; NID:G342338; PIDN:C/Superfamily: thioredoxin; thioredoxin homology
 C/Keywords: redox-active disulfide
 F/3-92/Domain: thioredoxin homology <THR>
 F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 42

S04107
 thioredoxin - mouse
 N/Alternate names: ATL-derived factor (ADF)
 C/Species: Mus musculus (house mouse)
 C/Date: 21-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 05-Oct-2004
 C/Accession: J04068; S44376; S04107
 R/Matsui, M.; Taniguchi, Y.; Hirota, K.; Takeo, M.; Yodoi, J.
 Gene 152, 165-171, 1995
 A/Title: Structure of the mouse thioredoxin-encoding gene and its processed pseudogene.
 A/Reference number: J04068; MUID:55137382; PMID:7835635
 A/Accession: J04068
 A/Molecule type: DNA
 A/Residues: 1-105 <MAT>
 A/Cross-references: UNIPROT:P10639; UNIPARC:UPI0000163891; DDBJ:D21855; NID:G517128
 R/Tagaya, Y.; Maeda, Y.; Mitsu, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai, E.
 EMBO J. 13, 2244, 1994
 A/Reference number: S44375; MUID:94244626; PMID:8187776
 A/Contents: extratum
 A/Accession: S44376
 A/Molecule type: mRNA
 A/Residues: 1-105 <TG1>
 A/Cross-references: UNIPARC:UPI0000163891; EMBL:X77585; NID:G453971; PIDN:CA54688.1; PI
 R/Tagaya, Y.; Maeda, Y.; Mitsu, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai, E.
 EMBO J. 8, 757-764, 1989
 A/Title: ATL-derived factor (ADF), an IL-2 receptor/Trac inducer homologous to thioredoxin
 A/Reference number: S04106; MUID:89251607; PMID:2785919
 A/Accession: S04107
 A/Molecule type: mRNA
 A/Residues: 1-93, 'N', '94-96, 'ALT', '100-104, 'S', <TG2>
 A/Cross-references: UNIPARC:UPI0000171E1E; GB:X77585
 C/Comment: This small ubiquitous protein functions in many intracellular biological path
 C/Genetic: A:Gene: MGI:Txn
 A/Cross-references: MGI:36258
 A/Map position: 4:24.6
 A/Intons: 29/2; 44/1; 84/2
 C/Superfamily: thioredoxin; thioredoxin homology

C/Keywords: redox-active disulfide
 F/3-92/Domain: thioredoxin homology <THR>
 F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 43

S04352
 thioredoxin - rat
 N/Alternate names: thioredoxin-related surface protein SASP
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Mar-1990 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C/Accession: S04352; S66372
 R/Tonnesen, K.F.; Robins, A.J.; Wells, J.R.E.
 Nucleic Acids Res. 17, 3973, 1989
 A/Title: Nucleotide sequence of a cDNA encoding rat thioredoxin.
 A/Reference number: S04352; MUID:89282399; PMID:2734107
 A/Accession: S04352
 A/Molecule type: mRNA
 A/Residues: 1-105 <TON>
 A/Cross-references: UNIPROT:P11232; UNIPARC:UPI000003066A; EMBL:X14878; NID:G57385; PIDN:
 R/Dean, M.F.; Martin, H.; Sansom, P.A.
 Biochem. J. 304, 861-867, 1994
 A/Title: Characterization of a thioredoxin-related surface protein.
 A/Reference number: S53453; MUID:95118305; PMID:7818492
 A/Accession: S66372
 A/Molecule type: protein
 A/Residues: 221 <DBA>
 A/Cross-references: UNIPARC:UPI0000171E1D
 A/Note: 12-Lys, 15-Gly, 16-Leu, 17-Gln, and 18-Leu were also found
 C/Superfamily: thioredoxin; thioredoxin homology
 C/Keywords: redox-active disulfide
 F/2-105/Product: thioredoxin #status experimental <MAT>
 F/3-92/Domain: thioredoxin homology <THR>
 F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 44

TXFK
 thioredoxin - coryneform bacterium ATCC11425
 C/Species: coryneform bacterium ATCC11425
 C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 05-Oct-2004
 C/Accession: A00281
 R/Meng, M.; Hogenkamp, H.P.C.
 J. Biol. Chem. 256, 9174-9182, 1981
 A/Title: Purification, characterization, and amino acid sequence of thioredoxin from Co
 A/Reference number: A00281; MUID:81244365; PMID:7021558
 A/Accession: A00281
 A/Molecule type: protein
 A/Residues: 1-105 <MEN>
 A/Cross-references: UNIPROT:P00275; UNIPARC:UPI0000136D69
 A/Note: the source was designated as Corynebacterium nephridii
 C/Comment: Thioredoxins are ubiquitous small hydrogen carrier proteins that participate
 C/Superfamily: thioredoxin; thioredoxin homology
 C/Keywords: redox-active disulfide
 F/8-91/Domain: thioredoxin homology <THR>
 F/30-33/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 45

S76386

thioredoxin M-1 - Synechocystis sp. (strain PCC 6803)

N:Alternate names: protein slr0233

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76386

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A:Reference number: S74322; PMID:97061201; PMID:8905231

A:Accession: S76386

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-105 <KAN>

A:Cross-references: UNIPROT:P52232; UNIPARC:UPI0000136D6; EMBL:D64000; GB:AE001339; NID

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: trxm-1

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 46

B97700

thioredoxin [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004

C:Accession: B97700

R:ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; PMID:21442074; PMID:11557893

A:Accession: B97700

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <KUR>

A:Cross-references: UNIPROT:Q92JRS; UNIPARC:UPI0000136E9A; GB:AE006914; PIDD:AAI02540.1;

C:Genetics:

A:Gene: trxA

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 47

AG2042

thioredoxin [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004

C:Accession: AG2042

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A:Reference number: AB1807; PMID:21595285; PMID:11759840

A:Accession: AG2042

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <KUR>

A:Cross-references: UNIPROT:Q8YV71; UNIPARC:UPI00000CE247; GB:BA000019; PIDD:BAW73592.1,

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all1893

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 48

D97279

thioredoxin [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004

C:Accession: D97279

R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.D.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc

A:Reference number: A96900; PMID:21359325; PMID:21359325

A:Accession: D97279

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <KUR>

A:Cross-references: UNIPROT:Q97EM7; UNIPARC:UPI00000CA715; GB:AE001437; PIDD:AAK81023.1,

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3083

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 49

A35135

thioredoxin - Rhodospirillum rubrum

C:Species: Rhodospirillum rubrum

C:Date: 27-Jul-1990 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: A35135; A30508

R:Fillie, S.; Breton, J.C.; Clement-Metral, J.D.; Galibert, F.

J. Bacteriol. 172, 1556-1561, 1990

A:Title: Cloning, nucleotide sequence, and expression of the Rhodospirillum rubrum

A:Reference number: A35135; PMID:90170874; PMID:2137818

A:Accession: A35135

A:Molecule type: DNA

A:Residues: 1-106 <PII>

A:Cross-references: UNIPROT:P08058; UNIPARC:UPI000016FF78; GB:M33806; NID:G152044; PIDD

A:Experimental source: strain Y
R:Clemens-Metral, J.D.; Holmgren, A.; Cambillau, C.; Joernvall, H.; Eklund, H.; Thomas, Eur. J. Biochem. 172, 413-419, 1998
A:Title: Amino acid sequence determination and three-dimensional modelling of thioredoxin
A:Reference number: A30508; MUID:88166714; PMID:3280308
A:Accession: A30508
A:Molecule type: protein
A:Residues: 2-63, 'Z', 65-106 <CUE>
A:Cross-references: UNIPARC:UPI0000171E23
A:Experimental source: strain Y
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 31 CGPC 34

RESULT 50
S33357
thioredoxin - Streptomyces aureofaciens (fragment)
C:Species: Streptomyces aureofaciens
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33357
R:Labudova, O.; Nemethova, M.; Turna, J.; Kollarova, M.
submitted to the EMBL Data Library, April 1993
A:Description: PCR cloning of a protein-coding part of the thioredoxin gene from Streptococcus
A:Reference number: S33357
A:Accession: S33357
A:Molecule type: DNA
A:Residues: 1-106 <LAB>
A:Cross-references: UNIPROT:P33791; UNIPARC:UPI0000136E9D; EMBL:X72799; NID:9297872; P11
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 31 CGPC 34

RESULT 51
H64622
thioredoxin - Helicobacter pylori
C:Species: Helicobacter pylori
A:Variety: strains J99, 26695
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: H64622; C71890
R:Tombl, J.F.; White, O.; Kellavag, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatkhat, H.G.; Glodok, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.; Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: H64622
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <TOM>
A:Cross-references: UNIPROT:P56430; UNIPARC:UPI0000136E82; GB:AE000594; GB:AE000511; NIT
A:Experimental source: strain 26695
R:Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

; Ives, C.; Gibson, R.; Werberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: C71890

A:Molecule type: DNA
A:Residues: 1-106 <ARN>
A:Cross-references: UNIPARC:UPI0000136E82; GB:AE001507; GB:AE001439; NID:94155326; PIDN
A:Experimental source: strain J99
C:Genetics:

A:Gene: trxA; HP0824
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 30 CGPC 33

RESULT 52
A49888
thioredoxin - Penicillium chrysogenum
C:Species: Penicillium chrysogenum
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 05-Oct-2004
C:Accession: A49888; S3886
R:Cohen, G.; Argaman, A.; Schreiber, R.; Mslorati, M.; Aharonowitz, Y.
J. Bacteriol. 176, 973-984, 1994
A:Title: The thioredoxin system of Penicillium chrysogenum and its possible role in pen
A:Reference number: A49888; MUID:94148789; PMID:8106340
A:Accession: A49888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <COH>
A:Cross-references: UNIPROT:P34723; UNIPARC:UPI0000136E91; EMBL:X76120; NID:9426468; P1
C:Genetics:
A:Gene: trxA
A:Insertions: 8/2
C:Superfamily: thioredoxin; thioredoxin homology
F:10-92/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 53
AG2579
thioredoxin C-1 trxA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004
C:Accession: AG2579
R:Wood, D.W.; Serubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavain, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2579
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <KUR>
A:Cross-references: UNIPROT:Q8UJA6; UNIPARC:UPI0000164451; GB:AE008688; PIDN:AL41053.1
A:Experimental source: strain C58 (Dupont)
C:Genetics:

A:Gene: trxA
A:Map position: circular chromosome
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 31 CGPC 34

RESULT 54

A32956
thioredoxin m - *Synechococcus* sp.

C:Species: *Synechococcus* sp.
C>Date: 17-Jul-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C/Accession: A32956; A30842
R:Miller, E.G.D.; Buchanan, B.B.

J. Biol. Chem. 264, 4008-4014, 1989

A>Title: Thioredoxin is essential for photosynthetic growth. The thioredoxin m gene of *A*
A:Reference number: A32956; MUID:89139466; PMID:2492995

A:Residues: 1-107 <MUL>
A:Molecule type: DNA

A:Cross-references: UNIPARC:UPI0000001823; GB:J04475; NID:g142153; PIDN:AAA23057.1; PID:
A>Note: the source is designated as *Anacystis nidulans* R2, which is also called *Synechoc*

C:Genetics:
A:Gene: trxm

C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide

F:10-93/Domain: thioredoxin homology <THR>
F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 55

TXAI
thioredoxin 1 - *Anabaena* sp.

C:Species: *Anabaena* sp.
C>Date: 31-Dec-1988 #sequence_revision 11-Apr-1997 #text_change 05-Oct-2004

C/Accession: I39624; A23910
R:Idm, C.

J. Bacteriol. 168, 1258-1264, 1986

A>Title: Cloning, expression, and characterization of the *Anabaena* thioredoxin gene in *E*
A:Reference number: I39624; MUID:87057030; PMID:3096973

A:Accession: I39624
A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA
A:Residues: 1-107 <RES>
A:Cross-references: UNIPARC:UPI00001655B5; GB:M14736; NID:g142117; PIDN:AAA22049.1; PID:

J. Biochem. 1985, 9567-9573, 1985
R:Biochem. 260, 9567-9573, 1985

A>Title: The primary structure of thioredoxin from the filamentous cyanobacterium *Anaba*
A:Reference number: A23910; MUID:85261357; PMID:3296769

A:Accession: A23910
A:Molecule type: protein

A:Residues: 2-107 <GLB>
A:Cross-references: UNIPARC:UPI0000136D66

A:Experimental source: PCC 7119, ATCC 29151
C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: heat-stable protein; redox-active disulfide
F:2-107/Product: thioredoxin #status experimental <MAT>

F:10-93/Domain: thioredoxin homology <THR>
F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 56

A26622
thioredoxin - *Chromatium vinosum*

C:Species: *Chromatium vinosum*
C>Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C/Accession: A26622
R:Johnson, R.S.; Blemann, K.

Biochemistry 26, 1209-1214, 1987

A>Title: The primary structure of thioredoxin from *Chromatium vinosum* determined by high
A:Reference number: A26622; MUID:87185419; PMID:3567166

A:Accession: A26622
A:Molecule type: protein

A:Residues: 1-107 <JOH>
A:Cross-references: UNIPROT:P09857; UNIPARC:UPI0000136E76

A>Note: unidentified residues are Ile or Leu
C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: heat-stable protein; redox-active disulfide
F:10-93/Domain: thioredoxin homology <THR>

F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 57

S31915
thioredoxin - red alga (*Cyanidium caldarium*)

C:Species: *Cyanidium caldarium*
C>Date: 03-Mar-1994 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C/Accession: S31915; S45488
R:Langsdorf, A.; Emich, A.; Zetsche, K.

submitted to the EMBL Data Library, February 1993
A:Description: A thioredoxin gene is located upstream of rbcLs in the unicellular red al

A:Reference number: S31915
A:Accession: S31915

A:Molecule type: DNA
A:Residues: 1-107 <LAN>

A:Cross-references: UNIPROT:P37395; UNIPARC:UPI0000136E7B; EMBL:Z21723; NID:g14402; PIDN:
R:Ohta, N.; Kawano, S.; Kuroiwa, T.

Curr. Genet. 26, 136-138, 1994

A>Title: Physical map of the plastid genome of the unicellular red alga *Cyanidium calda*
A:Reference number: S45488; MUID:95094309; PMID:8001167

A:Accession: S45488
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 'M', '6', 'IDEV', '11-12', 'DT', '15-16', 'LQ', '19', 'HQ', '22-38', 'A', '40', 'IL', '43-44', 'I', '46-4
A:Cross-references: UNIPARC:UPI000000A275B

C:Genetics:
A:Gene: trx

C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide

F:10-93/Domain: thioredoxin homology <THR>
F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 32 CGPC 35

RESULT 58

thioredoxin-like protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: S47867
R:Salz, H.K.; Flickinger, T.W.; Mitterdorf, E.; Pelllicena-Palle, A.; Petaschek, J.P.; Bro
Genetics 136, 1075-1086, 1994
A>Title: The *Drosophila* maternal effect locus *deadhead* encodes a thioredoxin homolog reg
A:Reference number: S47867, PMID:94274010; PMID:7516301
A:Accession: S47867
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <SAL>
A:Cross-references: UNIPROT:P47938; UNIPARC:UPI0000124A52; EMBL:L27072; NID:G435591; PIR
C:Genetics:
A:Gene: FlyBase:dhd
A:Cross-references: FlyBase:FBgn0011761
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 59

thioredoxin A - red alga (*Porphyra purpurea*) chloroplast
S73146
C:Species: *Porphyra purpurea*
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S73146
R:Reich, M.; Munnoliand, J.
Plant Mol. Biol. Rep. 13, 333-335, 1995
A>Title: Complete nucleotide sequence of the *Porphyra purpurea* chloroplast genome.
A:Reference number: S73108
A:Accession: S73146
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-107 <REI>
A:Cross-references: UNIPROT:P51225; UNIPARC:UPI0000136E93; EMBL:U88604; NID:G1276652; PI
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:
A:Gene: trxa
A:Genome: chloroplast
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 60
S46521
thioredoxin - *Porphyra yezoensis* chloroplast

C:Species: chloroplast *Porphyra yezoensis*
C>Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: S46521
R:Reynolds, A.E.; Chesnick, J.M.; Woolford, J.; Catcolico, R.A.
Plant Mol. Biol. 25, 13-21, 1994
A>Title: Chloroplast encoded thioredoxin genes in the red algae *Porphyra yezoensis* and *C*
A:Reference number: S46521; PMID:94272009; PMID:8003693
A:Accession: S46521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <REV>
A:Cross-references: UNIPROT:P50254; UNIPARC:UPI0000136B94; EMBL:X76612; NID:G509276; PIR
C:Genetics:
A:Genome: chloroplast
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 61

hypothetical protein Y44E3A.3 - *Caenorhabditis elegans*
T33843
C:Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33843
R:Woesner, J.; Graves, T.; Keppler, D.
submitted to the EMBL Data Library, November 1998
A>Description: The sequence of *C. elegans* cosmid Y44E3A.
A:Reference number: Z21422
A:Accession: T33843
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-107 <MOE>
A:Cross-references: UNIPROT:Q9TXV8; UNIPARC:UPI0000077021; EMBL:AF106589; PIDN:AACT8230
A:Experimental source: strain Bristol N2; clone Y44E3A
C:Genetics:
A:Gene: CESP:Y44E3A.3
A:Map position: 1
A:introns: 31/2
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 32 CGPC 35

RESULT 62

S46958
thioredoxin A - *Synechocystis* sp. (strain PCC 6803)
N:Alternate names: protein slr0623
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S46958; S76679
R:Navarro, F.; Florencio, F.J.
submitted to the EMBL Data Library, July 1994
A>Description: The gene encoding for thioredoxin (trxA) in the cyanobacterium *Synechoc*
A:Reference number: S46957
A:Accession: S46958
A:Molecule type: DNA

A;Residues: 1-107 <NAV>
A;Cross-references: UNIPROT:P52231; UNIPARC:UPI0000164C7C; EMBL:X80486; NID:9515939; PID: R; Kaneo, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamiu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76679
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-107 <RAN>
A;Cross-references: UNIPARC:UPI0000164C7C; EMBL:D64004; GB:AB001339; NID:91001701; PID: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: trxA
C;Superfamily: thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
F;10-93/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active <status predicted>

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
DB 32 CGPC 35

RESULT 63
T02814
thioredoxin TRXR1 [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: B81458; T02814
R;Wyle, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: B81458
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <PYL>
A;Cross-references: UNIPROT:Q25345; UNIPARC:UPI000007DADA; GB:AE001274; NID:93264850; PID: A;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
A;Gene: TRXR1
A;Map position: 1
C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
DB 31 CGPC 34

RESULT 64
B53307
thioredoxin - Streptomyces clavuligerus
C;Species: Streptomyces clavuligerus
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 05-Oct-2004
C;Accession: B53307
R;Cohen, G.; Yanko, M.; Mislovati, M.; Argaman, A.; Schreiber, R.; Av-Gay, Y.; Aharonov, J. Bacteriol. 175, 5159-5167, 1993
A;Title: Thioredoxin-thioredoxin reductase system of Streptomyces clavuligerus: sequence
A;Reference number: A53307; MUID:93352422; PMID:8349555
A;Accession: B53307
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-107 <COH>
A;Cross-references: UNIPROT:Q05739; UNIPARC:UPI0000136E9E; GB:Z21946; NID:9287916; PID: C;Genetics:
A;Gene: trxA
A;Start codon: GTG
C;Superfamily: thioredoxin; thioredoxin homology
F;11-93/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
DB 33 CGPC 36

RESULT 65
AD1813
thioredoxin [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004
C;Accession: AD1813
R;Kaneoko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyach, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *An*
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD1813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <KUR>
A;Cross-references: UNIPROT:P06544; UNIPARC:UPI00001655B5; GB:BA000019; PID:BA877576.1
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: trxA
C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
DB 32 CGPC 35

RESULT 66
AH3504
thioredoxin C-1 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 05-Oct-2004
C;Accession: AH3504
R;Daly-Vachio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3504
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <KUR>
A;Cross-references: UNIPROT:Q8YB56; UNIPROT:Q8FYX9; UNIPARC:UPI00000582C9; GB:AE008917;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI2022
A;Map position: 1
C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 67

E64047
Chloredoxin - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: E64047
R/Flaeschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; PMID:95350630; PMID:7542800
A/Accession: E64047
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-107 <TIGR>
A/Cross-references: UNIPROT:P43785; UNIPARC:UPI0000136E81; GB:U32693; GB:L42023; NID:G15
A/Note: named as homolog to a protein from *Anacyetis nidulans*
C/Superfamily: Chloredoxin; thioresoxin homology
C/Keywords: redox-active disulfide
F/10-93/Domains: thioresoxin homology <THR>
F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
|||||
Db 32 CGPC 35

RESULT 68

G82991
Chloredoxin PA5240 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: G82991
R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizioguchi, S.D.; Warren, P.; Hickey, M.J.; Braham, S.; Van, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, .; Loty, S.; Olson, M.V. Nature 406, 959-964, 2000
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A/Reference number: A82950; PMID:20437337; PMID:10984043
A/Accession: G82991
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-108 <STO>
A/Cross-references: UNIPROT:Q9X2T1; UNIPARC:UPI0000136E95; GB:AE004936; GB:AE004091; NID:G15
A/Experimental source: strain PA01
C/Genetics:
A/Gene: trxA; PA5240
C/Superfamily: thioresoxin; thioresoxin homology

Query Match 100.0%; Score 31; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
|||||
Db 33 CGPC 36

RESULT 69

B55124
thioresoxin - *Chlorobium limicola* f. sp. *thiosulfatophilum*

C/Species: *Chlorobium limicola* f. sp. *thiosulfatophilum*
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
C/Accession: B55124; A27801
R/Biemann, K.; Papayannopoulos, I.A. Acc. Chem. Res. 27, 370-378, 1994
A/Title: Amino acid sequencing of proteins.
A/Reference number: A55124
A/Accession: B55124
A/Molecule type: protein
A/Residues: 1-108 <BIR>

A/Cross-references: UNIPARC:UPI0000174DEC
A/Note: unidentified residues are Ile or Leu
A/Note: the species is identified as *Chlorobium thiosulfatophilum*
R/Matthews, W.R.; Johnson, R.S.; Corwell, K.L.; Johnson, T.C.; Buchanan, B.B.; Biemann, J. Biol. Chem. 262, 7537-7545, 1987
A/Title: Mass spectrometrically derived amino acid sequence of thioresoxin from *Chlorobium*
A/Reference number: A27801; PMID:87222370; PMID:3294835
A/Accession: A27801
A/Molecule type: protein
A/Residues: 1-15, 'XX', 18-41, 'X', 43-44, 'X', 46-53, 'XX', 56-65, 'X', 67-74, 'X', 76-78, 'XX', 81-85
A/Cross-references: UNIPARC:UPI0000174DBD
A/Experimental source: strain Tassajara
A/Note: unidentified residues are Ile or Leu
A/Note: the species is identified as *Chlorobium thiosulfatophilum*
C/Superfamily: Chloredoxin; thioresoxin homology
C/Keywords: photosynthesis; redox-active disulfide
F/10-93/Domains: thioresoxin homology <THR>
F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
|||||
Db 32 CGPC 35

RESULT 70

AD0471
thioresoxin 1 [imported] - *Yersinia pestis* (strain CO92)
C/Species: *Yersinia pestis*
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: AD0471
R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M.B.; Deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, Nature 413, 523-527, 2001
A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; PMID:21470413; PMID:11586360
A/Accession: AD0471
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-108 <KUR>
A/Cross-references: UNIPROT:Q8ZAD9; UNIPARC:UPI00000DC68C; GB:AL590842; PIDN:CAC93336.1
A/Genetics:
A/Gene: trxA
C/Superfamily: thioresoxin; thioresoxin homology

Query Match 100.0%; Score 31; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
|||||
Db 33 CGPC 36

Search completed: February 23, 2006, 00:42:24
Job time: 40.5 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:31:42 ; Search time 146.5 Seconds
(without alignments)
28.895 Million cell updates/sec

Title: US-10-660-118a-2
Perfect score: 31
Sequence: 1 XCGPCX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 1000 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	35	1 SCXP_ANDMA	P01498 androcyon
2	31	100.0	36	1 BS14_BUTSI	P59887 butrus sind
3	31	100.0	38	2 O46621_TAPIN	O46621 tapirus ind
4	31	100.0	42	2 O46620_EQUUS	O46620 equus asinu
5	31	100.0	42	2 Q23947_DROHY	Q23947 drosophila
6	31	100.0	49	2 Q23948_DROHY	Q23948 drosophila
7	31	100.0	51	2 Q8MLN5_DROME	Q8MLN5 drosophila
8	31	100.0	52	2 O6QAU0_DROMA	O6QAU0 drosophila
9	31	100.0	55	1 MS84C_DROME	O01644 drosophila
10	31	100.0	55	2 O6QAT9_DROSI	O6QAT9 drosophila
11	31	100.0	55	2 O6QAU1_DROMA	O6QAU1 drosophila
12	31	100.0	56	1 MS87F_DROME	P08175 drosophila
13	31	100.0	56	2 O595V9_NEILA	O595V9 neisseria l
14	31	100.0	56	2 O5F8A3_NEIG1	O5F8A3 neisseria g
15	31	100.0	56	2 Q7DDJ1_NEIMB	Q7DDJ1 neisseria m
16	31	100.0	56	2 O9UON3_NEIMA	O9UON3 neisseria m
17	31	100.0	58	2 O6QAT8_DROSI	O6QAT8 drosophila
18	31	100.0	59	1 SCCX_MESMA	O6QAT8 drosophila
19	31	100.0	59	1 SCCX_MESMA	O6QAT8 drosophila
20	31	100.0	60	2 O71DA0_DROYA	O9b1w4 mesobuthus
21	31	100.0	60	2 O8MSH6_DROYA	O8MSH6 drosophila
22	31	100.0	61	2 O8T4O3_DROME	O8T4O3 drosophila
23	31	100.0	62	1 SCIT_MESTA	O8T4O3 drosophila
24	31	100.0	63	1 MS84A_DROME	P81761 mesobuthus
25	31	100.0	64	2 O8MI19_SHEEP	O8MI19 ovis aries
26	31	100.0	66	2 O6IMK3_PIG	O6IMK3 sus scrofa
27	31	100.0	67	2 O9VW83_DROME	O9VW83 drosophila
28	31	100.0	69	2 O6ERU8_ORYSA	O6ERU8 oryza sativ
29	31	100.0	71	2 O7PK85_ANOGA	O7PK85 anopheles g
30	31	100.0	72	1 MS84D_DROME	O01645 drosophila
31	31	100.0	72	2 O5TSU4_ANOGA	O5TSU4 anopheles g

32	31	100.0	72	2 O4V3I2_DROME	O4V3I2 drosophila
33	31	100.0	72	2 O74DK8_GEOSL	O74DK8 geobacter s
34	31	100.0	72	2 O4KXV5_MOUSE	O4KXV5 mus musculu
35	31	100.0	73	2 O6ERU3_ORYSA	O6ERU3 oryza sativ
36	31	100.0	73	2 O9YH54_CHICK	O9YH54 gallus gall
37	31	100.0	74	1 MS84B_DROME	O01643 drosophila
38	31	100.0	75	2 O5YW29_NOCFA	O5YW29 nocardia fa
39	31	100.0	75	2 O82DM2_STEAM	O82DM2 streptomyce
40	31	100.0	75	2 O4RP51_TETNG	O4RP51 tetraodon n
41	31	100.0	76	2 O6UYH8_9CAUD	O6UYH8 burkholderi
42	31	100.0	76	2 O741I4_MYCPA	O741I4 mycobacteri
43	31	100.0	77	2 O8XHP3_CLOPE	O8XHP3 clostridium
44	31	100.0	77	2 O4SJ47_TETNG	O4SJ47 tetraodon n
45	31	100.0	80	2 O9VJMS_DROME	O9VJMS drosophila
46	31	100.0	80	2 O95JG5_BOVIN	O95JG5 bos taurus
47	31	100.0	80	2 O95JG6_BOVIN	O95JG6 bos taurus
48	31	100.0	80	2 O630I3_RAT	O630I3 rattus norv
49	31	100.0	80	2 O4T7B7_TETNG	O4T7B7 tetraodon n
50	31	100.0	82	2 O46622_CERSI	O46622 ceratotheri
51	31	100.0	83	2 O4ZC47_9VIRU	O4ZC47 bacterioph
52	31	100.0	84	2 O60744_HUMAN	O60744 homo sapien
53	31	100.0	84	2 O6J821_9VIRU	O6J821 actinoplane
54	31	100.0	84	2 O6WMB8_ORYSA	O6WMB8 oryza sativ
55	31	100.0	85	2 O16275_HUMAN	O16275 homo sapien
56	31	100.0	85	2 O5T936_HUMAN	O5T936 homo sapien
57	31	100.0	87	2 O8W710_9CAUD	O8W710 cyanophage
58	31	100.0	87	2 O9C922_ARATH	O9C922 arabidopsis
59	31	100.0	88	1 THIO2_DICDI	P29446 dictyostell
60	31	100.0	88	2 O5V0J2_HALMA	O5V0J2 haloarcula
61	31	100.0	88	2 O8P2O6_METMA	O8P2O6 methanosc
62	31	100.0	88	2 O71UV5_HORSE	O71UV5 equus cabal
63	31	100.0	88	2 O6ZHP3_BURMA	O6ZHP3 burkholderi
64	31	100.0	89	2 O9HMD0_HALSA	O9HMD0 halobacteri
65	31	100.0	89	2 O46618_EQUZE	O46618 equus zebra
66	31	100.0	89	2 O46619_EQUHM	O46619 equus hemio
67	31	100.0	89	2 O4HCJ2_9DBIO	O4HCJ2 deinococcus
68	31	100.0	89	2 O4LEN8_PAROL	O4LEN8 paraliichthy
69	31	100.0	89	2 O4LEP0_PAROL	O4LEP0 paraliichthy
70	31	100.0	90	2 O7R522_GIALA	O7R522 giardia lam
71	31	100.0	91	1 THIO_THIRO	P96132 thiocapsa r
72	31	100.0	92	2 O5S2Z0_HUMAN	O5S2Z0 homo sapien
73	31	100.0	93	2 O8TL30_METARC	O8TL30 methanosc
74	31	100.0	94	2 O4HC04_9DBIO	O4HC04 deinococcus
75	31	100.0	95	2 O4KXV3_PLACH	O4KXV3 plasmodium
76	31	100.0	96	2 O4Z5I8_PLABE	O4Z5I8 plasmodium
77	31	100.0	96	2 O8GM51_ARATH	O8GM51 arabidopsis
78	31	100.0	98	1 KRF1_LARNO	P02451 latius novae
79	31	100.0	98	2 O25549_NAEFO	O25549 naegleria f
80	31	100.0	98	2 O5LBI2_BACFN	O5LBI2 bacteroides
81	31	100.0	98	2 O64RG1_BACFR	O64RG1 bacteroides
82	31	100.0	99	2 O8AB91_BACTN	O8AB91 bacteroides
83	31	100.0	100	1 THIO_MTCGA	O924P9 mycoplasma
84	31	100.0	100	2 O9UN64_MYCGA	O9UN64 mycoplasma
85	31	100.0	100	2 O6KIE8_MYCOP	O6KIE8 mycoplasma
86	31	100.0	101	1 THIO1_CHLTE	O8K444 chlorella p
87	31	100.0	101	2 O4N2X5_THRPA	O4N2X5 thierleia p
88	31	100.0	101	2 O22031_CYACA	O22031 cyanidium c
89	31	100.0	101	2 O6KIE7_MYCOW	O6KIE7 mycoplasma
90	31	100.0	102	1 THIO_CHLVC	P52227 chlamydomon
91	31	100.0	102	1 THIO_CHLMU	O9PJK3 chlamydia m
92	31	100.0	102	1 THIO_CHLNP	O9Z7P3 chlamydia p
93	31	100.0	102	1 THIO_CHLNR	O84544 chlamydia t
94	31	100.0	102	1 THIO_CVAME	O22022 cyanidiosch
95	31	100.0	102	1 THIO_MYCGB	P47370 mycoplasma
96	31	100.0	102	1 THIO_MYCPN	P75512 mycoplasma
97	31	100.0	102	1 THIO_SCHPO	P14463 mycizosacch
98	31	100.0	102	1 TRX1_YEAST	P22217 saccharomyc
99	31	100.0	102	2 O9XT61_MACFA	O9XT61 macaca fasc
100	31	100.0	102	2 O5I731_CHLAB	O5I731 chlamydomon
101	31	100.0	102	2 O6F1T8_MESFL	O6F1T8 mecoplasma
102	31	100.0	102	2 O6WU60_MYCWS	O6WU60 mycoplasma
103	31	100.0	103	1 THIO_BACSV	P14949 bacillus su
104	31	100.0	103	1 THIO_LISIN	P04414 listeria in

105	31	100.0	103	1	THIO_LRSMO	P0a413	listeria mo	178	31	100.0	104	2	Q72ZM0	BACCI	Q72ZM0	bacillus ce
106	31	100.0	103	1	TRX2_YEAST	P22A03	saccharomyc	179	31	100.0	104	2	Q72QY0	LEBPC	Q72QY0	leptospira
107	31	100.0	103	2	Q75C00_ASHST	Q75C00	ashya goss	180	31	100.0	104	2	Q6HD04	BACCH	Q6HD04	bacillus th
108	31	100.0	103	2	Q6FND5_CANGA	Q6FND5	candida gla	181	31	100.0	104	2	Q6AYG6	BACCF	Q6AYG6	bacteroides
109	31	100.0	103	2	Q6B980_DEBHA	Q6B980	debariomyce	182	31	100.0	104	2	Q63S00	BACCC	Q63S00	bacillus ce
110	31	100.0	103	2	Q5ACN1_CANAL	Q5acn1	candida alb	183	31	100.0	104	2	Q5WEK7	BACSC	Q5WEK7	bacillus cl
111	31	100.0	103	2	Q7QC45_AMOGA	Q7qc45	anopheles g	184	31	100.0	104	2	Q5M212	STRT2	Q5M212	streptococ
112	31	100.0	103	2	Q5IER4_ENTHI	Q5ier4	entamoeba h	185	31	100.0	104	2	Q5LY08	STRT1	Q5LY08	streptococ
113	31	100.0	103	2	Q6Z832_ORISA	Q6Z832	crysa seriy	186	31	100.0	104	2	Q5HX18	CAMJR	Q5HX18	campylobact
114	31	100.0	103	2	Q7P4W8_FUSNV	Q7P4W8	fusobacteri	187	31	100.0	104	2	Q5HQ29	STABO	Q5HQ29	staphylococ
115	31	100.0	103	2	Q5FLM1_LACAC	Q5FLM1	lactobacilli	188	31	100.0	104	2	Q5HGT9	STAC	Q5HGT9	staphylococ
116	31	100.0	103	2	Q8RH23_FUSNN	Q8rh23	fusobacteri	189	31	100.0	104	2	Q81L73	BACAN	Q81L73	bacillus an
117	31	100.0	103	2	Q88V17_LACPL	Q88V17	lactobacilli	190	31	100.0	104	2	Q6S6E9	BACLD	Q6S6E9	bacillus l1
118	31	100.0	103	2	Q74KU7_LACJO	Q74KU7	lactobacilli	191	31	100.0	105	1	THI01_CORNE		THI01_CORNE	
119	31	100.0	103	2	Q720U6_LISMP	Q720U6	listeria mo	192	31	100.0	105	1	THI01_DICDI		THI01_DICDI	
120	31	100.0	104	1	THI03_DICDI	P29447	dicyostelli	193	31	100.0	105	1	THI01_SYNY3		THI01_SYNY3	
121	31	100.0	104	1	THIO_BOVIN	Q97680	bos taurus	194	31	100.0	105	1	THIO_ALIAC		THIO_ALIAC	
122	31	100.0	104	1	THIO_CALJA	Q9bd13	callithrix	195	31	100.0	105	1	THIO_PONPY		THIO_PONPY	
123	31	100.0	104	1	THIO_CHICK	P08629	gallus gall	196	31	100.0	105	1	THIO_RHOSH		THIO_RHOSH	
124	31	100.0	104	1	THIO_HORSE	P08629	gallus gall	197	31	100.0	105	1	THIO_RICCN		THIO_RICCN	
125	31	100.0	104	1	THIO_HUMAN	P10599	homo sapien	198	31	100.0	105	1	THIO_RICOB		THIO_RICOB	
126	31	100.0	104	1	THIO_MACMU	P29451	macaca mula	199	31	100.0	105	2	Q5T937	HUMAN	Q5T937	HUMAN
127	31	100.0	104	1	THIO_MOUSE	P29451	mus musculus	200	31	100.0	105	2	Q519H9	ENTHI	Q519H9	entamoeba h
128	31	100.0	104	1	THIO_PIG	Q98KX1	ophiophagus	201	31	100.0	105	2	Q54KN7	DICDI	Q54KN7	dicyostelli
129	31	100.0	104	1	THIO_RABIT	P82460	sus scrofa	202	31	100.0	105	2	Q5CR91	CRYPV	Q5CR91	cryptospori
130	31	100.0	104	1	THIO_RAT	P08628	cricetula	203	31	100.0	105	2	Q7PAB0	RICSEI	Q7PAB0	ricketsia
131	31	100.0	104	1	THIO_RHORU	P11222	rattus norv	204	31	100.0	105	2	Q68Y00	RICCY	Q68Y00	ricketsia
132	31	100.0	104	1	THIO_SHEEP	P10473	rhodospirill	205	31	100.0	105	2	Q97EM7	CLOAB	Q97EM7	clostridium
133	31	100.0	104	1	THIO_STAM	P50413	ovis aries	206	31	100.0	105	2	Q8VYTL	ANASP	Q8VYTL	anabaena sp
134	31	100.0	104	1	THIO_STAN	P0A043	staphylococ	207	31	100.0	105	2	Q8XMF0	CLOE	Q8XMF0	clostridium
135	31	100.0	104	1	THIO_STAN	P99122	staphylococ	208	31	100.0	105	2	Q890T2	CLOTE	Q890T2	clostridium
136	31	100.0	104	1	THIO_STAR	Q6ghn0	staphylococ	209	31	100.0	105	2	Q7VKR2	HAEDU	Q7VKR2	haemophilus
137	31	100.0	104	1	THIO_STAS	Q6gae9	staphylococ	210	31	100.0	105	2	Q7U534	SYNXP	Q7U534	synecococ
138	31	100.0	104	1	THIO_STAU	P0A0K6	staphylococ	211	31	100.0	105	2	Q5KMG6	GEOXA	Q5KMG6	geobacillus
139	31	100.0	104	1	THIO_STAW	P0A0K6	staphylococ	212	31	100.0	105	2	Q52KC4	MOUSE	Q52KC4	mus musculus
140	31	100.0	104	1	THIO_STABP	Q8cp15	staphylococ	213	31	100.0	105	2	Q8QD7	MELUD	Q8QD7	melospirac
141	31	100.0	104	1	Q6CN03_KULUA	Q6cn03	kluyveromyc	214	31	100.0	105	2	Q6GQ64	XENIA	Q6GQ64	xenopus lae
142	31	100.0	104	2	Q6C399_YARLI	Q6c399	yarrowia li	215	31	100.0	105	2	Q5XGB5	XENR	Q5XGB5	xenopus tiro
143	31	100.0	104	2	Q5KK55_RRYNE	Q5KK55	cryptococcu	216	31	100.0	106	1	Q5U566	XENLA	Q5U566	xenopus lae
144	31	100.0	104	2	Q5W388_RRYNE	Q5W388	cryptococcu	217	31	100.0	106	1	THI01_ANASO		THI01_ANASO	
145	31	100.0	104	2	Q9U1G7_FASHE	Q9U1G7	fasciola he	218	31	100.0	106	1	THI01_SYNFP		THI01_SYNFP	
146	31	100.0	104	2	Q9U544_FASHE	Q9U544	fasciola he	219	31	100.0	106	1	THI01_SYNFP		THI01_SYNFP	
147	31	100.0	104	2	Q9NIR2_PLAFA	Q9nir2	plasmodium	220	31	100.0	106	1	THI02_DROYA		THI02_DROYA	
148	31	100.0	104	2	Q962B7_BRABE	Q962B7	branchiosto	221	31	100.0	106	1	THIO_COBOM		THIO_COBOM	
149	31	100.0	104	2	Q9NFK9_PLARA	Q9nfx9	plasmodium	222	31	100.0	106	1	THIO_GEOCY		THIO_GEOCY	
150	31	100.0	104	2	Q7RH10_PLAFO	Q7RH10	plasmodium	223	31	100.0	106	1	THIO_HELPI		THIO_HELPI	
151	31	100.0	104	2	Q7KQL8_PLAFA	Q7Kql8	plasmodium	224	31	100.0	106	1	THIO_PASMU		THIO_PASMU	
152	31	100.0	104	2	Q6B963_SCHMA	Q6b963	schistosoma	225	31	100.0	106	1	THIO_PENCH		THIO_PENCH	
153	31	100.0	104	2	Q5DAX8_SCHMA	Q5dax8	schistosoma	226	31	100.0	106	1	THIO		THIO	
154	31	100.0	104	2	Q48985_MYCCA	Q48985	mycoplasma	227	31	100.0	106	1	THIO_STRAU		THIO_STRAU	
155	31	100.0	104	2	Q4HFK4_CAMCO	Q4hfK4	campylobact	228	31	100.0	106	2	THIO_SYNY3		THIO_SYNY3	
156	31	100.0	104	2	Q4HUN3_CAMLA	Q4hjn3	campylobact	229	31	100.0	106	2	Q9U515_MANSE		Q9U515_MANSE	
157	31	100.0	104	2	Q4HNN5_CAMOP	Q4hnn5	campylobact	230	31	100.0	106	2	Q4PNB0_IXOSC		Q4PNB0_IXOSC	
158	31	100.0	104	2	Q7M0Y9_CLOPA	Q7m0Y9	clostridium	231	31	100.0	106	2	Q963B4_AEDAE		Q963B4_AEDAE	
159	31	100.0	104	2	Q5LHJ1_BACFN	Q5lhj1	bacteroides	232	31	100.0	106	2	Q8T9N5_SCHNA		Q8T9N5_SCHNA	
160	31	100.0	104	2	Q4LSFO_STRAH	Q4LSfo	staphylococ	233	31	100.0	106	2	Q9U8F3_SCHNA		Q9U8F3_SCHNA	
161	31	100.0	104	2	Q8BDP9_STRRS	Q8bdp9	streptococ	234	31	100.0	106	2	Q9GMW8_MACRA		Q9GMW8_MACRA	
162	31	100.0	104	2	Q8I7L8_BACCR	Q8i7L8	bacillus ce	235	31	100.0	106	2	Q5VAN9_RHITT		Q5VAN9_RHITT	
163	31	100.0	104	2	Q9K8A8_BACHD	Q9k8A8	bacillus ce	236	31	100.0	106	2	Q4TMB6_GSPFN		Q4TMB6_GSPFN	
164	31	100.0	104	2	Q9PIY0_CAMJE	Q9piY0	campylobact	237	31	100.0	106	2	Q8KVV0_9PROT		Q8KVV0_9PROT	
165	31	100.0	104	2	Q9CF37_LACLA	Q9cf37	lactococcus	238	31	100.0	106	2	Q5NNI9_ZYMOA		Q5NNI9_ZYMOA	
166	31	100.0	104	2	Q97P68_STRPN	Q97p68	streptococcus	239	31	100.0	106	2	Q6NDN2_RHOXA		Q6NDN2_RHOXA	
167	31	100.0	104	2	Q8XHX1_CLOPE	Q8xhx1	clostridium	240	31	100.0	106	2	Q8UTJ6_AGRPS		Q8UTJ6_AGRPS	
168	31	100.0	104	2	Q8NZ17_STRPB	Q8nzi17	streptococ	241	31	100.0	106	2	Q89WD9_BRAJA		Q89WD9_BRAJA	
169	31	100.0	104	2	Q99Y75_STRPY	Q99y75	streptococ	242	31	100.0	106	2	Q8EWN2_MYCPB		Q8EWN2_MYCPB	
170	31	100.0	104	2	Q8EP16_OCEIH	Q8ep16	oceanobacilli	243	31	100.0	106	2	Q5L1P8_SILCO		Q5L1P8_SILCO	
171	31	100.0	104	2	Q8E3J7_STRPA3	Q8e3J7	streptococ	244	31	100.0	106	2	Q8DGN0_SYNTL		Q8DGN0_SYNTL	
172	31	100.0	104	2	Q8DXX8_STRAS	Q8dxx8	streptococ	245	31	100.0	106	2	Q7MSG6_WOLSV		Q7MSG6_WOLSV	
173	31	100.0	104	2	Q8DSD2_STRMU	Q8dsd2	streptococ	246	31	100.0	106	2	Q6MS96_PARWM		Q6MS96_PARWM	
174	31	100.0	104	2	Q83SH2_ENTFA	Q83sh2	enterococcus	247	31	100.0	106	2	Q4S0R5_TETNG		Q4S0R5_TETNG	
175	31	100.0	104	2	Q8A5L0_BACTN	Q8A5L0	bacteroides	248	31	100.0	107	1	THI01_DROME		THI01_DROME	
176	31	100.0	104	2	Q7MXW5_PORGI	Q7mxw5	porphyromon	249	31	100.0	107	1	THI01_DROYA		THI01_DROYA	
177	31	100.0	104	2	Q7CET1_STRP3	Q7cet1	streptococ	250	31	100.0	107	1	THIO_CHRVI		THIO_CHRVI	

251	31	100.0	107	1	THIO_CYACA	P37395 cyanidium c	324	31	100.0	108	2	O8YU9 ANASP	O8YU9 anabaena sp
252	31	100.0	107	1	THIO_ECHGR	O17485 echinococcu	325	31	100.0	108	2	O8Y05E RALSO	O8Y05E ralestonia s
253	31	100.0	107	1	THIO_HAEN	P43785 haemophilus	326	31	100.0	108	2	O8EJ06 SHEON	O8EJ06 shewanella
254	31	100.0	107	1	THIO_ICTPU	O9d613 ictalurus p	327	31	100.0	108	2	O8BDN7 VIBVO	O8BDN7 vibrio vuln
255	31	100.0	107	1	THIO_PORPU	P51225 porphyra pu	328	31	100.0	108	2	O8YKH6 VIBPA	O8YKH6 vibrio para
256	31	100.0	107	1	THIO_PORFE	P50254 porphyra ye	329	31	100.0	108	2	O8ZVN2 NITEU	O8ZVN2 nitrosomona
257	31	100.0	107	1	THIO_SYRCL	O05739 streptomyce	330	31	100.0	108	2	O7UJ35 RHODA	O7UJ35 rhodospirell
258	31	100.0	107	2	O7RXV8 NEUCR	O7RXV8 neutrospora	331	31	100.0	108	2	O7NXP2 CHRVO	O7NXP2 chromobacte
259	31	100.0	107	2	O7RXV8 NEUCR	O9c111 neurospora	332	31	100.0	108	2	O6MKD2 BDEBA	O6MKD2 deulfovibri
260	31	100.0	107	2	O5EN23 MAGGR	O5en23 magnaportia	333	31	100.0	108	2	O6AK04 DESPS	O6AK04 desulfobact
261	31	100.0	107	2	O51V99 MAGGR	O51V99 magnaportie	334	31	100.0	108	2	O6ABW1 LEXIX	O6ABW1 leifsonia x
262	31	100.0	107	2	O7PM26 ANOGA	O7pm26 anopheles g	335	31	100.0	108	2	O63U09 BURMA	O63U09 burkholderi
263	31	100.0	107	2	O81PJO DROME	O81PJO drosophila	336	31	100.0	108	2	O62UJ6 BURMA	O62UJ6 burkholderi
264	31	100.0	107	2	O9NG21 ANOGA	O9ng21 anopheles g	337	31	100.0	108	2	O5ZRE7 LEGSPH	O5ZRE7 legionella
265	31	100.0	107	2	O9NG23 TRYBA	O9ng23 trypanosoma	338	31	100.0	108	2	O5XOU3 LEGPA	O5XOU3 legionella
266	31	100.0	107	2	O25345 LEXMA	O25345 leishmania	339	31	100.0	108	2	O5W5L4 LEGPL	O5W5L4 legionella
267	31	100.0	107	2	O9YXV8 CABEL	O9YXV8 caenorhabdi	340	31	100.0	108	2	O5QYF9 IDILO	O5QYF9 idiomarina
268	31	100.0	107	2	O6B343 TRYCR	O6b343 trypanosoma	341	31	100.0	108	2	O5P1K6 ACOSE	O5P1K6 azotarcus sp
269	31	100.0	107	2	O617H0 CABBR	O617H0 caenorhabdi	342	31	100.0	108	2	O5NG78 FRATT	O5NG78 francisella
270	31	100.0	107	2	O5S1X7 IXOSC	O5s1x7 ixodes scap	343	31	100.0	108	2	O7ZUI4 BRARE	O7ZUI4 brachydanto
271	31	100.0	107	2	O67UL8 ORYSA	O67ul8 oryza sativ	344	31	100.0	109	1	THIO2_SYNY3	THIO2 syny3
272	31	100.0	107	2	O57AF5 BRUBA	O57af5 bruceella ab	345	31	100.0	109	1	THIO_CHIAU	THIO chauu
273	31	100.0	107	2	O5FGA3 EHRNG	O5fga3 entilichia r	346	31	100.0	109	1	THIO_EMENT	THIO ementi
274	31	100.0	107	2	O9AUR5 ACTAC	O9ajr5 actinobacill	347	31	100.0	109	1	THIO_GRIPA	THIO gripa
275	31	100.0	107	2	O79N44 SYNP7	O79n44 synchococc	348	31	100.0	109	2	O4W214 ASPEFU	O4W214 aspergillus
276	31	100.0	107	2	O6M1C7 CORGL	O6m1c7 corynebacte	349	31	100.0	109	2	O8MIN1 CAPHI	O8MIN1 capra hircu
277	31	100.0	107	2	O4ORGI HARI8	O4org1 haemophilus	350	31	100.0	109	2	O84XS1 CHLRE	O84XS1 chlamydomon
278	31	100.0	107	2	O6NEA2 CONDI	O6nea2 corynebacte	351	31	100.0	109	2	O4K3Z3 PEPF5	O4K3Z3 pseudomonas
279	31	100.0	107	2	O92TCS RHIME	O92tcs rhizobium m	352	31	100.0	109	2	O5PKK3 SALPA	O5PKK3 salmonella
280	31	100.0	107	2	O6G1B7 BARQU	O6g1b7 bartonella	353	31	100.0	109	2	O8ECG6 PSEPK	O8ECG6 pseudomonas
281	31	100.0	107	2	O6G588 BARHE	O6g588 bartonella	354	31	100.0	109	2	O87UQ3 PSESM	O87UQ3 pseudomonas
282	31	100.0	107	2	O8FXV9 BRUSU	O8fxv9 bruceella su	355	31	100.0	109	2	O60CP8 METCA	O60CP8 methyllococ
283	31	100.0	107	2	O98CM9 RHIL0	O98cm9 rhizobium l	356	31	100.0	109	2	O4S0R6 TETNG	O4S0R6 tetradodon n
284	31	100.0	107	2	O73GQ5 WOJPM	O73gq5 wolbachia p	357	31	100.0	110	1	THIO2_ANASP	THIO2 anasp
285	31	100.0	107	2	O8Y562 BRWME	O8y562 bruceella me	358	31	100.0	110	1	THIO_STRCO	THIO strco
286	31	100.0	107	2	O8PSW0 COREF	O8psw0 corynebacte	359	31	100.0	110	2	O4WV97 ASPEFU	O4WV97 aspergillus
287	31	100.0	107	2	O8DKP7 SYNEL	O8dkp7 synchococc	360	31	100.0	110	2	O6QUK5 PAXIN	O6QUK5 paxillus in
288	31	100.0	107	2	O7VBF6 PROMA	O7vbf6 prochlorococ	361	31	100.0	110	2	O5BHI0 EMENT	O5BHI0 ementi
289	31	100.0	107	2	O7V6M6 PROMA	O7v6m6 prochlorococ	362	31	100.0	110	2	O6ZYLO 9METZ	O6ZYLO 9metz
290	31	100.0	107	2	O7V126 PROMP	O7v126 prochlorococ	363	31	100.0	110	2	O4H9D7 9PEIO	O4H9D7 9peio
291	31	100.0	107	2	O7U898 SYNPX	O7u898 synchococc	364	31	100.0	110	2	O879K6 STREP3	O879K6 streptococ
292	31	100.0	107	2	O72B01 DESVH	O72b01 desulfocvibr	365	31	100.0	110	2	O5F8V8 NETG1	O5F8V8 neisseria g
293	31	100.0	107	2	O65827 MANSMT	O65827 manheimia	366	31	100.0	110	2	O9A218 CAUCR	O9A218 caulobacter
294	31	100.0	107	2	O5NF09 FRATT	O5nf09 francisella	367	31	100.0	110	2	O9UYI9 NEIMB	O9UYI9 neisseria m
295	31	100.0	107	2	O5MZR6 SYNP6	O5mzr6 synchococc	368	31	100.0	110	2	O9UTV5 NEIMA	O9UTV5 neisseria m
296	31	100.0	107	2	O5HAC6 EHRRM	O5hac6 entilichia r	369	31	100.0	110	2	O8YV7 ANASP	O8YV7 anabaena sp
297	31	100.0	107	2	O6D616 BRARE	O6d616 brachydanto	370	31	100.0	110	2	O88ZK9 LACPL	O88ZK9 lactobacill
298	31	100.0	108	1	THIO2_CHLTH	O8k449 chlorobium	371	31	100.0	110	2	O82FE7 STRAW	O82FE7 streptomyce
299	31	100.0	108	1	THIO2_CHLTH	P10472 chlorobium	372	31	100.0	110	2	O7M87 GLOVI	O7M87 gloeobacter
300	31	100.0	108	1	THIO_ECOLI	P00274 escherichia	373	31	100.0	110	2	O5YMS6 NOCEFA	O5YMS6 nocardiella fa
301	31	100.0	108	1	THIO_PSEAE	P09271 pseudomonas	374	31	100.0	111	2	O5TVVO ANOGA	O5TVVO anoga
302	31	100.0	108	1	THIO_THIFE	P52333 thiodacillium	375	31	100.0	111	2	O9ALAT SYNP7	O9ALAT synp7
303	31	100.0	108	2	O4WMD4 ASPEFU	O4wmd4 aspergillus	376	31	100.0	111	2	O5EUB4 9ENTR	O5EUB4 buchnera ap
304	31	100.0	108	2	O5JRY2 HDWAN	O5jry2 homo sapien	377	31	100.0	111	2	O5N062 SYNP6	O5N062 synchococc
305	31	100.0	108	2	O5T933 HDWAN	O5t933 homo sapien	378	31	100.0	111	2	O6MUC1 XEMIA	O6MUC1 xenopus lae
306	31	100.0	108	2	O9S5J2 DROME	O9s5j2 drosophila	379	31	100.0	112	1	THIO_MYCSM	THIO mycsm
307	31	100.0	108	2	O41OD7 9BIVA	O41od7 chlamys far	380	31	100.0	112	1	TRXH_CHLRE	TRXH chlre
308	31	100.0	108	2	O5TY47 ANOGA	O5ty47 anopheles g	381	31	100.0	112	2	O9U2Z9 CABEL	O9U2Z9 caenorhabdi
309	31	100.0	108	2	O6VH15 1POBA	O6vh15 ipomoea bat	382	31	100.0	112	2	O81EVA TRIVA	O81EVA trichomonas
310	31	100.0	108	2	O6IVR6 9GAMM	O6ivr6 uncultured	383	31	100.0	112	2	O6IVS9 TRIVA	O6IVS9 trichomonas
311	31	100.0	108	2	O7BK7 PRB01	O7bk7 gamma-prote	384	31	100.0	112	2	O6IVS8 TRIVA	O6IVS8 trichomonas
312	31	100.0	108	2	O4NK10 9MICC	O4nk10 arthrobacte	385	31	100.0	112	2	O5YBBI 9GLOI	O5YBBI helicospori
313	31	100.0	108	2	O4IH05 9BURK	O4ih05 burkholderi	386	31	100.0	112	2	O7WGP8 VIBVY	O7WGP8 vibrio vuln
314	31	100.0	108	2	O4O108 AZOVI	O4o108 azotobacter	387	31	100.0	112	2	O6LL16 PHOPR	O6LL16 photobacter
315	31	100.0	108	2	O6Q926 9GAMM	O6q926 uncultured	388	31	100.0	112	2	O67LQ7 SYMTH	O67LQ7 symbiodace
316	31	100.0	108	2	O5EBU4 VIBF1	O5ebu4 vibrio fisc	389	31	100.0	113	2	O8M120 SHEEP	O8M120 ovis aries
317	31	100.0	108	2	O4FY72 9GAMM	O4fy72 psychrobact	390	31	100.0	113	2	O6B8P1 GRATL	O6B8P1 gracilaria
318	31	100.0	108	2	O7MYL3 PHOHL	O7myl3 photorhabd	391	31	100.0	113	2	O8GUR9 PEA	O8GUR9 pieum sativ
319	31	100.0	108	2	O8ZAD9 YERP8	O8zad9 yerinia pe	392	31	100.0	113	2	O4UPY4 XANCP	O4UPY4 xanthomonas
320	31	100.0	108	2	O6G618 YERP8	O6g618 yerinia pe	393	31	100.0	113	2	O5GUR7 XANCP	O5GUR7 xanthomonas
321	31	100.0	108	2	O6CZ80 ERMCT	O6cz80 erwinia car	394	31	100.0	113	2	O6O826 METCA	O6O826 methyllococ
322	31	100.0	108	2	O5FT93 GLOUX	O5ft93 gluconobact	395	31	100.0	113	2	O8PF22 XANAC	O8PF22 xanthomonas
323	31	100.0	108	2	O9KV51_VIBCH	O9kv51 vibrio chol	396	31	100.0	113	2	O8PAD3_XANCP	O8PAD3 xanthomonas

397	31	100.0	113	2	Q879Y5_XYLEFT	Q879Y5_xylella fas	470	31	100.0	124	2	Q6M1N0_CORGL	Q6m1n0 corynebacte
398	31	100.0	114	1	THIO2_DROME	Q9v429 drosophila	471	31	100.0	124	2	Q8NLS8_CORGL	Q8nls8 corynebacte
399	31	100.0	114	1	TRXH1_ARATH	P29x44 arabiopsis	472	31	100.0	124	2	Q9KFM2_BACDH	Q9kfm2 bacillus ha
400	31	100.0	114	1	Y989_METUA	Q58396 methanococ	473	31	100.0	124	2	Q5YVL7_NOCFA	Q5yvl7 nocardia fa
401	31	100.0	114	2	Q6M0G2_METMP	Q6m0g2 methanococ	474	31	100.0	125	1	TRXH_PICMA	Q65045 picea maria
402	31	100.0	114	2	Q51FH8_ENTHI	Q51fh8 entamoeba h	475	31	100.0	125	2	Q5FYH5_PINTA	Q5f1h5 pinus taeda
403	31	100.0	114	2	Q7YZF7_CAEEL	Q7yzf7 caenorhabdi	476	31	100.0	125	2	Q5FYH8_PINTA	Q5f1h8 pinus taeda
404	31	100.0	114	2	Q9RYL2_DEIRA	Q9ryl2 drosococcus	477	31	100.0	125	2	Q5FYI9_PINTA	Q5f1i9 pinus taeda
405	31	100.0	114	2	Q67SM1_SWMTH	Q67sm1 symbiodace	478	31	100.0	125	2	Q5FYJ1_PINTA	Q5f1j1 pinus taeda
406	31	100.0	115	2	THIO1_CAEEL	Q09433 caenorhabdi	479	31	100.0	125	2	Q5FYJ5_PINTA	Q5f1j5 pinus taeda
407	31	100.0	115	1	THIO1_MYCOB	P0a617 mycobacteri	480	31	100.0	125	2	Q5FYU8_PINTA	Q5f1j8 pinus taeda
408	31	100.0	115	1	THIO1_MYCTU	P0a616 mycobacteri	481	31	100.0	125	2	Q5FYK2_PINTA	Q5f1k2 pinus taeda
409	31	100.0	115	2	Q751D5_ASHGO	Q751d5 ashya goss	482	31	100.0	125	2	Q5LIV9_ORISA	Q5l1v9 oryza sativ
410	31	100.0	115	2	Q5PES9_ANAMM	Q5p99 anaplasmata m	483	31	100.0	125	2	Q9LIDX4_WHEAT	Q9lidx4 triticum ae
411	31	100.0	115	2	Q5MZN0_SYMP6	Q5mzn0 synecchococ	484	31	100.0	125	2	Q4SLD3_TETNG	Q4slod3 tetradon n
412	31	100.0	116	1	TRXH_FRGES	Q96419 fagopyrum e	485	31	100.0	126	1	TRXH1_TOBAC	TRXH1 nicotiana t
413	31	100.0	116	2	ULB1_HCMVA	P16625 human cytom	486	31	100.0	126	1	TRXH_WHEAT	Q84394 nicotiana ae
414	31	100.0	116	2	Q4WB53_ASPEU	Q4wb53 aspergillus	487	31	100.0	126	1	Q8TGH7_PODAN	Q8tgh7 podispora a
415	31	100.0	116	2	Q6U838_PARBH	Q6u838 paracoccidi	488	31	100.0	126	2	Q685T8_9SCOR	Q685t8 mesobuthus
416	31	100.0	116	2	Q4ZZP9_PSESY	Q4zzp9 pseudomonas	489	31	100.0	126	2	Q685V0_9SCOR	Q685v0 mesobuthus
417	31	100.0	117	1	THIO_BORBU	Q51088 borrellia bu	490	31	100.0	126	2	Q685V4_9SCOR	Q685v4 mesobuthus
418	31	100.0	117	2	Q740Z6_MYCPA	Q740z6 mycobacteri	491	31	100.0	126	2	Q685X1_9SCOR	Q685x1 mesobuthus
419	31	100.0	117	2	Q66ZV3_BORGA	Q66zv3 borrellia ga	492	31	100.0	126	2	Q685X8_9SCOR	Q685x8 mesobuthus
420	31	100.0	117	2	Q93AQ3_MYCPA	Q93aq3 mycobacteri	493	31	100.0	126	2	Q685Y5_9SCOR	Q685y5 mesobuthus
421	31	100.0	118	1	LSHB_BALAC	P33088 balaeopter	494	31	100.0	126	2	Q685Y8_9SCOR	Q685y8 mesobuthus
422	31	100.0	118	1	LSHB_PHYCA	P25330 phyaelet ca	495	31	100.0	126	2	Q685Y9_BUTEU	Q685y9 buthus eup
423	31	100.0	118	1	TRXH2_TOBAC	Q07090 nicotiana t	496	31	100.0	126	2	Q685X9_9SCOR	Q685x9 mesobuthus
424	31	100.0	118	1	TRXH_RICCO	Q43636 ricinus com	497	31	100.0	126	2	Q685W5_9SCOR	Q685w5 mesobuthus
425	31	100.0	118	2	Q64BN2_9ARCH	Q64bn2 unclutired	498	31	100.0	126	2	Q67412_9ORTO	Q67412 influenza c
426	31	100.0	118	2	Q8WT16_DROPH	Q8wt16 drosophila	499	31	100.0	126	2	Q67413_INCNB	Q67413 influenza c
427	31	100.0	118	2	Q93X24_PEA	Q93x24 pisum sativ	500	31	100.0	126	2	Q67414_9ORTO	Q67414 influenza c
428	31	100.0	118	2	Q8GVD3_WHEAT	Q8gvd3 triticum ae	501	31	100.0	127	1	KRCL_CHICK	P25592 gallus gall
429	31	100.0	118	2	Q7XKX3_HORVD	Q7xkx3 hordeum vul	502	31	100.0	127	1	THIO_NEUCR	P42115 neuropep
430	31	100.0	118	2	Q5XA57_STRB6	Q5xa57 streptococ	503	31	100.0	127	1	TRX3_YEAST	P25372 saccharomy
431	31	100.0	119	1	THIO2_CAEEL	Q17424 caenorhabdi	504	31	100.0	127	1	TXNDB_HUMAN	Q6a555 homo sapien
432	31	100.0	119	2	Q5V6K7_HALMA	Q5v6k7 halocactula	505	31	100.0	127	1	TXNDB_MOUSE	Q69b22 mus musculu
433	31	100.0	119	2	Q46709_HALSA	Q46709 halobacteri	506	31	100.0	127	1	TXNDB_RAT	Q69bd1 rattus norv
434	31	100.0	119	2	Q7M3C7_RABIT	Q7m3c7 cryptolagus	507	31	100.0	127	2	Q8MMQ4_PIG	Q8mmq4 sus scrofa
435	31	100.0	119	2	Q9SP36_SECOE	Q9sp36 secale cere	508	31	100.0	127	2	Q6NBJ0_CORDI	Q6n6j0 corynebacte
436	31	100.0	119	2	Q5ZFA8_PLAMJ	Q5zfa8 plantago ma	509	31	100.0	127	2	Q7W131_BORBR	Q7w131 borstella
437	31	100.0	119	2	Q8F4W0_LEPIN	Q8f4w0 leprospira	510	31	100.0	127	2	Q7W665_BORBP	Q7w665 borstella
438	31	100.0	120	2	Q5URY3_HUMAN	Q5ury3 homo sapien	511	31	100.0	127	2	Q7VXN6_BORBP	Q7vxn6 borstella
439	31	100.0	120	2	Q4RI04_CAEEL	Q4ri04 caenorhabdi	512	31	100.0	128	1	LSHB_PROSU	Q9q749 phodopus su
440	31	100.0	120	2	Q9AR82_PEA	Q9ar82 pisum sativ	513	31	100.0	128	2	Q8SP15_HORSE	Q8sp15 equus cabal
441	31	100.0	120	2	Q4NLS3_9MICC	Q4nls3 arthropacte	514	31	100.0	129	1	DYLA_CHIRE	Q39591 chlamydomon
442	31	100.0	120	2	Q6SKX3_ARTXU	Q6skx3 arthropacte	515	31	100.0	129	2	Q9XIF4_ARATH	Q9xif4 arabiopsis
443	31	100.0	121	1	Y008_METKA	P94948 methanopyru	516	31	100.0	129	2	Q825V1_STRBW	Q825v1 streptomyce
444	31	100.0	121	2	Q94504_SCHPO	Q94504 schizosacch	517	31	100.0	129	2	Q64393_TRTTU	Q64393 triticum tu
445	31	100.0	121	2	Q8IKL4_PLAF7	Q8ikl4 plasmodium	518	31	100.0	130	2	Q8GUR8_PEA	Q8gur8 pisum sativ
446	31	100.0	121	2	Q7R8F6_PLAYO	Q7r8f6 plasmodium	519	31	100.0	130	2	Q7PT21_WHEAT	Q7pte21 triticum ae
447	31	100.0	121	2	Q61CC9_CABBR	Q61cc9 caenorhabdi	520	31	100.0	131	2	Q8M4B6_CARCA	Q8m4b6 capreolus c
448	31	100.0	121	2	Q4YYYS_PLABE	Q4yyys plasmodium	521	31	100.0	131	2	Q9SMG4_LOLPR	Q9smg4 lolium pere
449	31	100.0	121	2	Q9FRY3_ORISA	Q9fry3 oryza sativ	522	31	100.0	131	2	Q9SMG4_LOLPR	Q9smg4 lolium pere
450	31	100.0	121	2	Q6L4X5_ORISA	Q6l4x5 oryza sativ	523	31	100.0	131	2	Q9SMG6_HORBU	Q9smg6 hordeum bul
451	31	100.0	121	2	Q6AAH7_PROAC	Q6aah7 propionibac	524	31	100.0	131	2	Q8HEX0_WHEAT	Q8hex0 triticum ae
452	31	100.0	121	2	Q4TDS8_TETNG	Q4tds8 tetradon n	525	31	100.0	131	2	Q8GZK4_HORVD	Q8gzk4 hordeum vul
453	31	100.0	122	1	TRXH_ORISA	Q42443 oryza sativ	526	31	100.0	131	2	Q84X91_9POLA	Q84x91 leymus chin
454	31	100.0	122	2	Q7EXZ7_ORISA	Q7exz7 oryza sativ	527	31	100.0	131	2	Q9AS75_ORISA	Q9as75 oryza sativ
455	31	100.0	122	2	Q7XZX2_HORVD	Q7xzx2 hordeum vul	528	31	100.0	131	2	Q9S753_9POLA	Q9s753 phalaris co
456	31	100.0	122	2	Q4W1F6_MAIZE	Q4w1f6 zea mays (m	529	31	100.0	131	2	Q4NT79_9DELT	Q4nt79 anaeromyxob
457	31	100.0	123	2	Q9N1S1_CAPCA	Q9n1s1 capreolus c	530	31	100.0	132	2	Q8HEX4_ORISA	Q8hex4 oryza sativ
458	31	100.0	123	2	Q7XJ63_ARATH	Q7xj63 arabiopsis	531	31	100.0	133	1	TRXH2_ARATH	Q38875 arabiopsis
459	31	100.0	123	2	Q6VH14_IPOBA	Q6vh14 ipomoea bat	532	31	100.0	133	2	Q8HEX5_MAIZE	Q8hex5 zea mays (m
460	31	100.0	123	2	Q5JMR9_ORISA	Q5jmr9 oryza sativ	533	31	100.0	133	2	Q8GZT3_BRAIC	Q8gz3 brassica ca
461	31	100.0	123	2	Q4JSG8_CORUK	Q4jsg8 corynebacte	534	31	100.0	133	2	Q7D2B9_AGRYS	Q7d2b9 agrobacteri
462	31	100.0	123	2	Q7U0U5_MYCOB	Q7u0u5 mycobacteri	535	31	100.0	134	2	Q8L9A6_ARATH	Q8l9a6 arabiopsis
463	31	100.0	123	2	Q7DBE1_MYCTU	Q7dbe1 mycobacteri	536	31	100.0	134	2	Q8S1R5_ORISA	Q8s1r5 oryza sativ
464	31	100.0	123	2	Q8G4Z3_BIFPU	Q8g4z3 bifidobacte	537	31	100.0	134	2	Q9RD25_STRCO	Q9rd25 streptomyce
465	31	100.0	124	2	Q4V6C1_DROME	Q4v6c1 drosophila	538	31	100.0	135	2	Q70YJ4_HORVN	Q70yj4 hordeum vul
466	31	100.0	124	2	Q8SP29_PIG	Q8sp29 sus scrofa	539	31	100.0	135	2	Q6PY94_SOYBN	Q6py94 glycine max
467	31	100.0	124	2	Q9GKU0_CALVA	Q9gku0 callitrich	540	31	100.0	135	2	Q57HT5_SALCH	Q57ht5 salmonella
468	31	100.0	124	2	Q38456_BPPIH	Q38456 bacterioph	541	31	100.0	135	2	Q4LGI1_9BURK	Q4lgi1 burholderi
469	31	100.0	124	2	Q6RJ27_CAPAN	Q6rj27 capsicum an	542	31	100.0	135	2	Q9DEQ1_MOUSE	Q9deg1 mus musculu

543	31	100.0	135	2	Q9D6R7_MOUSE	Q9D6R7_mus musculus	616	31	100.0	142	2	Q9BD19_PANTIA	Q9BD19_pantthera ti
544	31	100.0	135	2	Q9D7C0_MOUSE	Q9D7C0_mus musculus	617	31	100.0	142	2	Q5ZF46_PLAMU	Q5ZF46_plantago ma
545	31	100.0	136	2	Q5UW65_HALMA	Q5UW65_haloarcula	618	31	100.0	142	2	Q4WMSX2_BACCE	Q4WMSX2_bacillus ce
546	31	100.0	136	2	Q8XK10_HUMAN	Q8XK10_homo sapien	619	31	100.0	142	2	Q81FMO_BACCR	Q81FMO_bacillus ce
547	31	100.0	136	2	Q8MN99_PTELY	Q8MN99_pteropus ly	620	31	100.0	142	2	Q9RY19_DEIRA	Q9RY19_delmococcus
548	31	100.0	136	2	Q8MNA0_CYNVA	Q8MNA0_cynoccephalu	621	31	100.0	142	2	Q5QZV7_IDILO	Q5QZV7_idiomarina
549	31	100.0	136	2	Q8MNA1_LORTA	Q8MNA1_loris tardi	622	31	100.0	142	2	Q8R3V1_MOUSE	Q8R3V1_mus musculus
550	31	100.0	136	2	Q8MNA2_GALSE	Q8MNA2_galago seme	623	31	100.0	143	1	LSHB_FELCA	Q8R3V1_felis silve
551	31	100.0	136	2	Q8MNA5_TARBA	Q8MNA5_tarsius ban	624	31	100.0	143	2	Q8S3L2_IPOBA	Q8S3L2_ipomoea bat
552	31	100.0	136	2	Q8MNB5_COLGU	Q8MNB5_colobus gue	625	31	100.0	143	2	Q8S3L2_IPOBA	Q8S3L2_ipomoea bat
553	31	100.0	136	2	Q8MNB6_PREBO	Q8MNB6_psephylic o	626	31	100.0	144	2	Q51010_ENTHI	Q51010_entamoeba h
554	31	100.0	136	2	Q8MNB7_MACMU	Q8MNB7_macaca mula	627	31	100.0	144	2	Q41UJ1_AZCVI	Q41UJ1_azotobacter
555	31	100.0	136	2	Q9JWZ3_PRUPE	Q9JWZ3_prunus pers	628	31	100.0	144	2	Q4KJF7_PSEF5	Q4KJF7_pseudomonas
556	31	100.0	136	2	Q4SEK3_TETNG	Q4SEK3_tetradodon n	629	31	100.0	144	2	Q7UJF3_RHOBA	Q7UJF3_rhodospirill
557	31	100.0	137	2	Q4PLX7_IKOSC	Q4PLX7_iodexs scap	630	31	100.0	144	2	Q8B8C1_PSEBP	Q8B8C1_pseudomonas
558	31	100.0	137	2	Q4NH78_9M1CC	Q4NH78_arctirobacte	631	31	100.0	145	1	THIO3_CORRE	P52228_corynebacte
559	31	100.0	137	2	Q5UR29_MIMIV	Q5UR29_mimivirius	632	31	100.0	145	2	Q61JZ7_CABBR	Q61JZ7_caenorhabdi
560	31	100.0	138	1	LSHB_CNFA	P18842_canis fam11	633	31	100.0	145	2	Q7XV06_ORYSA	Q7XV06_oryza sativ
561	31	100.0	138	2	Q64MX0_ORYSA	Q64MX0_oryza sativ	634	31	100.0	145	2	Q84XR9_CHLRE	Q84XR9_chlamydomon
562	31	100.0	138	2	Q624I3_ORYSA	Q624I3_oryza sativ	635	31	100.0	145	2	Q6NCU6_RHOPA	Q6NCU6_rhodopseu
563	31	100.0	138	2	Q7ZM11_CHICK	Q7ZM11_gallus gall	636	31	100.0	145	2	Q8ZBM4_YERPE	Q8ZBM4_yersinia pe
564	31	100.0	139	1	THIO2_ECOLI	P33636_escherichia	637	31	100.0	145	2	Q6CE40_YERPS	Q6CE40_yersinia pe
565	31	100.0	139	2	Q6CK18_KLUDA	Q6CK18_kluyveromyc	638	31	100.0	145	2	Q7NQ61_CHRVO	Q7NQ61_chromobacte
566	31	100.0	139	2	Q6ENV3_HUMAN	Q6ENV3_homo sapien	639	31	100.0	145	2	Q5P2H5_AZOSB	Q5P2H5_azotobacter
567	31	100.0	139	2	Q5TSB2_ANOGA	Q5TSB2_anopheles g	640	31	100.0	146	2	Q5N844_ORYSA	Q5N844_oryza sativ
568	31	100.0	139	2	Q9VUG9_DROME	Q9VUG9_drosophila	641	31	100.0	146	2	Q82EK3_STRAW	Q82EK3_streptomyce
569	31	100.0	139	2	Q7YRL0_PIG	Q7YRL0_sus scrofa	642	31	100.0	146	2	Q8Q2D6_MELUD	Q8Q2D6_melopsittac
570	31	100.0	139	2	Q57L52_SALCH	Q57L52_salmonella	643	31	100.0	147	2	Q5BHK3_SCMA	Q5BHK3_schistosoma
571	31	100.0	139	2	Q5LBI1_BACFN	Q5LBI1_bacteroides	644	31	100.0	147	2	Q89164_BRAJA	Q89164_bradyrhizob
572	31	100.0	139	2	Q73AT5_BACCI	Q73AT5_bacillus ce	645	31	100.0	148	2	Q5MIS6_AEDAL	Q5MIS6_aedes albop
573	31	100.0	139	2	Q8Z4J6_SALTI	Q8Z4J6_salmonella	646	31	100.0	148	2	Q9CASI_ARATH	Q9CASI_arabidopsis
574	31	100.0	139	2	Q8ZMX4_SALTY	Q8ZMX4_salmonella	647	31	100.0	148	2	Q4US63_XANCP	Q4US63_xanthomonas
575	31	100.0	139	2	Q5PID7_SARPA	Q5PID7_salmonella	648	31	100.0	148	2	Q5Z2A0_NOCFA	Q5Z2A0_nocardia fa
576	31	100.0	139	2	Q6DID1_ERNCT	Q6DID1_erwinia car	649	31	100.0	148	2	Q8PMZ8_XANCP	Q8PMZ8_xanthomonas
577	31	100.0	139	2	Q67747_AQUAE	Q67747_aquifex aeo	650	31	100.0	148	2	Q8PB82_XANCP	Q8PB82_xanthomonas
578	31	100.0	139	2	Q7NZ16_CHRVO	Q7NZ16_chromobacte	651	31	100.0	149	2	Q5JYTP_HUMAN	Q5JYTP_homo sapien
579	31	100.0	139	2	Q743D8_MYCPA	Q743D8_mycobacteri	652	31	100.0	149	2	Q8N1G6_CORGL	Q8N1G6_corynebacte
580	31	100.0	139	2	Q605Y8_METCA	Q605Y8_methylococc	653	31	100.0	149	2	Q988U5_RH10L	Q988U5_rhizobium l
581	31	100.0	139	2	Q62778_RAT	Q62778_rattus norv	654	31	100.0	150	2	Q5DRA0_SCHJA	Q5DRA0_schistosoma
582	31	100.0	140	1	TRKM_CHIRE	P23400_chlamydomon	655	31	100.0	150	2	Q84XS0_CHIRE	Q84XS0_chlamydomon
583	31	100.0	140	2	Q9C9Y6_ARATH	Q9C9Y6_arabidopsis	656	31	100.0	151	2	Q9SRD7_ARATH	Q9SRD7_arabidopsis
584	31	100.0	140	2	Q81SR5_BACAN	Q81SR5_bacillus an	657	31	100.0	151	2	Q826F1_STRAW	Q826F1_streptomyce
585	31	100.0	140	2	Q9C8C8_MYCLE	Q9C8C8_mycobacteri	658	31	100.0	152	2	Q6ER81_ORYSA	Q6ER81_oryza sativ
586	31	100.0	140	2	Q8BFL1_SHEON	Q8BFL1_shewanella	659	31	100.0	152	2	Q4UOW0_NICAL	Q4UOW0_nicotiana a
587	31	100.0	140	2	Q72IL5_THET2	Q72IL5_thermus the	660	31	100.0	152	2	Q84XS2_CHIRE	Q84XS2_chlamydomon
588	31	100.0	140	2	Q5S193_THET8	Q5S193_thermus the	661	31	100.0	152	2	Q8H6X3_TOBAC	Q8H6X3_nicotiana t
589	31	100.0	140	2	Q5Z0Y6_CHICK	Q5Z0Y6_gallus gall	662	31	100.0	152	2	Q4SKJ5_TETNG	Q4SKJ5_tetradodon n
590	31	100.0	141	1	LSHB_BOVIN	P04651_bos taurus	663	31	100.0	153	2	Q7XY47_GRIJA	Q7XY47_griifilhsia
591	31	100.0	141	1	LSHB_CERSI	P07635_ceratoheri	664	31	100.0	153	2	Q9FYJ3_ARATH	Q9FYJ3_arabidopsis
592	31	100.0	141	1	LSHB_HUMAN	P01329_homo sapien	665	31	100.0	153	2	Q4UNK3_RICFE	Q4UNK3_rickettsia
593	31	100.0	141	1	LSHB_MACFA	Q6E778_macaca fasc	666	31	100.0	154	1	KRSC_CHICK	P04459_gallus gall
594	31	100.0	141	1	LSHB_MOUSE	Q09108_mus musculu	667	31	100.0	154	2	Q4K890_PSEF5	Q4K890_pseudomonas
595	31	100.0	141	1	LSHB_PIG	P01332_sus scrofa	668	31	100.0	154	2	Q8BMC7_PSBPK	Q8BMC7_pseudomonas
596	31	100.0	141	1	LSHB_RAT	P01331_rattus norv	669	31	100.0	154	2	Q8AB92_BACFN	Q8AB92_bacteroides
597	31	100.0	141	1	LSHB_SHEEP	P01321_ovis aries	670	31	100.0	155	2	Q4KZQ3_PSESY	Q4KZQ3_pseudomonas
598	31	100.0	141	1	Q4JBR7_SUIAC	Q4JBR7_eulfolobus	671	31	100.0	155	2	Q8EF86_SHEON	Q8EF86_shewanella
599	31	100.0	141	2	Q6FVN1_CANGA	Q6FVN1_candida gla	672	31	100.0	155	2	Q8B5Z3_PSESM	Q8B5Z3_pseudomonas
600	31	100.0	141	2	Q61Y74_RABIT	Q61Y74_oryctolagus	673	31	100.0	155	2	Q64RGO_BACFR	Q64RGO_bacteroides
601	31	100.0	141	2	Q8H2R9_AILFU	Q8H2R9_aillurus ful	674	31	100.0	156	1	DYLS_CHIRE	Q622F8_caenorhabdi
602	31	100.0	141	2	Q8MN18_AILME	Q8MN18_ailluropoda	675	31	100.0	156	2	Q5FBE9_9ORTO	Q5FBE9_influenza c
603	31	100.0	141	2	Q4H6T8_9DELO	Q4H6T8_delmococcus	676	31	100.0	156	2	Q5FBE9_9ORTO	Q5FBE9_influenza c
604	31	100.0	141	2	Q6H100_BACHK	Q6H100_bacillus th	677	31	100.0	156	2	Q8QZG1_9ORTO	Q8QZG1_influenza c
605	31	100.0	141	2	Q63DH7_BACCH	Q63DH7_bacillus ce	678	31	100.0	156	2	Q8QZL6_9ORTO	Q8QZL6_influenza c
606	31	100.0	141	2	Q5LWAO_SILPO	Q5LWAO_silicibacte	679	31	100.0	156	2	Q8QZL6_9ORTO	Q8QZL6_influenza c
607	31	100.0	141	2	Q9RVS8_DEIRA	Q9RVS8_delmococcus	680	31	100.0	156	2	Q8QZM0_9ORTO	Q8QZM0_influenza c
608	31	100.0	141	2	Q7WH77_BORBA	Q7WH77_bordetella	681	31	100.0	156	2	Q8QZM1_9ORTO	Q8QZM1_influenza c
609	31	100.0	141	2	Q7W990_BORBA	Q7W990_bordetella	682	31	100.0	156	2	Q8QZM2_9ORTO	Q8QZM2_influenza c
610	31	100.0	141	2	Q7VYP8_BORPE	Q7VYP8_bordetella	683	31	100.0	156	2	Q8QZM3_9ORTO	Q8QZM3_influenza c
611	31	100.0	141	2	Q6F7Y4_ACTIAD	Q6F7Y4_actinetobact	684	31	100.0	156	2	Q8QZM4_9ORTO	Q8QZM4_influenza c
612	31	100.0	141	2	Q6UDC1_MERUN	Q6UDC1_merionas un	685	31	100.0	156	2	Q8QZM5_9ORTO	Q8QZM5_influenza c
613	31	100.0	141	2	Q6V3B5_MESAU	Q6V3B5_mesocricetu	686	31	100.0	156	2	Q6BCC2_9ORTO	Q6BCC2_influenza c
614	31	100.0	141	2	Q6V3B6_MASCO	Q6V3B6_mascowys co	687	31	100.0	156	2	Q6BCC3_9ORTO	Q6BCC3_influenza c
615	31	100.0	142	2	Q61985_CABEL	Q61985_caenorhabdi	688	31	100.0	156	2	Q6BCC4_9ORTO	Q6BCC4_influenza c

689	31	100.0	156	2	068CC5_9ORTO	068cc5_influenza c	762	31	100.0	158	2	Q7RU85_NEUCR	Q7ru85_neutropora
690	31	100.0	156	2	068CC6_9ORTO	068cc6_influenza c	763	31	100.0	158	2	Q94282_CABEL	Q94282_caenorhabdi
691	31	100.0	156	2	068CC7_9ORTO	068cc7_influenza c	764	31	100.0	159	2	Q93V09_ARATH	Q93v09_arabidopsis
692	31	100.0	156	2	068CC8_9ORTO	068cc8_influenza c	765	31	100.0	160	2	Q64CW9_GARCH	Q64cw9_uncultured
693	31	100.0	156	2	068CC9_9ORTO	068cc9_influenza c	766	31	100.0	160	2	Q8PUY7_METMA	Q8puv7_methanosarc
694	31	100.0	156	2	068CD0_9ORTO	068cd0_influenza c	767	31	100.0	160	2	Q4P051_USTMA	Q4p051_ustiliago ma
695	31	100.0	156	2	068CD1_9ORTO	068cd1_influenza c	768	31	100.0	160	2	Q854C9_9CAUD	Q854c9_oryza sativ
696	31	100.0	156	2	068CD2_9ORTO	068cd2_influenza c	769	31	100.0	160	2	Q7XDO6_ORYSA	Q7xd06_oryza sativ
697	31	100.0	156	2	068CD3_9ORTO	068cd3_influenza c	770	31	100.0	160	2	P95355_NEIG1	P95355_neisseria g
698	31	100.0	156	2	068CD4_9ORTO	068cd4_influenza c	771	31	100.0	160	2	O5FSK1_NEIG1	O5fsk1_neisseria g
699	31	100.0	156	2	068CD5_9ORTO	068cd5_influenza c	772	31	100.0	160	2	Q604X8_MERCA	Q604x8_methyloccoc
700	31	100.0	156	2	068CD6_9ORTO	068cd6_influenza c	773	31	100.0	160	2	Q9UWT2_NEIMA	Q9uwt2_neisseria m
701	31	100.0	156	2	068CD7_9ORTO	068cd7_influenza c	774	31	100.0	160	2	Q9XLR4_NEIMA	Q9xlr4_neisseria m
702	31	100.0	156	2	068CD8_9ORTO	068cd8_influenza c	775	31	100.0	160	2	Q63QP3_BURPS	Q63qp3_burkholderi
703	31	100.0	156	2	068CD9_9ORTO	068cd9_influenza c	776	31	100.0	161	2	Q8TIAL_METNAC	Q8tial_methanosarc
704	31	100.0	156	2	068CE0_9ORTO	068ce0_influenza c	777	31	100.0	161	2	Q8TG10_PODAN	Q8tg10_podospora a
705	31	100.0	156	2	068CE1_9ORTO	068ce1_influenza c	778	31	100.0	161	2	Q856T3_9CAUD	Q856t3_mycobacteri
706	31	100.0	156	2	068CE2_9ORTO	068ce2_influenza c	779	31	100.0	161	2	Q5L8X8_BACFN	Q5l8x8_bacteroides
707	31	100.0	156	2	068CE3_9ORTO	068ce3_influenza c	780	31	100.0	161	2	Q64SV7_BACFR	Q64sv7_bacteroides
708	31	100.0	156	2	068CE4_9ORTO	068ce4_influenza c	781	31	100.0	163	2	Q6ZSV7_HUMAN	Q6zsv7_homo sapien
709	31	100.0	156	2	068CE5_9ORTO	068ce5_influenza c	782	31	100.0	163	2	Q59J06_9BACT	Q59j06_uncultured
710	31	100.0	156	2	068CE6_9ORTO	068ce6_influenza c	783	31	100.0	163	2	Q8D6F4_VIBVU	Q8d6f4_vibrio vuln
711	31	100.0	156	2	068CE6_9ORTO	068ce6_influenza c	784	31	100.0	163	2	Q7MDA8_VIBVY	Q7mda8_vibrio vuln
712	31	100.0	156	2	Q91Q61_9ORTO	Q91q61_influenza c	785	31	100.0	164	2	VEGPA_CAVPO	VEGpa_cavia porce
713	31	100.0	156	2	Q9Q221_9ORTO	Q9q221_influenza c	786	31	100.0	164	2	Q8PY73_METMA	Q8py73_methanosarc
714	31	100.0	156	2	Q9Q224_9ORTO	Q9q224_influenza c	787	31	100.0	165	2	Q8PY73_METMA	Q8py73_methanosarc
715	31	100.0	156	2	Q9Q227_9ORTO	Q9q227_influenza c	788	31	100.0	165	1	THIOM_BOVIN	Q95108_bos taurus
716	31	100.0	156	2	Q9Q232_9ORTO	Q9q232_influenza c	789	31	100.0	166	1	THIOM_HUMAN	Q99757_homo sapien
717	31	100.0	156	2	Q9Q235_9ORTO	Q9q235_influenza c	790	31	100.0	166	1	THIOM_MOUSE	Q97493_mus musculu
718	31	100.0	156	2	Q9Q238_9ORTO	Q9q238_influenza c	791	31	100.0	166	1	THIOM_RAT	Q97615_rattus norv
719	31	100.0	156	2	Q9Q241_9ORTO	Q9q241_influenza c	792	31	100.0	166	2	Q6FPH0_HUMAN	Q6tph0_homo sapien
720	31	100.0	156	2	Q9Q244_9ORTO	Q9q244_influenza c	793	31	100.0	166	2	Q5K553_9BACT	Q5k553_uncultured
721	31	100.0	156	2	Q9Q247_9ORTO	Q9q247_influenza c	794	31	100.0	166	2	Q6N4H2_RHOPA	Q6n4h2_rhodopseu
722	31	100.0	156	2	Q9Q250_9ORTO	Q9q250_influenza c	795	31	100.0	166	2	Q545D5_MOUSE	Q545d5_mus musculu
723	31	100.0	156	2	Q9Q253_9ORTO	Q9q253_influenza c	796	31	100.0	166	2	Q6P131_BRARB	Q6p131_brachydanio
724	31	100.0	156	2	Q8B040_9ORTO	Q8b040_influenza c	797	31	100.0	167	1	TRKM_MITZE	Q41664_zea mays (m
725	31	100.0	156	2	Q8B041_9ORTO	Q8b041_influenza c	798	31	100.0	167	2	Q6HSW8_ORYSA	Q6hsw8_oryza sativ
726	31	100.0	156	2	Q8B042_9ORTO	Q8b042_influenza c	799	31	100.0	167	2	Q8L7S9_ARATH	Q8l7s9_arabidopsis
727	31	100.0	156	2	Q8B043_9ORTO	Q8b043_influenza c	800	31	100.0	167	2	Q5UR27_MIMIV	Q5ur27_mimivirus.
728	31	100.0	156	2	Q8B044_9ORTO	Q8b044_influenza c	801	31	100.0	169	1	LSHB_EQUAS	P19794_equus asinu
729	31	100.0	156	2	Q8B045_9ORTO	Q8b045_influenza c	802	31	100.0	169	1	LSHB_EOUBU	Q46641_equus burch
730	31	100.0	156	2	Q8B046_9ORTO	Q8b046_influenza c	803	31	100.0	169	1	LSHB_HORSE	P08751_equus caball
731	31	100.0	156	2	Q8B047_9ORTO	Q8b047_influenza c	804	31	100.0	169	2	Q66PC5_RHITR	Q66pc5_rhizobium t
732	31	100.0	156	2	Q8B048_9ORTO	Q8b048_influenza c	805	31	100.0	169	2	Q7MXC8_PORGI	Q7mxc8_porphyromon
733	31	100.0	156	2	Q8B049_9ORTO	Q8b049_influenza c	806	31	100.0	169	2	Q6MLM7_BDEBA	Q6mlm7_bdellovibri
734	31	100.0	156	2	Q8B050_9ORTO	Q8b050_influenza c	807	31	100.0	170	2	Q8KDH8_CHLTE	Q8kdh8_chlorobium
735	31	100.0	156	2	Q8B051_9ORTO	Q8b051_influenza c	808	31	100.0	170	2	Q7ZYG6_XENIA	Q7zyg6_xenopus lae
736	31	100.0	156	2	Q8B052_9ORTO	Q8b052_influenza c	809	31	100.0	170	2	Q64JU6_XENTR	Q64j16_xenopus tto
737	31	100.0	156	2	Q8B053_9ORTO	Q8b053_influenza c	810	31	100.0	172	1	TRXM_ORYSA	Q92520_oryza sativ
738	31	100.0	156	2	Q8B054_9ORTO	Q8b054_influenza c	811	31	100.0	172	2	Q6NPF9_ARATH	P48384_pisum sativ
739	31	100.0	156	2	Q8B055_9ORTO	Q8b055_influenza c	812	31	100.0	172	1	Q50039_MYCLE	Q50039_mycobacteri
740	31	100.0	156	2	Q8B056_9ORTO	Q8b056_influenza c	813	31	100.0	172	2	TRXM3_ARATH	Q99877_arabidopsis
741	31	100.0	156	2	Q8B057_9ORTO	Q8b057_influenza c	814	31	100.0	173	1	Q9VM81_DROME	Q9vm81_drosophila
742	31	100.0	156	2	Q8B058_9ORTO	Q8b058_influenza c	815	31	100.0	173	2	Q84XR8_CHLRE	Q84xr8_chlamydomon
743	31	100.0	156	2	Q8B059_9ORTO	Q8b059_influenza c	816	31	100.0	173	2	Q6H7E4_ORYSA	Q6h7e4_oryza sativ
744	31	100.0	156	2	Q8B060_9ORTO	Q8b060_influenza c	817	31	100.0	173	2	Q681Y9_ARATH	Q681y9_arabidopsis
745	31	100.0	156	2	Q8B061_9ORTO	Q8b061_influenza c	818	31	100.0	173	2	Q67ZH7_ARATH	Q67zh7_arabidopsis
746	31	100.0	156	2	Q8B062_9ORTO	Q8b062_influenza c	819	31	100.0	173	2	Q67XN4_ARATH	Q67xn4_arabidopsis
747	31	100.0	156	2	Q8B063_9ORTO	Q8b063_influenza c	820	31	100.0	173	2	Q4NX02_9DELT	Q4nx02_aeaeromyxob
748	31	100.0	156	2	Q8B064_9ORTO	Q8b064_influenza c	821	31	100.0	174	2	Q8NDY2_HUMAN	Q8ndy2_homo sapien
749	31	100.0	156	2	Q8B065_9ORTO	Q8b065_influenza c	822	31	100.0	174	2	Q4VX49_HUMAN	Q4vx49_homo sapien
750	31	100.0	156	2	Q8B066_9ORTO	Q8b066_influenza c	823	31	100.0	174	2	Q623W5_CAEBR	Q623w5_caenorhabdi
751	31	100.0	156	2	Q8B067_9ORTO	Q8b067_influenza c	824	31	100.0	174	2	Q8XVP6_RALISO	Q8xvp6_ralstonia s
752	31	100.0	156	2	Q8B068_9ORTO	Q8b068_influenza c	825	31	100.0	175	2	TRXM_WHEAT	Q92p21_triticum ae
753	31	100.0	156	2	Q4U6Y3_9ORTO	Q4u6y3_influenza c	826	31	100.0	175	1	Q9AV49_CUCME	Q9av49_cucumis mel
754	31	100.0	156	2	Q4U6Y4_9ORTO	Q4u6y4_influenza c	827	31	100.0	175	2	Q9LKW0_LYCPS	Q9lkw0_lycopersico
755	31	100.0	156	2	Q4U6Y5_9ORTO	Q4u6y5_influenza c	828	31	100.0	175	2	Q9LVI2_ARATH	Q9lvi2_arabidopsis
756	31	100.0	156	2	Q4U6Y6_9ORTO	Q4u6y6_influenza c	829	31	100.0	175	2	Q5ND46_TRITUV	Q5nd46_triticum tu
757	31	100.0	157	1	THIOR_DROME	Thior_drosophila	830	31	100.0	175	2	Q7P629_FUSNV	Q7p629_fusobacteri
758	31	100.0	157	1	VHCB_METYO	Vhcb_methanococc	831	31	100.0	177	1	TRXM_BRANA	Q9xg60_braesica na
759	31	100.0	157	2	Q8A7R8_BACTN	Q8a7r8_bacteroides	832	31	100.0	177	2	Q66PE5_9RHIZ	Q66pe5_mesorhizobi
760	31	100.0	157	2	VG09_ICHV1	VG09_ictaluriid h	833	31	100.0	177	2	Q7WS25_BRECH	Q7ws25_brevibacill
761	31	100.0	158	1			834	31	100.0				

835	31	100.0	178	1	TRXF1_ARATH	09xfth8	arabidopsis	908	31	100.0	192	2	066PE4_9RHIZ	066PE4	rhizobium s
836	31	100.0	178	2	083WD6_MICGR	083w737	microdomosp	909	31	100.0	192	2	04HB83_9DEIO	04hb83	deinococcus
837	31	100.0	179	1	TRXW1_ARATH	083737	caulobacter	910	31	100.0	193	1	TRXW4_ARATH	083w4	arabidopsis
838	31	100.0	179	2	09AD7_CAUCR	09ad7	caulobacter	911	31	100.0	194	2	064764_ARATH	064764	arabidopsis
839	31	100.0	180	2	07XND0_ORYSA	07xnd0	oryza sativ	912	31	100.0	194	2	066PC8_RHILE	066pc8	rhizobium l
840	31	100.0	180	2	095AH9_PEA	095ah9	pisum sativ	913	31	100.0	195	2	05YJQ5_9ASPA	05yj05	hyacinthus
841	31	100.0	180	2	07XBR5_ORYSA	07xbr5	oryza sativ	914	31	100.0	196	2	04NY01_9DELT	04ny01	anaeromyxob
842	31	100.0	180	2	066PD0_RHILE	066pd0	rhizobium l	915	31	100.0	197	2	06ZN00_HUMAN	06zn00	homo sapien
843	31	100.0	180	2	066PE8_RHIME	066pe8	rhizobium m	916	31	100.0	197	2	06M138_BDEBA	06m138	bdellovibri
844	31	100.0	181	1	TRXW_SPTOL	07591	spinacia ol	917	31	100.0	197	2	073SQ1_MYCPA	073sq1	mycobacteri
845	31	100.0	181	1	06QAT5_DROMA	06qat5	drosophila	918	31	100.0	198	2	072H15_THRT2	072h15	thermus tne
846	31	100.0	181	2	06QAT6_DROSI	06qat6	drosophila	919	31	100.0	198	2	083368_9GARM	083368	murine leuk
847	31	100.0	181	2	06QAT7_DROSI	06qat7	drosophila	920	31	100.0	199	2	06CAU8_YARLI	06cau8	yarowia l1
848	31	100.0	181	2	06JRE3_NICBE	06jre3	nicotiana b	921	31	100.0	201	1	SYA_RHILV	064973	rhizobium l
849	31	100.0	181	2	06JRE38_NICBE	06jre38	nicotiana b	922	31	100.0	202	2	09NPF2_HUMAN	09nfp2	homo sapien
850	31	100.0	181	2	04SS63_TETNG	04ss63	tetradodon n	923	31	100.0	202	2	04USY3_CORKJ	04usy3	corynebacte
851	31	100.0	182	1	TRXF_BRANA	04897	brassica na	924	31	100.0	202	2	073K50_TRADE	073k50	treponema d
852	31	100.0	182	1	TRXF_PBA	029450	pisum sativ	925	31	100.0	203	2	06AQD6_DBSPS	06aqd6	desulfotale
853	31	100.0	182	1	TRXX_ARATH	081d49	arabidopsis	926	31	100.0	204	2	086XZ5_HUMAN	086xz5	homo sapien
854	31	100.0	182	2	07ZAP9_HUMAN	07zap9	homo sapien	927	31	100.0	205	2	075FA5_ASHGO	075fa5	ashbya gos
855	31	100.0	183	2	08LFA3_ARATH	08lfa3	arabidopsis	928	31	100.0	205	2	06ZRD4_HUMAN	06zrd4	homo sapien
856	31	100.0	183	2	09W7X9_ARATH	09w7x9	arabidopsis	929	31	100.0	205	2	07F449_ORYSA	07f449	oryza sativ
857	31	100.0	183	2	066PE1_RHIME	066pe1	rhizobium m	930	31	100.0	205	2	084634_CHLTR	084634	chlamydia t
858	31	100.0	183	2	066PE6_9BRAD	066pe6	bradyrhizob	931	31	100.0	206	2	06QPD9_9ADEN	06qpd9	simian aden
859	31	100.0	184	2	08HY70_MUSVT	08hy70	muscula vis	932	31	100.0	207	2	05JRY5_HUMAN	05jry5	homo sapien
860	31	100.0	184	2	04NOC9_9DELT	04nc9	anaeromyxob	933	31	100.0	207	2	04LLZ3_9BURK	04llz3	burkholderi
861	31	100.0	184	2	04MTIO_BACCE	04mtio	bacillus ce	934	31	100.0	208	2	0582P3_9TRYP	0582p3	trypanosoma
862	31	100.0	184	2	073AC8_BACCI	073ac8	bacillus ce	935	31	100.0	208	2	05QGR1_MASBA	05qgr1	maestigmoeb
863	31	100.0	184	2	081P76_BACCR	081p76	bacillus an	936	31	100.0	208	2	070K47_9ACTO	070k47	gordonia we
864	31	100.0	184	2	081S90_BACAN	081s90	bacillus an	937	31	100.0	208	2	07UV64_RHOBA	07uv64	rhodospirill
865	31	100.0	184	2	06HKG7_BACHK	06hkg7	bacillus th	938	31	100.0	208	2	06QPA3_9ADEN	06qpa3	simian aden
866	31	100.0	184	2	063D26_BACGZ	063d26	bacillus ce	939	31	100.0	209	2	05Z300_NOCFA	05z300	nocardia fa
867	31	100.0	184	2	08RYO6_CORRF	08ryo6	corynebacte	940	31	100.0	211	2	04HX91_GIBZE	04hx91	gibberella
868	31	100.0	185	1	TFZLY_HUMAN	08lieu	homo sapien	941	31	100.0	211	2	09VW14_DROME	09vw14	drosophila
869	31	100.0	185	1	TRXF2_ARATH	09xfth9	arabidopsis	942	31	100.0	211	2	0671A5_SYMTW	0671a5	syndiotabac
870	31	100.0	185	2	09WZJ6_MACMU	09wzj6	macaca mula	943	31	100.0	212	2	06XN29_RHOER	06xn29	rhodococcus
871	31	100.0	185	2	097R36_STEPPN	097r36	streptococc	944	31	100.0	212	2	05VPE1_NOCFA	05vpe1	nocardia fa
872	31	100.0	185	2	09RXW6_DEIRA	09rxw6	deinococcus	945	31	100.0	213	2	04X9X7_PLACH	04x9x7	plasmodium
873	31	100.0	186	1	TRXW2_ARATH	09seu8	arabidopsis	946	31	100.0	214	1	VEGPA_CANPA	09glf5	canis famli
874	31	100.0	186	2	08LG26_ARATH	08lg26	arabidopsis	947	31	100.0	214	2	09GLF5_PIG	09glf5	sus scrofa
875	31	100.0	186	2	056YG4_ARATH	056yg4	arabidopsis	948	31	100.0	214	2	066PD1_9RHIZ	066pd1	uncultured
876	31	100.0	186	2	066PC4_RHILE	066pc4	rhizobium l	949	31	100.0	214	2	066PD2_9RHIZ	066pd2	uncultured
877	31	100.0	186	2	066PC7_RHILE	066pc7	rhizobium l	950	31	100.0	214	2	066PD3_9RHIZ	066pd3	uncultured
878	31	100.0	186	2	050189_MYCHY	050189	mycoplasma	951	31	100.0	214	2	066PD5_9RHIZ	066pd5	uncultured
879	31	100.0	186	2	06ZCX6_BURKA	06zcx6	burkholderi	952	31	100.0	214	2	066PD6_9RHIZ	066pd6	uncultured
880	31	100.0	187	2	06ZVA2_HUMAN	06zva2	homo sapien	953	31	100.0	214	2	066PD7_9RHIZ	066pd7	uncultured
881	31	100.0	187	2	08S091_ORYSA	08s091	oryza sativ	954	31	100.0	214	2	066PE0_9RHIZ	066pe0	uncultured
882	31	100.0	187	2	08DTZ1_STMMU	08dtz1	streptococc	955	31	100.0	214	2	066PE2_9RHIZ	066pe2	uncultured
883	31	100.0	188	2	066PC9_RHILE	066pc9	rhizobium l	956	31	100.0	214	2	066PE3_9RHIZ	066pe3	uncultured
884	31	100.0	188	2	08RZV7_MOUSE	08rzv7	mus musculu	957	31	100.0	215	1	NRG2D_RAT	066pe3	uncultured
885	31	100.0	189	2	096MK4_HUMAN	096mk4	homo sapien	958	31	100.0	216	1	NRG2D_HUMAN	066pe4	uncultured
886	31	100.0	189	2	0951LQ4_FELCA	0951lq4	felis silve	959	31	100.0	216	1	NRG2D_MACPA	066pe5	uncultured
887	31	100.0	189	2	0655X0_ORYSA	0655x0	oryza sativ	960	31	100.0	216	1	NRG2D_MACMU	066pe6	uncultured
888	31	100.0	189	2	08H2V6_ORYSA	08h2v6	oryza sativ	961	31	100.0	216	1	NRG2D_PANTR	066pe7	uncultured
889	31	100.0	189	2	066PE7_9BRAD	066pe7	bradyrhizob	962	31	100.0	216	2	08WJH1_PONPY	08wjh1	pongo pygma
890	31	100.0	190	1	TRXF_SPTOL	099856	spinacia ol	963	31	100.0	216	2	08WJH1_PONPY	08wjh1	pongo pygma
891	31	100.0	190	1	VEGPA_BOVIN	015591	bos taurus	964	31	100.0	216	2	07ORD4_MACMU	07ord4	macaca mula
892	31	100.0	190	1	VEGPA_HORSE	099xrt0	equus cabal	965	31	100.0	216	2	08W2X9_ORYSA	08w2x9	oryza sativ
893	31	100.0	190	1	VEGPA_PIG	049151	sus scrofa	966	31	100.0	216	2	049816_MYCLE	049816	mycobacteri
894	31	100.0	190	1	TRXF_SHEEP	077643	ovis aries	967	31	100.0	216	2	07U1U8_MYCBO	07u1u8	mycobacteri
895	31	100.0	191	1	TRXF_MESCR	081332	mesembryant	968	31	100.0	216	2	066392_MYCTU	066392	mycobacteri
896	31	100.0	191	2	09NBE0_RIPPA	09nbe0	ricefla pach	969	31	100.0	217	2	05AT09_EMENT	05at09	aspergillus
897	31	100.0	191	2	095ME5_MACPA	095me5	macaca fasc	970	31	100.0	217	2	0658N4_HUMAN	0658n4	homo sapien
898	31	100.0	191	2	04NMH0_BACCE	04nmh0	bacillus ce	971	31	100.0	217	2	0726Q0_DESHV	0726q0	desulfovibr
899	31	100.0	191	2	08DQ10_STRR6	08dq10	streptococc	972	31	100.0	218	2	07PPY7_ANOGA	07ppy7	anopheles g
900	31	100.0	191	2	0733M6_BACCI	0733m6	bacillus ce	973	31	100.0	218	2	09PJB4_CHLAMU	09pjb4	chlamydia m
901	31	100.0	191	2	081AF8_BACCR	081af8	bacillus an	974	31	100.0	219	2	08N4R2_HUMAN	08n4r2	homo sapien
902	31	100.0	191	2	081Y83_BACAN	081y83	bacillus ce	975	31	100.0	220	2	09GBV5_HUMAN	09gbv5	homo sapien
903	31	100.0	191	2	06HF17_BACHK	06hf17	bacillus th	976	31	100.0	220	2	09ZVT3_ARATH	09zvt3	arabidopsis
904	31	100.0	191	2	0637L5_BACGZ	0637l5	bacillus ce	977	31	100.0	220	2	05TMM0_NOCFA	05tmm0	nocardia fa
905	31	100.0	192	2	09YEH7_ABRPE	09yeh7	aeropyrum p	978	31	100.0	220	2	098253_MCV1	098253	molluscum c
906	31	100.0	192	2	06VQ14_HYDMA	06vq14	hydra magni	979	31	100.0	220	2	04TGPF_TETNG	04tgpf	tetradodon n
907	31	100.0	192	2	066NM9_RHILE	066nm9	rhizobium l	980	31	100.0	222	2	07S153_NEUCR	07s153	neurospora

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881 31 100.0 222 2 Q6SN38_CERMO Q6sn38_cercoptihc
882 31 100.0 222 2 Q6SN76_9PRIM Q6sn76_cercocebub
883 31 100.0 222 2 Q6SNH6_COLGU Q6snh6_colobus_gue
884 31 100.0 222 2 Q6SNP3_PAPPA Q6snp3_papio_papio
885 31 100.0 222 2 Q6LDI1_ARATH Q6ldi1_arabidopsis
886 31 100.0 222 2 Q6ASV5_PROAC Q6asv5_propionibac
887 31 100.0 222 2 Q6RG01_FUSNN Q6rg01_fusobacteri
888 31 100.0 222 2 Q6CB61_MYCLE Q6cb61_mycobacteri
889 31 100.0 223 2 Q6Z5M4_OREYA Q6z5m4_oryza_sativ
890 31 100.0 223 2 Q6GMH2_STRGL Q6gmh2_atricipovce
891 31 100.0 223 2 Q6JNF4_ARTNI Q6jnf4_arthrobacte
892 31 100.0 223 2 Q6Z234_RAT Q6z234_rattus_norv
893 31 100.0 224 2 Q6NAB0_HUMAN Q6nab0_homo_sapien
894 31 100.0 224 2 Q6UMD8_HUMAN Q6umd8_homo_sapien
895 31 100.0 224 2 Q6K4P2_DROME Q6k4p2_drosophila
896 31 100.0 225 2 Q6C708_MOUSE Q6c708_mus_musculu
897 31 100.0 225 2 Q6BK39_RAT Q6bk39_rattus_norv
898 31 100.0 225 2 Q6P346_MOUSE Q6p346_mus_musculu
899 31 100.0 225 2 Q4REX3_TETNG Q4rex3_tetradon_n
1000 31 100.0 226 2 Q7UL27_RHOBA Q7ul27_rhodopirell

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ALIGNMENTS

RESULT 1

SCXP_1 ANDMA STANDARD; PRT; 35 AA.

AC P01456; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Neurotoxin P2.
 OS Androctonus mauretanicus mauretanicus (Scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butridae; Butthoidea; Butthidae; Androctonus.
 OX NCBI_TaxID=6860;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Venom.
 RX MEDLINE=5193276; PubMed=3992595; DOI=10.1016/0041-0101(85)90114-X;
 RA Rosso J.-P., Rochat H.;
 RT "Characterization of ten proteins from the venom of the Moroccan
 scorpion Androctonus mauretanicus mauretanicus, six of which are toxic
 to the mouse."
 RL Toxicon 23:113-125(1985).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the short scorpion toxin family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC -----
 CC PIR: A01758; NTSRPM.
 DR HSSP; P15222; 1S1S.
 DR InterPro; IPR007958; toxin_5.
 DR Pfam; PF05294; Toxin_5; 1.
 KM Direct protein sequencing; Neurotoxin; Toxin.
 FT DISULFID 1 18 By similarity.
 FT DISULFID 4 25 By similarity.
 FT DISULFID 15 30 By similarity.
 FT DISULFID 19 32 By similarity.
 SQ SEQUENCE 35 AA; 3673 MW; 21365926289B5A CRC64;

Query Match 100.0%; Score 31; DB 1; Length 35;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

||||

Db 1 CGPC 4

RESULT 2

BS14_BUTSI STANDARD; PRT; 36 AA.

AC P59887; 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chlorotoxin-like peptide Bs 14 (Bs14).
 OS Butrus sindicus (Scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butthidae; Butthoidea; Butthidae; Mesobuthus.
 OX NCBI_TaxID=42519;
 RN [1]
 RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99157745; PubMed=10048185; DOI=10.1016/S1095-6433(98)10140-X;
 RA Ali S.A., Stoeva S., Schuetz J., Kaye R., Abbasi A., Zaidi Z.H.,
 RA Voelter W.;
 RT "Purification and primary structure of low molecular mass peptides
 from scorpion (Butrus sindicus) venom."
 RL Comp. Biochem. Physiol. 121A:323-332(1998).
 CC -1- FUNCTION: Probable chloride channel ligand, which blocks small-
 CC conductance chloride channels (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- MASS SPECTROMETRY: MW=3848.3; METHOD=MALDI; RANGE=1-36;
 CC NOT=Ref.1.
 CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Chloride
 CC channel inhibitor subfamily.

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 CC removed.
 CC -----
 CC InterPro; IPR007958; toxin_5.
 DR Pfam; PF05294; Toxin_5; 1.
 KM Chloride channel inhibitor; Direct protein sequencing;
 KW Ionic channel 1 18 By similarity.
 FT DISULFID 1 18 By similarity.
 FT DISULFID 4 25 By similarity.
 FT DISULFID 15 30 By similarity.
 FT DISULFID 19 32 By similarity.
 SQ SEQUENCE 36 AA; 3847 MW; 536117F8E5015A0 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 36;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

||||

Db 1 CGPC 4

RESULT 3

O46621_TAPIN PRELIMINARY; PRT; 38 AA.

AC O46621; 01-JUN-1998 (TREMBREL. 06, Created)
 DT 01-JUN-1998 (TREMBREL. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBREL. 23, Last annotation update)
 DE Luteinizing hormone beta-subunit (Fragment).
 DE Name=LH-beta;
 OS Tapirus indicus (Asiatic tapir) (Malayan tapir).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Laurasiatheria; Perissodactyla; Tapiridae;
 OC Tapirus.
 OX NCBI_TaxID=9802;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Fischer S., Velts J., Meyer H.H.D.;
 RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF047606; AAC04364.1; -, Genomic_DNA.
 DR HSSP; P01233; IHCN.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR006208; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 FT NON_TER
 SQ SEQUENCE 38 AA; 3928 MW; 5DBB7A21170C80A0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 7 CGPC 10

RESULT 4
 ID Q46620 EQUAS PRELIMINARY; PRT; 42 AA.
 AC Q46620;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Testis-specific RNA.
 GN Name=Mst87Fb; Synonyms=Dhtc2;
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;

GN Name=IH/CG-beta;
 OS Equus asinus somalicus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=73336;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA Fischer S., Velts J., Meyer H.H.D.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF047605; AAC04363.1; -, Genomic_DNA.
 DR HSSP; P01233; IHCN.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0005213; F:structural constituent of chorion (sensu In. . .; IEA.
 DR InterPro; IPR006208; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 KM Chorion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 42 AA; 4332 MW; 7D4A6C35B138589D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 6 CGPC 9

RESULT 5
 ID Q23947 DROHY PRELIMINARY; PRT; 49 AA.
 AC Q23947;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Testis-specific RNA.
 GN Name=Mst87Fa; Synonyms=Dhtc3;
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;

GN Name=Mst87Fa; Synonyms=Dhtc3;
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Kuech A., Buenemann H.;
 RA Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X58114; CAA41117.1; -, Genomic_DNA.
 DR FlyBase; FBgn0015096; Dhyd\Mst87Fa.
 SQ SEQUENCE 49 AA; 4610 MW; BE158FEC51369F01 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 3 CGPC 6

RESULT 6
 ID Q23948 DROHY PRELIMINARY; PRT; 49 AA.
 AC Q23948;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Testis-specific RNA.
 GN Name=Mst87Fb; Synonyms=Dhtc2;
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;

GN Name=Mst87Fb; Synonyms=Dhtc2;
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA Kuech A., Buenemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X58114; CAA41118.1; -, Genomic_DNA.
 DR FlyBase; FBgn0015097; Dhyd\Mst87Fb.
 SQ SEQUENCE 49 AA; 4550 MW; 24758FEC51369F1D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 3 CGPC 6

RESULT 7
 ID Q8MLN5 DROME PRELIMINARY; PRT; 51 AA.
 AC Q8MLN5;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE CG30430-PA (IP04475D).
 GN Name=CG30430; ORFNames=CG30430;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]

GN Name=CG30430; ORFNames=CG30430;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Domnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ilegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Zhang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zhibs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommler B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kelniker J.S., Bergman C.M., Krommler B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertman B.P.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.,
 RT "Protophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RP NUCLEOTIDE SEQUENCE.

RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Celniker S.,
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A5003466; AAM68330.1; -; Genomic_DNA.
 DR EMBL; BT023672; AAY85072.1; -; mRNA.
 DR EMBL; CC30430; Drosophila melanogaster.
 DR FlyBase; FBgn0050430; CG30430.
 SQ SEQUENCE 51 AA; 5077 MW; 0C26A637E5D2949B CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 RESULT 8
 Q6QAU0 DROMA PRELIMINARY; PRT; 52 AA.
 ID Q6QAU0 DROMA PRELIMINARY;
 AC Q6QAU0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE M8T84DC.
 GN Name=M8T84DC; ORFName=CG17945;
 OS Drosophila mauritiana (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7226;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=952;
 RX PubMed=15486701; DOI=10.1007/s00239-004-2622-Y;
 RA Michalak P., Noor M.A.F.,
 RT "Association of misexpression with sterility in hybrids of *Drosophila*
 RT simulans and *D. mauritiana*.";
 RL J. Mol. Evol. 59:277-282(2004).
 DR EMBL; AY549566; AAS55565.1; -; Genomic DNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0042742; P:defense response to bacteria; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IPR001450; 4Fe4S_Ferredoxin.
 DR InterPro; IPR006081; Defensin_alpha.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS00269; DEFENSIN; 1.
 DR PROSITE; PS01208; VWF_C_1.
 SQ SEQUENCE 52 AA; 4908 MW; DE0F3DB43F68EE3A CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 RESULT 9
 MS84C DROME
 ID MS84C DROME STANDARD; PRT; 55 AA.
 AC Q01644; Q9VIA0;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Male specific sperm protein M8T84DC.

GN Name=Mt84Dc; ORFNames=CG17945;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Oregon-R.
 RX MEDLINE=9212953; PubMed=1684716; DOI=10.1016/0925-4773(91)90064-D;
 RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U., Schaefer M.,
 RT "A cluster of four genes selectively expressed in the male germ line
 of Drosophila melanogaster."
 RL Mech. Dev. 35:143-151(1991).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkeley.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sturgeon G.G., Wortman J.R., Landell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adayant A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu P., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boltekar S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,
 RA Cherry J.M., Chew S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evans G.L., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Fosler A., Gong F., Gortelli J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Houston D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jafari M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasok P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveli J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 [3]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminck J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Brentenourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -1- TISSUE SPECIFICITY: Testis.
 CC -1- DEVELOPMENTAL STAGE: Primary spermatocytes.
 CC -1- DOMAIN: This protein is mostly composed of repetitive C-G-P
 motifs.

CC -1- SIMILARITY: Belongs to the MST(3)CGP family.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

 CC EMBL: X67703; CAA47939.1; -; Genomic DNA.
 DR EMBL: AE003672; AAF54025.1; -; Genomic DNA.
 DR PIR: S25774; S25774.
 DR Ensemble: CG17945; Drosophila melanogaster.
 DR FlyBase: FBgn004174; Mt84Dc.
 DR InterPro: IPR005634; MSSP.
 DR Pfam: PF03940; MSSP; 1.
 KW Developmental protein; Differentiation; Multigene family; Repeat;
 KW Spermatogenesis.
 SQ SEQUENCE 55 AA; 5225 MW; 95A12F3ABC8BBD6C CRC64;

 QY 2 CGPC 5
 ||||
 Db 3 CGPC 6

 RESULT 10
 Q6QAT9 DROSI
 ID Q6QAT9 DROSI PRELIMINARY; PRT; 55 AA.
 AC Q6QAT9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MST84DC.
 GN Name=Mt84Dc; ORFNames=CG17945;
 OS Drosophila simulans (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7240;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ottawa;
 RX PubMed=15486701; DOI=10.1007/s00239-004-2622-Y;
 RA Michaelak P., Noor M.A.F.,
 RT "Association of misexpression with sterility in hybrids of Drosophila
 simulans and D. mauritiana."
 RL J. Mol. Evol. 59:277-282(2004).
 DR EMBL: AY54957; AAS55566.1; -; Genomic DNA.
 DR InterPro: IPR001450; 4Fe4S_Ferredoxin.
 DR InterPro: IPR005634; MSSP.
 DR InterPro: IPR001007; VWF_C.
 DR Pfam: PF03940; MSSP; 1.
 DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE: PS01208; VWF_C; 1.
 DR PROSITE: PS01208; VWF_C; 1.
 SQ SEQUENCE 55 AA; 5165 MW; 95A12F27D07B6F6C CRC64;

 QY 2 CGPC 5
 ||||
 Db 3 CGPC 6

 Query Match 100.0%; Score 31; DB 1; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 RESULT 11
 Q6QAU1 DROMA
 ID Q6QAU1 DROMA PRELIMINARY; PRT; 55 AA.
 AC Q6QAU1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE MST8D.C.
 GN Name=Mst84Dc; ORFNames=CG17945;
 OS Drosophila mauritiana (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7226;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MS11.
 RC PubMed=15486701; DOI=10.1007/s00239-004-2622-Y;
 RA Michalak P., Noor M.A.F.;
 RT "Association of misexpression with sterility in hybrids of Drosophila
 simulans and D. mauritiana."
 RL J. Mol. Evol. 59:277-282(2004).
 DR EMBL; AY549955; AAS55564.1; -; Genomic_DNA.
 DR InterPro; IPR001450; 4Fe4s_Ferredoxin.
 DR InterPro; IPR005634; MSSP_
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF03940; MSSP_1.
 DR PROSITE; PS00198; 4Fe4s_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_1; 1.
 DR SEQUENCE 55 AA; 5165 MW; 95A12P27D07B6F6C CRC64;

Query Match 100.0%; Score 31; DB 2; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 3 CGPC 6

RESULT 12
 MS87F_DROME
 ID MS87F_DROME STANDARD; PRT; 56 AA.
 AC P08175; Q9VFO6;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 GN Male specific sperm protein Mst87F.
 DE Name=Mst87F; Synonyms=mst(3)g1-9; ORFNames=CG17956;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Canton-S;
 RC MEDLINE=8821557; PubMed=2835228;
 RA Kuhn R., Schaefer U., Schaefer M.;
 RT "Cis-acting regions sufficient for spermatocyte-specific
 transcriptional and spermatid-specific translational control of the
 Drosophila melanogaster gene mst(3)g1-9."
 RL EMBO J. 7:447-454(1988).

RT RT
 RL RT
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkelley;
 RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballieu R.M., Baxu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Modarres C., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).

RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.U., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.B.,
 RA Smith C.D., Tupy J.L., Whitefield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

CC -1- TISSUE SPECIFICITY: Testis.
 CC -1- DEVELOPMENTAL STAGE: Primary spermatocytes.
 CC -1- DOMAIN: This protein is mostly composed of repetitive C-G-P motifs.
 CC -1- SIMILARITY: Belongs to the MST(3)CGP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC CC
 CC DR EMBL; Y00831; CA66761.1; -; Genomic DNA.
 DR EMBL; AB003702; AAF54994.1; -; Genomic DNA.
 DR PIR; S00340; WTFP.
 DR HSSP; P01180; LJK6.
 DR Ensembl; CG17956; Drosophila melanogaster.
 DR FlyBase; FBgn002862; Mst87F.
 KW Developmental protein; Differentiation; Multigene family; Repeat;
 KW Spermatogenesis.
 SQ SEQUENCE 56 AA; 5233 MW; 830CD13212C34A47 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 3 CGPC 6

RESULT 13
 Q595V9_NEILTA

ID Q595V9 NEI1A PRELIMINARY; PRT; 56 AA.
 AC Q595V9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DR Rubredoxin.
 OS Neisseria lactamica.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_Taxid=486;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA van Pammel M.W.J., Bart A., Luyf A.C.M., van Kampen A.H.C.,
 RT "Identification of anomalous sequences in Neisseria lactamica expands
 RL the neisserial gene pool."; Genomic DNA.
 DR EMBL; AY532628; AAW21818.1; -; Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 KW Electron transport; Iron; Metal-binding; Rubredoxin.
 SQ SEQUENCE 56 AA; 6345 MW; 17DACA86E7DB8CF CRC64;

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 6 CGPC 9

RESULT 14
 Q5F8A3 NEIG1 PRELIMINARY; PRT; 56 AA.
 ID Q5F8A3;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DR Putative rubredoxin.
 OS OrderedLocustNames=NGO0885;
 OC Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_Taxid=242231;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Lewis L.A., Gillaapy A.F., McLaughlin R.E., Gibson M., Ducey T.F.,
 RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
 RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
 RA Kenyon S.W., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
 RT "The complete genome sequence of Neisseria gonorrhoeae."
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE004969; AAW89584.1; -; Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 DR InterPro; IPR004039; Rubredox.
 DR InterPro; IPR001052; Rubredoxin.
 DR Pfam; PF00301; Rubredoxin; 1.
 DR PRINTS; PR00163; RUBREDOXIN.
 DR PRODOM; PD001610; Rubredoxin.
 DR PROSITE; PS00202; RUBREDOXIN; 1.
 DR PROSITE; PS0903; RUBREDOXIN LIKE; 1.
 KW Complete proteome; Electron transport; Iron; Metal-binding;
 KW Rubredoxin.
 SQ SEQUENCE 56 AA; 6345 MW; 17DACA86E7DB8CF CRC64;

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 6 CGPC 9

RESULT 15
 Q7DDJ1 NEIMB PRELIMINARY; PRT; 56 AA.
 ID Q7DDJ1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DR Rubredoxin.
 OS OrderedLocustNames=MNB0993;
 OC Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_Taxid=491;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=MCS8 / Serogroup B;
 RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
 RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
 RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
 RA Dodson R.J., Nelson W.C., Gwin M.L., Deboy R.T., Peterson J.D.,
 RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
 RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
 RA Ciltone H., Clark B.B., Cotton M.D., Uteerback T.R., Khouri H.M.,
 RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizzo M.,
 RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
 RA Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MCS8.";
 RL Science 287:1809-1815 (2000).
 DR EMBL; AE002098; AAF41396.1; -; Genomic DNA.
 DR HSP; P24297; 1105.
 DR TIGR; NMB0993; -;
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 DR InterPro; IPR004039; Rubredox.
 DR InterPro; IPR001052; Rubredoxin.
 DR Pfam; PF00301; Rubredoxin; 1.
 DR PRINTS; PR00163; RUBREDOXIN.
 DR PRODOM; PD001610; Rubredoxin.
 DR PROSITE; PS00202; RUBREDOXIN; 1.
 DR PROSITE; PS0903; RUBREDOXIN LIKE; 1.
 KW Complete proteome; Electron transport; Iron; Metal-binding;
 KW Rubredoxin.
 SQ SEQUENCE 56 AA; 6369 MW; F2CE9EAB6E7DB8C9 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 6 CGPC 9

RESULT 16
 Q9JON3 NEIMA PRELIMINARY; PRT; 56 AA.
 ID Q9JON3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DR Putative rubredoxin.
 OS OrderedLocustNames=MNA1201;
 OC Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_Taxid=656599;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=22491 / Serogroup A / Serotype 4a;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parthill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Fellwell T., Hamlin N., Holroyd S.,
 RA Jagals K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.,
 RT "Complete DNA sequence of a serogroup A strain of *Neisseria*
 RT meningitidis 22491.";
 RL Nature 404:502-506 (2000).
 DR EMBL, AL162755; CAB84462.1; -; Genomic_DNA.
 DR PIR, H81133; H81133.
 DR HSSP, P24297; IRWD.
 DR GO, GO:0005489; F:electron transporter activity; IEA.
 DR GO, GO:0046872; F:metal ion binding; IEA.
 DR GO, GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR004039; Rubredoxin.
 DR Pfam: PF0301; Rubredoxin.
 DR PRINTS: PR00163; RUBREDOXIN.
 DR ProDom: PD001610; Rubredoxin; 1.
 DR PROSITE: PS00202; RUBREDOXIN; 1.
 DR PROSITE: PS00903; RUBREDOXIN LIKE; 1.
 KW Complete proteome; Electron transport; Iron; Metal-binding;
 KW Rubredoxin.
 SQ SEQUENCE 56 AA; 6369 MW; F2CE9EA86E7DB8C9 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 6 CGPC 9

RESULT 17
 Q6QAT8 DROSI
 ID Q6QAT8_DROSI PRELIMINARY; PRT; 58 AA.
 AC Q6QAT8;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE MST84DC.
 GN Name=Mst84DC; ORFNames=CG17945;
 OS Drosophila simulans (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCB1_TaxID=7240;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Valparaiso;
 RX PubMed=15486701; DOI=10.1007/s00239-004-2622-Y;
 RA Michalak P., Noor M.A.F.,
 RT "Association of misexpression with sterility in hybrids of *Drosophila*
 RT simulans

Query Match 100.0%; Score 31; DB 2; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 3 CGPC 6

RESULT 18
 SCCT MESMA
 ID SCCT MESMA STANDARD; PRT; 59 AA.
 AC 09UAD0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Neurotoxin BmKCT precursor (C1-channel toxin) (CT neurotoxin) (Short-chain toxin KCT) (BmKCL1) (TXCL1).
 DE Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butridae; Butioidae; Butridae; Mesobuthus.
 OC NCB1_TaxID=34649;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Venom gland;
 RX MEDLINE=20175769; PubMed=10708793; DOI=10.1016/S0041-0101(99)00212-3;
 RA Zeng X.-C., Li W.-X., Zhu S.-Y., Peng F., Zhu Z.-H., Wu K.-L.,
 RA Yang F.-H.,
 RT "Cloning and characterization of a cDNA sequence encoding the
 RT precursor of a chlorotoxin-like peptide from the Chinese scorpion
 RT *Buthus martensii* Karach.";
 RL Toxicon 38:1009-1014(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Wu J.-J., Dai L., Chi C.-W.,
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Venom gland;
 RA Shunyi Z., Wenxin L.,
 RT "cDNA encoding a putative insect toxin from BmK.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Shunyi Z., Wenxin L.,
 RT "Genomic DNA of a scorpion Cl-channel toxin.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Chloride channel ligand. Blocks small-conductance
 CC chloride channels (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Chloride
 CC channel inhibitor subfamily.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL: AF135821; AA001185.1; -; mRNA.
 CC EMBL: AF079059; AA047373.1; -; Genomic_DNA.
 CC EMBL: AF159976; AA061823.1; -; mRNA.
 CC EMBL: AF419252; AA032699.1; -; Genomic_DNA.
 CC HSSP: P15222; 1S1S.
 DR InterPro: IPR007958; toxin_5.
 DR Pfam: PF05294; Toxin_5; 1.
 KW Chloride channel inhibitor; Ionic channel inhibitor; Neurotoxin;
 KW Signal; Toxin.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 59 Neurotoxin BmKCT.
 FT DISULFID 25 42 By similarity.
 FT DISULFID 28 49 By similarity.
 FT DISULFID 39 54 By similarity.
 FT DISULFID 43 56 By similarity.
 SQ SEQUENCE 59 AA; 6467 MW; C9FAABAFCB8B02EA CRC64;

Query Match 100.0%; Score 31; DB 1; Length 59;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 25 CGPC 28

RESULT 19

SCCX MESMA STANDARD; PRT; 59 AA.
ID SCX_MESMA
AC Q9BJM4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Neurotoxin Bm12-b precursor.
OS Mesobuthus marseus (Manchurian scorpion) (Butus marseus);
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Scorpiones;
OC Butidae; Butiidae; Butidae; Mesobuthus.
OX NCBI_TaxId=34649;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xu C.-Q., Chi C.-W.;
RT "A novel neurotoxin from scorpion BmK.";
Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Chloride channel ligand. Blocks small-conductance
chloride channels (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Chloride
channel inhibitor subfamily.

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removed.

CC EMBL: A327643; AAK1644.1; -; mRNA.
DR HSP; P15222; ISIS.
DR InterPro; IPR007958; toxin_5.
DR Pfam; PF05294; Toxin_5; 1.
KW Chloride channel inhibitor; Ionic channel inhibitor; Neurotoxin;
KW Signal; Toxin.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 59 Neurotoxin Bm12-b.
FT DISULFID 25 42 By similarity.
FT DISULFID 28 49 By similarity.
FT DISULFID 39 54 By similarity.
FT DISULFID 43 56 By similarity.
SQ SEQUENCE 59 AA; 6484 MW; C2BABAFCB8BD9EA CRC64;

Query Match 100.0%; Score 31; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 25 CGPC 28

RESULT 20

Q71DA0 DROXA PRELIMINARY; PRT; 60 AA.
ID Q71DA0 DROXA PRELIMINARY;
AC Q71DA0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG4959 (Fragment).
OS Drosophila yakuba (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxId=7245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;
RA Domazet-Loso T., Tautz D.;
RT "An evolutionary analysis of orphan genes in Drosophila.";
Genome Res. 13:2213-2219(2003).
DR EMBL; AF531969; AAQ09868.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6105 MW; BF1072E1DA7C14AA CRC64;

Query Match 100.0%; Score 31; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 41 CGPC 44

RESULT 21

Q8MSH6 DROME PRELIMINARY; PRT; 60 AA.
ID Q8MSH6;
AC Q8MSH6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GH21.762p.
GN ORFNames=CG4959;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guatin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118808; AAM50668.1; -; mRNA.
DR FlyBase; FBgn0028883; CG4959.
SQ SEQUENCE 60 AA; 6117 MW; BEFF72E1C0CC14BC CRC64;

Query Match 100.0%; Score 31; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 41 CGPC 44

RESULT 22

Q8T403 DROME PRELIMINARY; PRT; 61 AA.
ID Q8T403 DROME PRELIMINARY;
AC Q8T403;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE A123551P (CG31740-PA).
GN ORFNames=CG31740;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Drensek D., Fafan D., Frise E.,
 RA George R., Gonzalez W., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munoz J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwe R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Fostel A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jaitani B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jermal M.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.C., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassenaar D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Wooley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Ye X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RL "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RL *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [4]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RL "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RL a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [5]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter C., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RL "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RL systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [6]
 RN NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RL "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RN NUCLEOTIDE SEQUENCE.
 RP FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY089413; AAL90151.1; -; mRNA.
 DR EMBL: AE003657; AAN1177.1; -; Genomic DNA.
 DR Ensembl: CG31740; *Drosophila melanogaster*.
 DR FlyBase: FBgn0051740; CG31740.
 SQ SEQUNCE 61 AA; 5965 MW; 94390FEB1D8B44D4 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Gaps 0;
 Matches 4; Conservative 0; Indels 0;
 Db 34 CGPC 37
 Qy 2 CGPC 5
 Db 34 CGPC 37
 RESULT 23
 SCIT_MESRA STANDARD; PRT; 62 AA.
 AC P81761; O870X4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Lepidopteran-selective toxin precursor (Butar) (BrCh12).
 OS Mesobuthus tamulus (Eastern Indian scorpion) (Butus tamulus).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butridae; Buthoidea; Butridae; Mesobuthus.
 OX NCBI_TaxID=34647;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Venom gland;
 RA Newton K.A., Armugam A., Strong P.N., Jeyaseelan K.;
 RL "Insect toxin from Mesobuthus tamulus.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN PROTEIN SEQUENCE OF 25-61, FUNCTION, SUBCELLULAR LOCATION, TISSUE
 RP SPECIFICITY, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX PubMed=11782289; DOI=10.1186/1472-2091-2-16;
 RA Widiyagiti R., Inceoglu B., Herrmann R., Derbel M., Choudary P.V.,
 RA Hammoek B.D.;
 RL "Isolation and characterization of a novel lepidopteran-selective
 RL toxin from the venom of South Indian red scorpion, Mesobuthus
 RL tamulus.";
 RL BMC Biochem. 2:16-16(2001).
 CC -1- FUNCTION: Induces flaccid paralysis in *H. virescens* larvae. Is not
 CC toxic to *S. falculata* larvae or mice.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- MASS SPECTROMETRY: MW=3856.77; METHOD=Electrospray; RANGE=25-61;
 CC NOTE=Ref.2.
 CC -1- SIMILARITY: Belongs to the short scorpion toxin family.

RA Durbin K.J., Evangelista C.C., Ferraz N.S., Periera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glöckner A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kudrya C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Moberly C., Morris J., Mostreli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacible J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RT Science 287:2185-2195(2000).
RX [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hirdekar P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shy S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- DEVELOPMENTAL STAGE: Primary spermatocytes.
CC -1- DOMAIN: This protein is mostly composed of repetitive C-G-P
CC motifs.
CC -1- SIMILARITY: Belongs to the MST(3) GCP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X67703; CAA47937.1; -; Genomic DNA.
DR EMBL; AE003672; AAF54022.1; -; Genomic DNA.
DR PIR; S25772; S25772.
DR Ensembl; CG17946; Drosophila melanogaster.
DR FlyBase; FBgn0004172; Msc84Da.
DR InterPro; IPR005634; MSSP.
DR Pfam; PF03940; MSSP; 1.
KW Developmental protein; differentiation; Multigene family; Repeat;
KW Spermatogenesis.
SQ SEQUENCE 63 AA; 5806 MW; BF64CD74CBCEFD3F CRC64;

Query Match 100.0%; Score 31; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
Db 17 CGPC 20

RESULT 25
O8MT19_SHEEP PRELIMINARY; PRT; 64 AA.
ID O8MT19_SHEEP PRELIMINARY; PRT; 64 AA.
JC O8MT19;

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DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vascular endothelial growth factor 188 isoform (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
RN
[1]
RP NUCLEOTIDE SEQUENCE.
RC TRISSE-Placental artery endothelium;
RA Chung J.-Y., Teo S.C.M., Wen Y.-X., Magness R.R., Zheng J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF534638; AAN04109.1; -, mRNA.
DR SMR; Q8M119; 15-64.
DR InterPro; IPR001212; Somatomedin_B.
DR PRINTS; PR00022; SOMATOMEDINB.
FT NON TER 1 1
SQ SEQUENCE 64 AA; 7674 MW; 8BF719596DDEF6B6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 16 CGPC 19

RESULT 26
Q6IWK3 PIG PRELIMINARY; PRT; 66 AA.
ID Q6IWK3_PIG PRELIMINARY; PRT; 66 AA.
AC Q6IWK3_PIG PRELIMINARY; PRT; 66 AA.
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxID=9823;
RN
[1]
RP NUCLEOTIDE SEQUENCE.
RA Teyade C., Black G.P., Crox A.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY616676; AAT3876.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Growth factor; Mitogen.
FT NON TER 1 1
SQ SEQUENCE 66 AA; 7796 MW; 2D3E1D07B63620 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 56 CGPC 59

RESULT 27
Q9VM83 DROME PRELIMINARY; PRT; 67 AA.
ID Q9VM83_DROME PRELIMINARY; PRT; 67 AA.

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AC Q9VM83;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE CG17376-PB, isoform B (GH22658p).
GN ORFNames=CG17376;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandel M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.B., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleib J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RN
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Munz D.M., Nelson C.R.,
RA Pacleib J.M., Park S., Pfeiffer B.D., Richards S., Sodegren E.J.,
RA Svirskas R., Taber P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatin genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN
[3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

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[4]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22426069; Pubmed=12537572;
 RX Hiraideky P., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Misra S., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.B.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celisner S., Carlson M., Wan K., Pfeiffer B., Friese E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Sylvestras R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG Flybase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkeley.
 RA Stapleton M., Carlson J., Chavez C., Friese E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Rubin G.M., Celisner S.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003615; AAF52440.1; -; Genomic_DNA.
 DR EMBL; BT011549; AAS15685.1; -; mRNA.
 DR Ensembl; CG17376; Drosophila melanogaster.
 DR Flybase; FBgn0042189; CG17376.
 SQ SEQUENCE 67 AA; 6871 MW; B9442P2C7B567C76 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 8 CGPC 11

RESULT 28
 ID O6EPUB ORYSA PRELIMINARY; PRT; 69 AA.
 AC O6EPUB;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE Hypothetical protein OSUNBA0016D04.29.
 GN Name=OSUNBA0016D04.29;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCB1_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nippondare(GAS) genomic DNA, chromosome 2, BAC
 RT clone:OSUNBA0016D04.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005800; BAD23238.1; -; Genomic_DNA.
 DR Gramene; O6EPUB; -;
 KW Hypothetical protein.
 SQ SEQUENCE 69 AA; 7109 MW; 97BA6730BE5730A6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 31 CGPC 34

RESULT 29
 ID O7PK85 ANOGA PRELIMINARY; PRT; 71 AA.
 AC O7PK85;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DE ENSANGP00000023827 (Fragment).
 GN ORFNames=ENSANG00000020560;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OC NCB1_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008980; EAA43469.2; -; Genomic_DNA.
 DR InterPro; IPR005634; MSSP.
 DR Pfam; PF03940; MSSP; 1.
 FT NON_TER 1 71
 FT NON_TER 71 71
 SQ SEQUENCE 71 AA; 6483 MW; 192B4F10CC5613BE CRC64;

Query Match 100.0%; Score 31; DB 2; Length 71;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 2 CGPC 5

RESULT 30
 ID MS84D DROME STANDARD; PRT; 72 AA.
 AC 001645; OSV199;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Male specific sperm protein Mst84D.
 GN Name=Mst84D; ORFNames=CG17935;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCB1_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=Oregon-R;
 RX MEDLINE=92102953; Pubmed=1684716; DOI=10.1016/0925-4773(91)90064-D;
 RA Kuhn R., Kuhn C., Boerscher D., Glaetzer K.H., Schaefer U., Schaefer M.;
 RT "A cluster of four genes selectively expressed in the male germ line
 RT of Drosophila melanogaster.";

RL Mech. Dev. 35:143-151 (1991).
 [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=Berkley;
 RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Adair J.F., Agbayani A., An H.-J., Andrews-Planck C., Baldwin D.,
 RA Bailly R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchen M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshnell A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sider-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195 (2000).
 [3]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D.N.J., Dysdale R.A.,
 RA Harris N.L., Richter J., Russe S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -1- TISSUE SPECIFICITY: Testis.
 CC -1- DEVELOPMENTAL STAGE: Primary spermatocyte.
 CC -1- DOMAIN: This protein is mostly composed of repetitive C-G-P
 motifs.
 CC -1- SIMILARITY: Belongs to the MST(3)CGP family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: X67703; CAA47940.1; -; Genomic DNA.
 DR EMBL: AF003672; AA954026.1; -; Genomic DNA.
 DR PIR: S25775; S25775.
 DR Ensemble: CG17935; Drosophila melanogaster.
 DR FlyBase: FBgn004175; Mst84Dd.

DR InterPro: IPR005634; MSSP.
 DR Pfam: PF03940; MSSP; 1.
 KM Developmental protein; Differentiation; Multigene family; Repeat;
 KW Spermatogenesis.
 FT CONFLICT 13 Missing (in Ref. 1).
 SQ SEQUENCE 72 AA; 6840 MW; 8CE374495F88ABA CRC64;
 Query Match 100.0%; Score 31; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 10 CGPC 13
 RESULT 31
 QSTSUA ANOGA
 ID QSTSUA ANOGA PRELIMINARY; PRT; 72 AA.
 AC QSTSUA;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE ENSANGP0000029185 (Fragment).
 GN ORFNames=ENSANG0000023294;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OC NCBI_Taxid=180454;
 RX NUCLEOTIDE SEQUENCE.
 RP STRAIN=PEST;
 RC The Anopheles gambiae Sequence Committee;
 RT Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 DR EMBL: AAAB01008900; BAI40455.1; -; Genomic DNA.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0005179; F:hormone activity; IEA.
 DR InterPro: IPR000381; Inhibin_betaab.
 DR PRINTS: PR00671; INHIBINB.
 FT NON TER 1 1
 FT NON TER 72 72
 SQ SEQUENCE 72 AA; 6596 MW; DA63390CA9DF3A01 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 38 CGPC 41
 RESULT 32
 Q4V3L2 DROME
 ID Q4V3L2 DROME PRELIMINARY; PRT; 72 AA.
 AC Q4V3L2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE I002161P
 GN Name=Mst84Dd;
 OS Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Celniker S.;
 RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; FRO23344; AAY55760.1; -; mRNA.
 SQ SEQUENCE 72 AA; 6840 MW; 8CE374495F88ABA CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 10 CGPC 13
 RESULT 33
 ID 074DK8_GROSL PRELIMINARY; PRT; 72 AA.
 AC 074DK8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocustNames=GSU1308;
 OC Geobacter sulfurreducens;
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteriaceae; Geobacter.
 OK NCBI_TaxID=35554;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Heideberg J.F., Wu D., Wu M., Ward N.L., Benan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., Debey R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Uterback T.R.,
 RA Van Aken S.E., Loyley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 RT environments."
 RL Science 302:1967-1969(2003).
 DR EMBL; AE017180; AAR34684.1; -; Genomic_DNA.
 DR TIGR; GSU1308; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 72 AA; 8191 MW; F25B550B9D43BB9 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 38 CGPC 41
 RESULT 34
 ID 04KKY5_MOUSE PRELIMINARY; PRT; 72 AA.
 AC 04KKY5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN Name=Pkd1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oaw and Lamb;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Roak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oaw and Lamb;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC099589; AAG95989.1; -; mRNA.
 DR MGI; MGI:97603; Pkd1.
 KW Hypothetical protein.
 SQ SEQUENCE 72 AA; 7108 MW; 37F5B94C6918C0FD CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 30 CGPC 33
 RESULT 35
 ID 06EPJ3_ORYZA PRELIMINARY; PRT; 73 AA.
 AC 06EPJ3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein OSJNBa0016D04.34.
 GN Name=OSJNBa0016D04.34;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaristidae; Oryzaceae; Oryza.
 OK NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 2, BAC
 RT clone:OSJNBa0016D04.34."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005800; BAC29333.1; -; Genomic_DNA.
 DR Gramene; 06EPJ3; -;
 KW Hypothetical protein.
 SQ SEQUENCE 73 AA; 7746 MW; 3EF220FB4F36D10A CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 CGPC 5
      ||||
Db      37 CGPC 40

RESULT 36
QYH54 CHICK PRELIMINARY; PRT; 73 AA.
ID QYH54 CHICK PRELIMINARY;
AC QYH54;
DT 01-MAY-1999 (TREMURel. 10, Created)
DT 01-MAY-1999 (TREMURel. 10, Last sequence update)
DT 01-JUN-2003 (TREMURel. 24, Last annotation update)
DE Keratin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RX NCLECTIDE SEQUENCE.
RP MEDLINE=85122780; PubMed=2578818; DOI=10.1016/0167-4781(85)90049-1;
RA Wilton S.D., Crocker L.A., Rogers G.E.;
RT "Isolation and characterization of keratin mRNA from the scale
RT epidermis of the embryonic chick.";
RL Biochim. Biophys. Acta 824:201-208(1985).
DR EMBL; M25641; AAA48932.1; -; mRNA.
DR PIR; A60136; A60136.
DR Ensembl; ENSGALG0000009189; Gallus gallus.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR003461; Keratin.
DR Pfam; PF02422; Keratin; 1.
KW Keratin.
PT NON TER.
SQ SEQUENCE 73 AA; 7468 MB; B108CEBA52106B5F CRC64;
      1 1
      |||
Query Match 100.0%; Score 31; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      70 CGPC 73

RESULT 37
MS84B DROME STANDARD; PRT; 74 AA.
ID MS84B DROME STANDARD;
AC Q01643; Q8M2E2; Q9V1A1;
DT 01-JUL-1993 (Rel. 26, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Male specific sperm protein Mst84b.
GN Name=Mst84b; ORFNames=CG17934;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RX NCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND
RP DEVELOPMENTAL STAGE.
RC STRAIN=Oregon-R;
RX MEDLINE=2102953; PubMed=1684716; DOI=10.1016/0925-4773(91)90064-D;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U., Schaefer M.;
RT "A cluster of four genes selectively expressed in the male germ line
RT of Drosophila melanogaster.";
RL Mech. Dev. 35:143-151(1991).
[2]
RX NCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

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RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amand R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chang M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busan D.A., Butler H., Cadiu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fester C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kesteven J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskae R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Weasman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[3]
GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bellocourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[4]
NCLECTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Berkely; TISSUE=Testis;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Garin H., Krommiller B., Pacle J.M., Park S., Wan K.H.,
RA Rubin G.M., Celnik S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.6(2002).
-1- TISSUE SPECIFICITY: Testis.
-1- DEVELOPMENTAL STAGE: Primary spermatocytes.
-1- DOMAIN: This protein is mostly composed of repetitive C-G-P motifs.
-1- SIMILARITY: Belongs to the MST(3)GSP family.
-1- CAUTION: Ref.4 sequence differs from that shown due to wrong choice of frame.
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

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CC -----
DR EMBL: X67703: CAA47938.1; -; Genomic DNA.
DR EMBL: AF003672: AAF54024.1; -; Genomic DNA.
DR EMBL: AY113221: AAM29226.1; ALT_SEQ; mRNA.
DR PIR: S25773; S25773.
DR HSSP: Q9S7B3; IEHH.
DR Ensembl: CG17934; Drosophila melanogaster.
DR FlyBase: FBgn0004173; MstB4D.
DR InterPro: IPR005634; MSSP.
DR Pfam: PF03940; MSSP; 1.
KW Developmental protein; Differentiation; Multigene family; Repeat;
KW Spermatogenesis.
FT COMPBIAS 2 74 Cys/Gly/Pro-rich.
FT CONFLICT 42 42 C -> W (in Ref. 1).
FT CONFLICT 60 60 P -> L (in Ref. 1).
SQ SEQUENCE 74 AA; 6725 MW; CC6FF07A7B7CABC CRC64;

Query Match 100.0%; Score 31; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 9 CGPC 12

RESULT 38
Q5TW29_NOCFA PRELIMINARY; PRT; 75 AA.
ID O5YW29;
AC O5YW29;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative ferredoxin.
GN OrderedLocustNames=hf24450;
OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.,
RT "The complete genomic sequence of Nocardia farcinica IFM 10152."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL: AP006618; BAD57292.1; -; Genomic DNA.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0005506; F:iron ion binding; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR001450; 4Fe4S_Fe_S_bd.
DR Pfam: PF00037; Fer4; 2.
DR PRINTS: PR00353; 4FE4SFDOXIN.
DR PROSITE: PS00198; 4FE4SFDOXIN; 1.
KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
KW Metal-binding; Transport.
SQ SEQUENCE 75 AA; 8193 MW; F6994795E7B2D209 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 54 CGPC 57

RESULT 39
Q82DW2_STRAW PRELIMINARY; PRT; 75 AA.
ID Q82DW2;
AC Q82DW2;

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DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ferredoxin.
GN Name=fdx; OrderedLocustNames=SAV4856;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR EMBL: BA000030; BAC72568.1; -; Genomic DNA.
DR HSSP: P00214; IPRM.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0005506; F:iron ion binding; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR001450; 4Fe4S_Fe_S_bd.
DR Pfam: PF00037; Fer4; 2.
DR PRINTS: PR00353; 4FE4SFDOXIN.
DR PROSITE: PS00198; 4FE4SFDOXIN; 1.
KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
KW Metal-binding; Transport.
SQ SEQUENCE 75 AA; 8139 MW; 8070930081708437 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 54 CGPC 57

RESULT 40
Q4RP51_TETNG PRELIMINARY; PRT; 75 AA.
ID Q4RP51;
AC Q4RP51;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 1 SCAFI5008, whole genome shotgun sequence.
GN ORFNames=GSTENG0031275001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphna; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Uallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozout-Coataz C., Benoit A.,
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dastiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

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RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,
 RA Cruaud C., Duprat S., Brothier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapuis C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volf J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.",
 RL Nature 431:946-957(2004).

RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FE8-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CA90105008; CAG09831.1; -; Genomic DNA.
 SQ SEQUENCE 75 AA; 7913 MW; 4918F75E5D548359 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
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 DB 17 CGPC 20

RESULT 41
 06UYH8_9CAUD
 ID 06UYH8_9CAUD PRELIMINARY; PRT; 76 AA.

AC 06UYH8;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Putative head-tail joining protein.
 OS Burkholderia cepacia phage BcepNazgul.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales.
 OK NCBI_TaxID=242861;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA Sumner E.J., Peek M.L., Halburton J.R., Hall E., Heusinkveld K.,
 RA Simmer J., No E.G., Gonzalez C.F., Young R.F.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A3537582; AA063363.1; -; Genomic DNA.
 DR GO; GO:0019067; P:Viral assembly, maturation, egress, and rel. .; IEA.
 DR InterPro; IPR004174; gpW.
 DR ProDom; PD019366; gpW; 1.
 SQ SEQUENCE 76 AA; 8345 MW; 9DBFDD73E5A96799 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 60 CGPC 63

RESULT 42
 074114_MYCPA
 ID 074114_MYCPA PRELIMINARY; PRT; 76 AA.

AC 074114;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN Ordered locus names=MAP1106;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;

OC Mycobacterium avium complex (MAC).
 OK NCBI_TaxID=1770;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K10;
 RA Li U., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A5017230; AAS03423.1; -; Genomic DNA.
 DR HSSP; P00214; 1B0T.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_Fe_s_bd.
 DR Pfam; PF00037; Fer4; 2.
 DR PRINTS; PR00353; 4FE4SFRDOXIN.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN_1.
 KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
 KW Metal-binding; Transport.
 SQ SEQUENCE 76 AA; 8289 MW; 8CF5D7803D838F6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 55 CGPC 58

RESULT 43
 08XHP3_CLOPE
 ID 08XHP3_CLOPE PRELIMINARY; PRT; 77 AA.

AC 08XHP3;
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Probable glutaredoxin.
 GN Ordered locus names=CPE2439;
 OC Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OK NCBI_TaxID=1502;
 RN (1)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=J3 / Type A;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
 RA Shimizu T., Ohnishi K., Hirakawa H., Onshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hatohori M., Kohara S., Hayashi H.,
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; BA000016; BAB82145.1; -; Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR011911; Glrx_Yrnb.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR TRIGPfam; TIGR02196; Glrx_Yrnb; 1.
 KW Complete proteome.
 SQ SEQUENCE 77 AA; 8641 MW; 3337E0EB2A301508 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 10 CGPC 13

RESULT 44
 04S347_TETNG
 ID 04S347_TETNG PRELIMINARY; PRT; 77 AA.

AC Q4S47;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAR14576, whole genome shotgun sequence.
 GN ORFNames=GSTEN00017363001;
 OS Tetradodon nigrovittatus (Green Puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;
 OC Tetradontidae; Tetradontidae; Tetradon.
 NC NCB1_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicad S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Catellico L., Poulain J., De Berardinis V.,
 RA Crnaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McSwan P., Bosak S.,
 RA Kellis M., Volt J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetradodon nigrovittatus reveals
 RT the early vertebrate proto-karyotype.",
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RC Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAEB01014576; CAF99335.1; -!- Genomic DNA.
 SQ SEQUENCE 77 AA; 9043 MW; 25F48C1751A7D3A3 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
 ||||
 Db 25 CGPC 28

RESULT 45
 OSYUM5 DROME PRELIMINARY; PRT: 80 AA.
 ID OSYUM5_DROME PRELIMINARY; PRT: 80 AA.
 AC OSYUM5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG13245-PA.
 GN Name=CG13245; ORFNames=CG13245;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.C., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Heit G., Nelson C.R., Milos G.L.G.,
 RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.A., Bouck J., Brokstein P., Brottier P.,
 RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Fabois B., Delcher A., Deng Z., Dugan A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulj D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milne N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.",
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celisner S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.",
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celisner S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective.",
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktoglu L., Berman B.P.,
 RA Bertencourt B.R., Celisner S.E., de Grey A.D.N.-J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.",
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celisner S., Carlson J., Van K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.",
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]

```

RP NUCLEOTIDE SEQUENCE.
RG Phase:
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -i- INTERACTION:
CC Q9XIN4:Brk; NDExp=1; IntAct=EBI-85165, EBI-159245;
CC CC Q9VAV1:CG9706; NDExp=1; IntAct=EBI-85165, EBI-177365;
CC EMBL; AB003649; AAF53497.1; -; Genomic_DNA.
DR Intact; Q9VAV5; -.
DR Ensemble; CG13245; Drosophila melanogaster.
DR Flybase; FBgn0045627; CG13245.
SQ SEQUENCE 80 AA; 8815 MW; EB81323487838A0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 34 CGPC 37

RESULT 46
Q95JG5_BOVIN PRELIMINARY; PRT; 80 AA.
AC Q95JG5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Natural killer cell receptor group D variant 2 (Fragment).
GN Name=KLRG;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=21351526; PubMed=11457486; DOI=10.1016/S0165-2427(01)00295-1;
RA Govaerts M.M., Goddeeris B.M.; cell receptors NKG2-D and NKR-P1
RT "Homologues of natural killer cell receptors NKG2-D and NKR-P1
RT expressed in cattle.";
RL Vet. Immunol. Immunopathol. 80:339-344(2001).
DR EMBL; AF322885; AAK73810.1; -; mRNA.
DR HSSP; O54709; 1H08.
DR SMR; Q95JG5; 1-80.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; Antifreezeit.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEIT.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.
DR KEGG; K00007; Gly_knot.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 9401 MW; 87A0D11CB3CB5FA0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 4 CGPC 7

RESULT 47
Q95JG6_BOVIN PRELIMINARY; PRT; 80 AA.
AC Q95JG6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

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DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Natural killer cell receptor group D variant 1 (Fragment).
GN Name=KLRG;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=21351526; PubMed=11457486; DOI=10.1016/S0165-2427(01)00295-1;
RA Govaerts M.M., Goddeeris B.M.;
RT "Homologues of natural killer cell receptors NKG2-D and NKR-P1
RT expressed in cattle.";
RL Vet. Immunol. Immunopathol. 80:339-344(2001).
DR EMBL; AF322884; AAK73809.1; -; mRNA.
DR HSSP; O54709; 1H08.
DR SMR; Q95JG6; 1-80.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; Antifreezeit.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEIT.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.
DR KEGG; K00007; Gly_knot.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 9429 MW; 87A0D11CA1405FA0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 4 CGPC 7

RESULT 48
Q63013_RAT PRELIMINARY; PRT; 80 AA.
AC Q63013;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Testicular luteinizing hormone beta subunit.
GN Name=TLHB3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague Dawley;
RX MEDLINE=95283549; PubMed=7763258;
RX Zhang F.P., Rannikko A., Huttanen L.;
RT "Isolation and characterization of testis-specific cDNAs for
RT luteinizing hormone beta-subunit in the rat.";
RL Biochem. Biophys. Res. Commun. 210:858-865(1995).
DR EMBL; U25803; AAC52251.1; -; mRNA.
DR PIR; I65235; 165235.
DR HSSP; P01233; 1HCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneb.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.

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DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ SEQUENCE 80 AA; 8515 MW; F9EA66C2FD6FC97D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 49

Q4T7B7 TETNG PRELIMINARY; PRT; 80 AA.

AC Q4T7B7;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome undetermined SCAR8161, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00005813001;
OS Tetraodon nigrovittatus (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;

RN [1]
RA NUCLEOTIDE SEQUENCE.

RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicand S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Antouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skali Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schacher V., Quetier F., Saurin W., Scapellato C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.,
RT "Genome duplication in the teleost fish Tetraodon nigrovittatus reveals
RN the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).

RN [2]
RA NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01008161; CAF91215.1; -; Genomic_DNA.

FT NON_TER 1 1
FT NON_TER 80 80
SQ SEQUENCE 80 AA; 8611 MW; 64705ABEA4A5620E CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 50

O46622 CERSI PRELIMINARY; PRT; 82 AA.

DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Luteinizing hormone beta-subunit (Fragment).

GN Name=LH-beta;
OS Ceratotherium simum simum.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Rhinocerotidae;
OC Ceratotherium.
OX NCBI_TaxID=73337;

RN [1]

RA Fischer S., Velts J., Meyer H.H.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047607; AAC04365.1; -; Genomic_DNA.
DR HSSP; P01233; 1HCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.

DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.

DR SMART; SM00068; GHF; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

FT NON_TER 1 1
SQ SEQUENCE 82 AA; 8643 MW; 270411BA19B78A37 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 51 CGPC 54

RESULT 51

Q4ZC47 9VIRU PRELIMINARY; PRT; 83 AA.

AC Q4ZC47;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE ORF063.
OS Bacteriophage EW.
OC Viruses.

OX NCBI_TaxID=320841;
RN [1]

RA NUCLEOTIDE SEQUENCE.

RX PubMed=15788529; DOI=10.1073/pnas.0501140102;
RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
RT "The complete genomes and proteomes of 27 *Staphylococcus aureus*
RT bacteriophages.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179 (2005).

DR EMBL; AY954959; AAX91390.1; -; Genomic_DNA.
SQ SEQUENCE 83 AA; 8546 MW; 710CC35BBAB2C31 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 51 CGPC 54

RESULT 52

O60744 HUMAN PRELIMINARY; PRT; 84 AA.

DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Thiorodoxin delta 3 (Fragment).

GN Name=TXN delta 3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=liver;
RA Wang Y., Wang Y.G., Zhang Y., Yuan Y., Ma D.;
RT "An alternative splice variant of human thioredoxin.";
RL Chin. Sci. Bull. 43:292-295(1998).
DR EMBL: AF65241; AAC17430.1; -, mRNA.
DR HSSP: P10599; IERT.
DR SMR: O60744; 1-84.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR006663; Thioredoxin.
DR InterPro: IPR006663; Thioredoxin_dom2.
DR InterPro: IPR012336; Thioredoxin-like.
DR Pfam: PF00085; Thioredoxin_fold.
DR PRINTS: PR00421; THIOREDOXIN.
DR PROSITE: PS00194; THIOREDOXIN, 1.
KM Redox-active center. 1
FT NON_TER 1
SQ SEQUENCE 84 AA; 9321 MW; 818FB84BA86E5721 CRC64;
FT 1
Query Match 100.0%; Score 31; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 31 CGPC 34
RESULT 53
Q6J821_9VIRU
ID Q6J821_9VIRU PRELIMINARY; PRT; 84 AA.
AC Q6J821;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Pas10.
GN Name=Pas10;
OS Actinoplanes phage phiAsp2.
OC Viruses.
OX NCBI_TaxID=279303;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15215690; DOI=10.1023/B:VIRU.0000032795.17713.6c;
RA Jarling M., Bartkowiak K., Pape H., Meinhardt F.;
RT "The Genome of phiAsp2, an Actinoplanes Infecting Phage.";
RL Virus Genes 29:117-129(2004).
DR EMBL: AY576796; AAT36758.1; -, Genomic DNA.
DR SQUEL: 84 AA; 8995 MW; C1ECF12181EB7C72 CRC64;
Query Match 100.0%; Score 31; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 2 CGPC 5
RESULT 54
Q6MWB8_ORYSA
ID Q6MWB8_ORYSA PRELIMINARY; PRT; 84 AA.
AC Q6MWB8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE B1358B12.4 protein.
GN Name=B1358B12.4;

OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartidae; Oryzaceae; Oryza.
OX NCBI_TaxID=59947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Yang K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Wu Y., Sun T., Lei H., Li T., Wang J.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Wang J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Yan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Y.J., Zhang L.,
RA Liu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Yang K., Zhou B., Chen Z.H.,
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX842605; CAE75995.1; -, Genomic DNA.
DR Gramene: Q6MWB8; -;
DR InterPro: IPR006461; DUF_A_thal_cys.
DR Pfam: PF04749; PLAC8; 1.
SQ SEQUENCE 84 AA; 9417 MW; FOBA5C9C390BC7C9 CRC64;
Query Match 100.0%; Score 31; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 37 CGPC 40
RESULT 55
Q16275_HUMAN
ID Q16275_HUMAN PRELIMINARY; PRT; 85 AA.
AC Q16275;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Type I hair keratin (fragment).
GN Name=Type I hair keratin;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95092656; PubMed=7528047;
RA Bowden P.E., Hainey S., Parker G., Hodgins M.B.;
RT "Sequence and expression of human hair keratin genes.";
RL J. Dermatol. Sci. 7:0-0(0).
CC -1- SIMILARITY: Belongs to the intermediate filament family.
DR EMBL: S75797; AAB32812.1; -, Genomic DNA.
DR GO: GO:0005882; C:intermediate filament; IEA.
DR GO: GO:0005198; P:structural molecule activity; IEA.
DR InterPro: IPR001664; IF.
DR Pfam: PF00038; Filament; 1.

DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
FT NON TER 85
SQ SEQUENCE 85 AA; 9314 MW; 4041B8DF0CC18414 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 77 CGPC 80

RESULT 56

05T936 HUMAN
ID 05T936_HUMAN PRELIMINARY; PRT; 85 AA.
AC 05T936;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Thioresdoxin.
GN Name=TXN; ORFNames=RP11-427L11.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Williams S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL158158; CAL14067.1; -; Genomic_DNA.
DR SMR; 05T936; 1-85

DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006662; Thioresdoxin.

DR InterPro; IPR012336; Thioresdoxin-dom2.

DR Pfam; PF00085; Thioresdoxin; 1.

DR PRINTS; PR00421; THIOREDOXIN.

DR PROSITE; PS00194; THIOREDOXIN; 1.

DR Redox-active center.

SQ SEQUENCE 85 AA; 9452 MW; 3CC6254BD6A1D66F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 57

08W710 9CAUD
ID 08W710_9CAUD PRELIMINARY; PRT; 87 AA.
AC 08W710;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Thioresdoxin C3.

OS Cyanophage P60.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.

OX NCBI_TaxID=151528;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=21972319; PubMed=11976141;

RX DOI=10.1128/AEM.68.5.2589-2594.2002;

RA Chen F.; Lu J.;

RT "Genomic sequence and evolution of marine cyanophage P60: a new

insight on lytic and lysogenic phages.";

Appl. Environ. Microbiol. 68:2589-2594(2002).

DR EMBL; AF38467; AAU73267.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioresdoxin.
DR PRINTS; PR00421; THIOREDOXIN.

SQ SEQUENCE 87 AA; 9991 MW; FFBCC315381DD7F81 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 14 CGPC 17

RESULT 58

09C922 ARATH
ID 09C922_ARATH PRELIMINARY; PRT; 87 AA.
AC 09C922;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Putative thioresdoxin; 109829-109566.

GN Name=FLG24.26;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Lin X.; Kaul S.; Town C.D.; Benito M.; Creasy T.H.; Haas B.J.; Wu D.;

RA Maiz R.; Roming C.M.; Koo H.; Fujii C.Y.; Uteback T.R.;

RA Barnstead M.E.; Bowman C.L.; White O.; Nieman W.C.; Fraser C.M.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Town C.D.; Kaul S.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC019018; AAG52290.1; -; Genomic_DNA.

DR HSSP; P23400; 1DBY.

DR GO; GO:0005489; F:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006662; Thioresdoxin.

DR InterPro; IPR006663; Thioresdoxin-dom2.

DR InterPro; IPR012336; Thioresdoxin-like.

DR Pfam; PF00085; Thioresdoxin_fold.

DR PRINTS; PR00421; THIOREDOXIN.

DR PROSITE; PS00194; THIOREDOXIN; 1.

SQ SEQUENCE 87 AA; 10318 MW; 5AEBB56E7A44189 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 13 CGPC 16

RESULT 59

TH102 DICDI
ID TH102_DICDI STANDARD; PRT; 88 AA.
AC P29446;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Thioresdoxin 2 (Fragment).

GN Name=trxB; Synonyms=trx2;

OS Dictyostelium discoideum (slime mold).

OC Eukaryota; Metazoa; Dictyostelida; Dictyostelium.

```

OX NCBI_TaxID=44689;
RN [1]
RT NUCLEOTIDE SEQUENCE.
RX MEDLINE=92250653; PubMed=1577820;
RA Wettstein B., Jacquot J.-P., Veron M.;
RT "Thioredoxins from Dictyostelium discoideum are a developmentally
regulated multigene family."
RL J. Biol. Chem. 267:9895-9904(1992).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: M91382; AAA3259.1; -; mRNA.
DR F1R; B46264; B46264.
DR HSP; P10599; IERV.
DR DictyBase: DDB0001983; TRX2.
DR InterPro: IPR006663; Thioredox.
DR InterPro: IPR012335; Thioredoxin-dom2.
DR InterPro: IPR012335; Thioredoxin-like.
DR InterPro: IPR012335; Thioredoxin_fold.
DR Pfam: PF00085; Thioredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN_1.
DR Electrophoresis; MultiGene family; Redox-active center; Transport.
KM ELECTRON TRANSPORT; MultiGene family; Redox-active center; Transport.
FT ACT_SITE 31 31 Nucleophile (By similarity).
FT ACT_SITE 34 34 Nucleophile (By similarity).
FT SITE 25 25 Deprotonates C-terminal active site Cys
FT SITE 32 32 (By similarity).
FT SITE 32 32 Contributes to redox potential value (By
FT SITE 33 33 similarity).
FT SITE 33 33 Contributes to redox potential value (By
FT DISULFID 31 34 similarity).
FT NON_TER 88 88 Redox-active (By similarity).
SQ SEQUENCE 88 AA; 10103 MW; CEC73BCEFA607C CRC64;

Query Match 100.0%; Score 31; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
Db 31 CGPC 34

RESULT 60
Q5V0J2 HALMA PRELIMINARY; PRT; 88 AA.
ID Q5V0J2 HALMA PRELIMINARY; PRT; 88 AA.
AC Q5V0J2; 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Thioredoxin.
GN Name=trx3; OrderedLocustNames=trxA2110;
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RT NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Faciolletti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;

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RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT the Dead Sea."
RL Genome Res. 14:2221-2234(2004).
DR EMBL; AY596297; AA46961.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR005746; Thioredoxin.
DR InterPro; IPR006663; Thioredoxin-dom2.
DR Pfam; PF00085; Thioredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAMs; TIGR01068; Thioredoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN_1.
KM Complete proteome.
SQ SEQUENCE 88 AA; 10011 MW; CFE9B8FAC1F69857 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
Db 13 CGPC 16

RESULT 61
Q8PZ06 METMA PRELIMINARY; PRT; 88 AA.
ID Q8PZ06 METMA PRELIMINARY; PRT; 88 AA.
AC Q8PZ06;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thioredoxin.
GN OrderedLocustNames=MM0436;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RT NUCLEOTIDE SEQUENCE.
RC STRAIN=Gael / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=2210827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartesch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wieser A., Baumer S., Jacobi C.,
RA Bueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea."
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013269; AAM30132.1; -; Genomic DNA.
DR HSP; P80579; 1NM2.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR006663; Thioredox-dom2.
DR InterPro; IPR005746; Thioredoxin.
DR InterPro; IPR012335; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF00085; Thioredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAMs; TIGR01068; Thioredoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN_1.
KM Complete proteome.
SQ SEQUENCE 88 AA; 9914 MW; D448923BF5845FA5 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
Db 13 CGPC 16

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RESULT 62
Q71UV5 HORSE
ID Q71UV5_HORSE PRELIMINARY; PRT; 88 AA.
AC Q71UV5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE luteinizing hormone/chorionic gonadotropin beta-subunit (Fragment).
GN Name=lH/CG-beta;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fischer S., Velts J., Meyer H.H.D.;
RL Submitted (PEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047604; AAC04362.1; -; Genomic_DNA.
DR GO; GO:0005576; Cerebral cellular region; IEA.
DR GO; GO:0005179; F: hormone activity; IEA.
DR InterPro; IPR006208; Cys knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHF; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Choriion.
FT NON_TER 1 1
FT NON_TER 88 88
SQ SEQUENCE 88 AA; 9153 MW; 32E7DB6CF7B1C9CF CRC64;
Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 43 CGPC 46

RESULT 63
Q62H93 BURMA PRELIMINARY; PRT; 88 AA.
ID Q62H93_BURMA PRELIMINARY; PRT; 88 AA.
AC Q62H93;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein
GN OrderedLocNames=BMA2369;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=ATCC 23344;
RC PubMed=15377793; DOI=10.1073/pnas.040306101;
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M., Sarrifa S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M., Durkin A.S., Gilm M.L., Haft D.H., Khouri H.M., Kolony J.F., Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL; CP000010; AAU50201.1; -; Genomic_DNA.
DR TIGR; BMA2369; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 88 AA; 9445 MW; 74D511CDE7B2ECD6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 72 CGPC 75

RESULT 64
Q9HMD0 HALSA PRELIMINARY; PRT; 89 AA.
ID Q9HMD0;
AC Q9HMD0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Thioredoxin.
GN Name=trxA2; OrderedLocNames=VNG2600G;
OS Halobacterium salinarum (Halobacterium halobium).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
NCBI_TaxID=2242;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA Ng W.V., Kennedy S.P., Mahaisa G.G., Bergquist B., Pan M., Shukla H.D., Laszky S.R., Baliga N.S., Thorsson V., Shrogha J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Geo Y.A., Leitbauer B., Keller K., Cruz R., Danon M.J., Hough D.W., Maddock D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlshocher M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Edhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005133; AAG20641.1; -; Genomic_DNA.
DR PIR; B84409; B84409.
DR HSSP; P10599; 1ERY.
DR GO; GO:0005489; F: electron transporter activity; IEA.
DR GO; GO:0006118; P: electron transport; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR005746; Thioredoxin.
DR InterPro; IPR006663; Thioredox_dom2.
DR Pfam; PF00085; Thioredoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioredoxin; 1.
KW Complete proteome.
SQ SEQUENCE 89 AA; 10019 MW; BDF97B3496F70BFF CRC64;
Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 13 CGPC 16

RESULT 65
O46618 EQUZE PRELIMINARY; PRT; 89 AA.
ID O46618_EQUZE PRELIMINARY; PRT; 89 AA.
AC O46618;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE luteinizing hormone/chorionic gonadotropin beta-subunit (Fragment).
GN Name=lH/CG-beta;
OS Equus zebra hartmannae.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

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OX NCBI_TaxID=73335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fischer S., Velts J., Meyer H.H.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047602; AAC04360.1; -; Genomic_DNA.
DR HSSP; P01233; IHCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. .; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KM Choriion.
FT NON_TER 1
FT TER 89
SQ SEQUENCE 89 AA; 9325 MW; 2AD973AECTEAC5C8 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 66
O46619 EQUHM PRELIMINARY; PRT; 89 AA.
ID O46619 EQUHM PRELIMINARY;
AC O46619;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lateinizing hormone/chorionic gonadotrophin beta-subunit
DE (Fragment).
GN Name=LH/CG-Beta;
OS Equus hemionus (Kulan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9794;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fischer S., Velts J., Meyer H.H.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047603; AAC04361.1; -; Genomic_DNA.
DR HSSP; P01233; IHCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. .; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KM Choriion.
FT NON_TER 1
FT TER 89
SQ SEQUENCE 89 AA; 9369 MW; E0EEF73778C5566 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 50 CGPC 53

RESULT 67
O4HCJ2_9DEIO

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ID O4HCJ2_9DEIO PRELIMINARY; PRT; 89 AA.
AC O4HCJ2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DgeODRAFT_2284;
OS Deinococcus geothermophilus DSM 11300.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=319795;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Copeland A., Lucas S., Lapidus A., Barry K., Deter C., Glavina T.,
Hammon N., Istrani S., Plutnick S., Richardson P.;
RT "Sequencing of the draft genome assembly of Deinococcus geothermophilus
RT DSM 11300."
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Deinococcus geothermophilus
RT DSM 11300."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHE01000001; EAL84178.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 89 AA; 9776 MW; 1ABEA48510AB827A CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 65 CGPC 68

RESULT 68
O4LEN8 PAROL
ID O4LEN8 PAROL PRELIMINARY; PRT; 89 AA.
AC O4LEN8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hepcidin 2;
GN Name=JF-hep 2;
OS Paralichthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hiroto I., Nozaki R., Ono Y., Kurobe T., Ohira T., Aoki T.;
RT "Two different types of hepcidins from Japanese flounder Paralichthys
RT olivaceus."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB198063; BAB06235.1; -; Genomic_DNA.
SQ SEQUENCE 89 AA; 9729 MW; 04CBB16152953F00 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

```

Db 83 CGPC 86

RESULT 69
QALEPO PAROL PRELIMINARY; PRT; 89 AA.
AC QALEPO;
DT 13-SRP-2005 (TREMBlrel. 31, Created)
DT 13-SRP-2005 (TREMBlrel. 31, last sequence update)
DT 13-SRP-2005 (TREMBlrel. 31, last annotation update)
DE Hepcidin 2.
GN Name=JF-hep 2;
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hirono I., Nozaki R., Ono Y., Kurobe T., Ohira T., Aoki T.;
RT "Two different types of hepcidins from Japanese Flounder Paralicthys
RT olivaceus.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB198061; BAE06233.1; -; mRNA.
SQ SEQUENCE 89 AA; 9771 MW; D9AE7173C29CB412 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 83 CGPC 86

RESULT 70
Q7RS22 GIALA PRELIMINARY; PRT; 90 AA.
AC Q7RS22;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
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DE GIP 81 67830 68102
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RT Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACB0100003; EAA42709.1; -; Genomic DNA.
SQ SEQUENCE 90 AA; 10714 MW; D84C31177BA31834 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 74 CGPC 77

Search completed: February 23, 2006, 00:41:45
Job time: 177.5 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:42:19 ; Search time 34.5 Seconds
(without alignments)
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Title: US-10-660-118a-2

Perfect score: 31
Sequence: 1 XCGPCX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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398	25	80.6	12	2	US-09-910-009A-463	Sequence 463, App	471	25	80.6	99	2	US-09-452-991A-24967	Sequence 24967, A
399	25	80.6	13	2	US-09-910-009A-452	Sequence 452, App	472	25	80.6	99	2	US-09-248-796A-27022	Sequence 27022, A
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401	25	80.6	16	2	US-09-954-987B-199	Sequence 199, App	474	25	80.6	105	1	US-08-103-170-12	Sequence 12, Appl1
402	25	80.6	17	2	US-09-910-009A-414	Sequence 414, App	475	25	80.6	106	2	US-10-232-858-78	Sequence 78, Appl1
403	25	80.6	32	2	US-08-632-511A-6	Sequence 6, Appl1	476	25	80.6	106	2	US-09-338-063A-78	Sequence 78, Appl1
404	25	80.6	32	2	US-09-091-590A-12	Sequence 12, Appl1	477	25	80.6	106	2	US-10-104-047-2975	Sequence 2975, Ap
405	25	80.6	32	2	US-09-488-200-6	Sequence 6, Appl1	478	25	80.6	110	2	US-09-902-540-11228	Sequence 11228, A
406	25	80.6	38	2	US-09-270-767-60645	Sequence 60645, A	479	25	80.6	111	1	US-08-543-238-8	Sequence 8, Appl1
407	25	80.6	40	2	US-09-270-767-61997	Sequence 61997, A	480	25	80.6	111	1	US-08-420-526-8	Sequence 8, Appl1
408	25	80.6	45	2	US-08-803-954B-10	Sequence 10, Appl1	481	25	80.6	114	2	US-09-774-639-156	Sequence 156, App
409	25	80.6	46	2	US-09-270-767-58428	Sequence 58428, A	482	25	80.6	116	2	US-09-540-236-3774	Sequence 3774, Ap
410	25	80.6	49	2	US-09-461-325-425	Sequence 425, App	483	25	80.6	120	2	US-09-252-991A-22272	Sequence 22272, A
411	25	80.6	49	2	US-10-012-542-425	Sequence 425, App	484	25	80.6	120	2	US-09-710-279-2214	Sequence 2214, Ap
412	25	80.6	49	2	US-10-115-123-425	Sequence 425, App	485	25	80.6	123	2	US-09-489-039A-12685	Sequence 12685, A
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416	25	80.6	53	4	PCT-US95-05744-53	Sequence 53, Appl1	489	25	80.6	126	2	US-09-328-352-7886	Sequence 7886, Ap
417	25	80.6	57	2	US-09-621-976-7258	Sequence 7258, Ap	490	25	80.6	126	2	US-09-270-767-43094	Sequence 43094, A
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419	25	80.6	62	2	US-09-252-991A-25973	Sequence 25973, A	492	25	80.6	127	2	US-09-489-039A-13310	Sequence 13310, A
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422	25	80.6	65	2	US-10-012-542-457	Sequence 457, App	495	25	80.6	132	2	US-09-523-323-55	Sequence 55, Appl1
423	25	80.6	66	2	US-10-115-123-457	Sequence 457, App	496	25	80.6	132	2	US-10-104-047-3315	Sequence 3315, Ap
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425	25	80.6	67	2	US-09-910-009A-168	Sequence 168, App	498	25	80.6	136	2	US-09-252-991A-26088	Sequence 26088, A
426	25	80.6	67	2	US-09-910-009A-327	Sequence 327, App	499	25	80.6	137	2	US-09-252-991A-20915	Sequence 20915, A
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430	25	80.6	69	2	US-09-627-775-11	Sequence 11, Appl1	503	25	80.6	143	2	US-10-232-858-77	Sequence 77, Appl1
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432	25	80.6	69	2	US-09-910-009A-108	Sequence 108, App	505	25	80.6	145	2	US-10-232-858-15	Sequence 15, Appl1
433	25	80.6	69	2	US-09-910-009A-342	Sequence 342, App	506	25	80.6	145	2	US-09-338-063A-15	Sequence 15, Appl1
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435	25	80.6	76	2	US-09-621-976-5646	Sequence 5646, Ap	508	25	80.6	147	2	US-09-527-236A-20	Sequence 20, Appl1
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444	25	80.6	81	2	US-09-252-991A-28421	Sequence 28421, A	517	25	80.6	154	2	US-10-232-858-13	Sequence 13, Appl1
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446	25	80.6	84	2	US-09-248-796A-23070	Sequence 23070, A	519	25	80.6	157	2	US-09-270-767-37143	Sequence 37143, A
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448	25	80.6	84	2	US-09-338-063A-82	Sequence 82, Appl1	521	25	80.6	158	2	US-09-422-680A-24	Sequence 24, Appl1
449	25	80.6	87	2	US-09-252-991A-20264	Sequence 20264, A	522	25	80.6	159	2	US-09-461-697-978	Sequence 46, Appl1
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457	25	80.6	94	2	US-08-974-549A-334	Sequence 334, App	530	25	80.6	168	2	US-09-252-991A-30752	Sequence 30752, A
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461	25	80.6	94	2	US-09-721-456-334	Sequence 334, App	534	25	80.6	175	2	US-09-252-991A-16749	Sequence 16749, A
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464	25	80.6	97	2	US-09-025-596-53	Sequence 53, Appl1	537	25	80.6	187	2	US-09-199-637A-287	Sequence 287, App
465	25	80.6	97	2	US-09-073-661-53	Sequence 53, Appl1	538	25	80.6	187	2	US-09-252-991A-21454	Sequence 21454, A

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545	25	80.6	194	2	US-09-252-991A-24154	Sequence 24154, A	618	25	80.6	254	2	US-10-286-606-27	Sequence 27, App1
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547	25	80.6	196	2	US-09-513-999C-4249	Sequence 4249, Ap	620	25	80.6	255	1	US-08-236-912A-8	Sequence 8, App1
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553	25	80.6	199	1	US-08-465-500-4	Sequence 4, App1	626	25	80.6	255	2	US-09-578-764A-2	Sequence 2, App1
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562	25	80.6	204	2	US-09-999-833A-36	Sequence 36, App1	635	25	80.6	259	2	US-09-976-594-229	Sequence 229, App
563	25	80.6	204	2	US-10-020-445A-36	Sequence 36, App1	636	25	80.6	259	2	US-09-919-035-109	Sequence 109, App
564	25	80.6	205	2	US-09-949-016-9980	Sequence 9980, Ap	637	25	80.6	259	6	5212074-3	Patent No. 5212074
565	25	80.6	205	2	US-09-949-016-9981	Sequence 9981, Ap	638	25	80.6	263	2	US-09-107-532A-6468	Sequence 6468, Ap
566	25	80.6	205	2	US-09-949-016-9982	Sequence 9982, Ap	639	25	80.6	265	2	US-09-903-456-77	Sequence 77, App1
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568	25	80.6	207	2	US-08-795-445A-47	Sequence 47, App1	641	25	80.6	269	2	US-09-252-991A-29917	Sequence 29917, A
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570	25	80.6	207	2	US-08-974-186-47	Sequence 47, App1	643	25	80.6	271	2	US-09-248-796A-14877	Sequence 14877, A
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572	25	80.6	207	2	US-08-706-945D-133	Sequence 133, App	645	25	80.6	272	2	US-10-232-858-75	Sequence 75, App1
573	25	80.6	207	2	US-08-577-788C-47	Sequence 47, App1	646	25	80.6	272	2	US-09-338-063A-75	Sequence 75, App1
574	25	80.6	207	2	US-09-603-208A-68	Sequence 68, App1	647	25	80.6	274	2	US-09-949-016-9095	Sequence 9095, Ap
575	25	80.6	207	2	US-09-605-703B-1726	Sequence 1726, Ap	648	25	80.6	276	2	US-09-270-767-45156	Sequence 45156, A
576	25	80.6	211	2	US-10-104-047-3219	Sequence 3219, Ap	649	25	80.6	277	1	US-08-147-984-2	Sequence 2, App1
577	25	80.6	211	2	US-09-949-016-11620	Sequence 11620, A	650	25	80.6	277	2	US-08-195-967-2	Sequence 2, App1
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579	25	80.6	217	2	US-09-902-540-15578	Sequence 15578, A	652	25	80.6	277	2	US-08-472-940-2	Sequence 2, App1
580	25	80.6	219	1	US-08-152-019A-32	Sequence 32, App1	653	25	80.6	277	2	US-09-573-986-12	Sequence 12, App1
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582	25	80.6	225	2	US-09-252-991A-24245	Sequence 24245, A	655	25	80.6	277	2	US-09-804-200-2	Sequence 2, App1
583	25	80.6	225	2	US-09-252-991A-29348	Sequence 29348, A	656	25	80.6	277	2	US-08-469-633A-4	Sequence 4, App1
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592	25	80.6	229	2	US-09-992-598-424	Sequence 424, App	665	25	80.6	284	1	US-09-055-095-1	Sequence 1, App1
593	25	80.6	230	2	US-09-252-991A-31737	Sequence 31737, A	666	25	80.6	293	1	US-08-264-53A-9	Sequence 9, App1
594	25	80.6	235	2	US-09-620-405B-487	Sequence 487, App	667	25	80.6	293	1	US-08-083-959A-4	Sequence 4, App1
595	25	80.6	235	2	US-09-328-352-6597	Sequence 6597, Ap	668	25	80.6	293	1	US-08-465-500-9	Sequence 9, App1
596	25	80.6	235	2	US-09-604-287A-467	Sequence 467, App	669	25	80.6	293	1	US-08-346-126-9	Sequence 9, App1
597	25	80.6	235	2	US-09-604-287A-467	Sequence 487, App	670	25	80.6	293	1	US-08-346-126-9	Sequence 9, App1
598	25	80.6	235	2	US-09-604-287A-467	Sequence 487, App	671	25	80.6	293	1	US-08-346-126-9	Sequence 9, App1
599	25	80.6	236	2	US-09-707-767-46803	Sequence 46803, A	672	25	80.6	293	2	US-08-893-828-9	Sequence 8, App1
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605	25	80.6	246	2	US-10-104-047-2232	Sequence 2232, Ap	678	25	80.6	301	2	US-09-949-016-9189	Sequence 9189, Ap
606	25	80.6	246	2	US-10-104-047-2243	Sequence 2243, Ap	679	25	80.6	301	2	US-09-902-540-11985	Sequence 11985, A
607	25	80.6	247	2	US-10-126-279-29	Sequence 29, App1	680	25	80.6	303	2	US-09-461-325-466	Sequence 426, App
608	25	80.6	247	2	US-10-286-606-29	Sequence 29, App1	681	25	80.6	303	2	US-10-012-542-466	Sequence 426, App
609	25	80.6	247	2	US-10-104-047-2790	Sequence 2790, Ap	682	25	80.6	304	2	US-10-115-123-466	Sequence 304, App
610	25	80.6	248	2	US-09-552-991A-17358	Sequence 17358, A	683	25	80.6	304	2	US-09-893-737-304	Sequence 304, App
611	25	80.6	249	2	US-09-252-991A-28972	Sequence 28972, A	684	25	80.6	305	2	US-09-252-991A-26204	Sequence 26204, A

685	25	80.6	312	2	US-09-270-767-39065	Sequence 39065, A	758	25	80.6	391	2	US-10-232-856-106	Sequence 106, App
686	25	80.6	312	2	US-09-270-767-54282	Sequence 54282, A	759	25	80.6	391	2	US-09-338-063A-106	Sequence 106, App
687	25	80.6	314	1	US-08-460-309-19	Sequence 19, Appl	760	25	80.6	393	2	US-10-232-856-79	Sequence 79, Appl
688	25	80.6	314	1	US-08-125-077-19	Sequence 19, Appl	761	25	80.6	393	2	US-09-338-063A-79	Sequence 79, Appl
689	25	80.6	314	2	US-09-949-001-23	Sequence 23, Appl	762	25	80.6	394	2	US-10-232-856-9	Sequence 9, Appl
690	25	80.6	315	2	US-09-172-952-13	Sequence 13, Appl	763	25	80.6	394	2	US-09-338-063A-9	Sequence 9, Appl
691	25	80.6	317	1	US-08-118-770-10	Sequence 10, Appl	764	25	80.6	396	2	US-09-489-039A-10242	Sequence 10242, A
692	25	80.6	317	4	PCT-US93-08528-10	Sequence 10, Appl	765	25	80.6	396	2	US-09-489-039A-12215	Sequence 12215, A
693	25	80.6	321	2	US-10-232-858-80	Sequence 80, Appl	766	25	80.6	398	2	US-10-104-047-2769	Sequence 2769, App
694	25	80.6	321	2	US-09-338-063A-80	Sequence 80, Appl	767	25	80.6	399	2	US-10-232-858-73	Sequence 73, Appl
695	25	80.6	322	2	US-09-252-991A-3141	Sequence 3141, A	768	25	80.6	399	2	US-09-949-002-437	Sequence 437, App
696	25	80.6	325	1	US-08-292-549-2	Sequence 2, Appl	769	25	80.6	399	2	US-09-338-063A-73	Sequence 73, Appl
697	25	80.6	325	1	US-09-042-785A-9	Sequence 9, Appl	770	25	80.6	401	2	US-08-974-022-6	Sequence 6, Appl
698	25	80.6	325	4	PCT-US91-02207-2	Sequence 2, Appl	771	25	80.6	401	2	US-09-153-927-1	Sequence 1, Appl
699	25	80.6	326	1	US-08-292-549-4	Sequence 4, Appl	772	25	80.6	401	2	US-09-042-785A-12	Sequence 12, Appl
700	25	80.6	326	2	US-10-232-858-71	Sequence 71, Appl	773	25	80.6	401	2	US-08-795-445A-6	Sequence 6, Appl
701	25	80.6	326	2	US-09-338-063A-71	Sequence 71, Appl	774	25	80.6	401	2	US-08-974-186-6	Sequence 6, Appl
702	25	80.6	326	4	PCT-US91-02207-4	Sequence 4, Appl	775	25	80.6	401	2	US-08-795-446B-6	Sequence 6, Appl
703	25	80.6	327	2	US-09-290-640-66	Sequence 66, Appl	776	25	80.6	401	2	US-09-153-927-1	Sequence 1, Appl
704	25	80.6	327	2	US-09-665-615B-66	Sequence 66, Appl	777	25	80.6	401	2	US-09-072-993C-1	Sequence 128, App
705	25	80.6	327	2	US-10-232-858-72	Sequence 72, Appl	778	25	80.6	401	2	US-08-577-788C-6	Sequence 6, Appl
706	25	80.6	327	2	US-09-338-063A-72	Sequence 72, Appl	779	25	80.6	401	2	US-08-577-788C-56	Sequence 56, Appl
707	25	80.6	328	2	US-09-252-991A-23826	Sequence 23826, A	780	25	80.6	401	2	US-08-577-788C-56	Sequence 56, Appl
708	25	80.6	328	2	US-09-252-991A-26586	Sequence 26586, A	781	25	80.6	401	2	US-09-064-832-2	Sequence 2, Appl
709	25	80.6	329	2	US-09-336-910A-5	Sequence 5, Appl	782	25	80.6	401	2	US-10-332-858-5	Sequence 5, Appl
710	25	80.6	334	2	US-09-949-016-8549	Sequence 8549, Ap	783	25	80.6	401	2	US-10-332-858-62	Sequence 62, Appl
711	25	80.6	334	2	US-09-949-016-8571	Sequence 8571, Ap	784	25	80.6	401	2	US-10-332-858-63	Sequence 63, Appl
712	25	80.6	339	2	US-09-171-461-36	Sequence 36, Appl	785	25	80.6	401	2	US-10-332-858-65	Sequence 65, Appl
713	25	80.6	339	2	US-09-252-991A-25235	Sequence 25235, A	786	25	80.6	401	2	US-10-332-858-66	Sequence 66, Appl
714	25	80.6	339	2	US-09-970-711-36	Sequence 36, Appl	787	25	80.6	401	2	US-10-332-858-66	Sequence 66, Appl
715	25	80.6	345	2	US-09-403-768-4	Sequence 36, Appl	788	25	80.6	401	2	US-09-338-063A-5	Sequence 5, Appl
716	25	80.6	345	2	US-09-252-991A-32869	Sequence 32869, A	789	25	80.6	401	2	US-09-338-063A-62	Sequence 62, Appl
717	25	80.6	348	2	US-09-830-807-43	Sequence 43, Appl	790	25	80.6	401	2	US-09-338-063A-63	Sequence 63, Appl
718	25	80.6	348	2	US-09-006-353A-13	Sequence 13, Appl	791	25	80.6	401	2	US-09-338-063A-64	Sequence 64, Appl
719	25	80.6	349	2	US-09-573-986-13	Sequence 13, Appl	792	25	80.6	401	2	US-09-338-063A-65	Sequence 65, Appl
720	25	80.6	349	2	US-09-780-996A-7	Sequence 7, Appl	793	25	80.6	401	2	US-09-338-063A-65	Sequence 65, Appl
721	25	80.6	350	2	US-10-726-721A-7	Sequence 7, Appl	794	25	80.6	402	2	US-09-470-67-61551	Sequence 61551, A
722	25	80.6	350	2	US-10-046-433-41	Sequence 41, Appl	795	25	80.6	419	2	US-09-252-991A-21423	Sequence 21423, A
723	25	80.6	351	2	US-10-232-858-74	Sequence 74, Appl	796	25	80.6	423	2	US-09-252-991A-18123	Sequence 18123, A
724	25	80.6	351	2	US-09-338-063A-74	Sequence 74, Appl	797	25	80.6	425	2	US-09-538-092-1366	Sequence 1366, Ap
725	25	80.6	353	2	US-09-252-991A-26394	Sequence 26394, A	798	25	80.6	427	2	US-09-328-952-5312	Sequence 5312, Ap
726	25	80.6	353	2	US-10-104-047-2052	Sequence 2052, Ap	799	25	80.6	430	2	US-09-352-991A-25287	Sequence 25287, A
727	25	80.6	355	1	US-08-292-549-6	Sequence 6, Appl	800	25	80.6	434	2	US-09-452-991A-21735	Sequence 21735, A
728	25	80.6	355	2	US-09-006-353A-14	Sequence 14, Appl	801	25	80.6	435	2	US-09-252-991A-21698	Sequence 21698, A
729	25	80.6	355	2	US-09-403-768-6	Sequence 6, Appl	802	25	80.6	437	2	US-09-353-332-2	Sequence 2, Appl
730	25	80.6	356	2	US-09-573-986-14	Sequence 14, Appl	803	25	80.6	447	2	US-09-949-016-10334	Sequence 10334, A
731	25	80.6	356	2	US-09-235-103-2	Sequence 2, Appl	804	25	80.6	450	2	US-09-896-720-2	Sequence 2, Appl
732	25	80.6	356	2	US-09-235-103-4	Sequence 4, Appl	805	25	80.6	458	2	US-09-949-016-8791	Sequence 8791, Ap
733	25	80.6	356	2	US-09-235-103-13	Sequence 13, Appl	806	25	80.6	456	1	US-08-194-338-11	Sequence 11, Appl
734	25	80.6	357	2	US-09-270-767-60452	Sequence 60452, A	807	25	80.6	466	2	US-09-826-509-515	Sequence 515, App
735	25	80.6	359	2	US-10-232-858-70	Sequence 70, Appl	808	25	80.6	466	2	US-09-252-991A-31436	Sequence 31436, A
736	25	80.6	359	2	US-09-338-063A-70	Sequence 70, Appl	809	25	80.6	469	2	US-09-393-117-7	Sequence 7, Appl
737	25	80.6	362	2	US-10-232-858-11	Sequence 11, Appl	810	25	80.6	480	1	US-08-201-118-1	Sequence 1, Appl
738	25	80.6	362	2	US-09-338-063A-11	Sequence 11, Appl	811	25	80.6	480	1	US-08-201-118-3	Sequence 3, Appl
739	25	80.6	363	2	US-10-232-858-69	Sequence 69, Appl	812	25	80.6	480	1	US-08-201-118-7	Sequence 7, Appl
740	25	80.6	363	2	US-09-338-063A-69	Sequence 69, Appl	813	25	80.6	480	1	US-08-201-118-11	Sequence 11, Appl
741	25	80.6	364	2	US-08-706-945D-142	Sequence 142, App	814	25	80.6	480	1	US-08-201-118-11	Sequence 11, Appl
742	25	80.6	365	2	US-09-503-219B-8	Sequence 8, Appl	815	25	80.6	480	1	US-08-201-118-11	Sequence 13, Appl
743	25	80.6	365	2	US-10-039-659A-10	Sequence 10, Appl	816	25	80.6	480	1	US-08-238-821B-13	Sequence 13, Appl
744	25	80.6	366	2	US-09-252-991A-31958	Sequence 31958, A	817	25	80.6	480	1	US-08-238-821B-13	Sequence 13, Appl
745	25	80.6	368	2	US-09-949-016-8818	Sequence 8818, Ap	818	25	80.6	480	1	US-08-238-821B-3	Sequence 3, Appl
746	25	80.6	376	2	US-09-949-016-7545	Sequence 7545, Ap	819	25	80.6	480	1	US-08-238-821B-7	Sequence 7, Appl
747	25	80.6	377	2	US-09-270-767-44972	Sequence 44972, A	820	25	80.6	480	1	US-08-238-821B-9	Sequence 9, Appl
748	25	80.6	377	2	US-09-949-016-8141	Sequence 8141, Ap	821	25	80.6	480	1	US-08-238-821B-9	Sequence 9, Appl
749	25	80.6	380	2	US-10-232-858-4	Sequence 4, Appl	822	25	80.6	480	1	US-08-238-821B-11	Sequence 11, Appl
750	25	80.6	380	2	US-09-338-063A-4	Sequence 4, Appl	823	25	80.6	480	1	US-08-238-821B-13	Sequence 13, Appl
751	25	80.6	386	2	US-09-086-483A-2	Sequence 2, Appl	824	25	80.6	480	2	US-09-949-016-5989	Sequence 5989, Ap
752	25	80.6	386	2	US-09-130-491-6	Sequence 6, Appl	825	25	80.6	480	2	US-09-949-016-5990	Sequence 5990, Ap
753	25	80.6	386	2	US-09-580-212-2	Sequence 2, Appl	826	25	80.6	480	4	PCT-US95-05744-1	Sequence 1, Appl
754	25	80.6	386	2	US-09-759-402-2	Sequence 2, Appl	827	25	80.6	480	4	PCT-US95-05744-3	Sequence 3, Appl
755	25	80.6	386	2	US-09-949-002-357	Sequence 357, App	828	25	80.6	480	4	PCT-US95-05744-5	Sequence 5, Appl
756	25	80.6	389	2	US-09-252-991A-31590	Sequence 31590, A	829	25	80.6	480	4	PCT-US95-05744-7	Sequence 7, Appl
757	25	80.6	390	2	US-09-949-016-10020	Sequence 10020, A	830	25	80.6	480	4	PCT-US95-05744-9	Sequence 9, Appl

831	25	80.6	490	4	PCT-US95-05744-11	Sequence 11, Appl	904	25	80.6	700	2	US-08-933-711B-5	Sequence 5, Appl
832	25	80.6	492	4	PCT-US95-05744-13	Sequence 13, Appl	905	25	80.6	709	2	US-08-753-247-6	Sequence 6, Appl
833	25	80.6	490	2	US-09-252-991A-18218	Sequence 18218, A	906	25	80.6	713	2	US-08-753-247-9	Sequence 9, Appl
834	25	80.6	495	2	US-09-949-016-10481	Sequence 10481, A	907	25	80.6	716	2	US-09-312-283C-183	Sequence 183, Appl
835	25	80.6	495	2	US-09-949-016-10532	Sequence 10532, A	908	25	80.6	719	2	US-08-753-247-12	Sequence 12, Appl
836	25	80.6	495	2	US-09-949-016-10533	Sequence 10533, A	909	25	80.6	721	2	US-09-134-000C-5466	Sequence 5466, Ap
837	25	80.6	498	1	US-07-688-352C-20	Sequence 20, Appl	910	25	80.6	722	2	US-09-107-532A-3970	Sequence 3970, Ap
838	25	80.6	498	1	US-08-474-379C-20	Sequence 20, Appl	911	25	80.6	724	2	US-09-252-991A-10945	Sequence 10945, A
839	25	80.6	498	2	US-09-146-249A-20	Sequence 20, Appl	912	25	80.6	762	2	US-09-489-039A-10008	Sequence 10008, A
840	25	80.6	498	2	US-08-206-188B-20	Sequence 20, Appl	913	25	80.6	771	2	US-09-188-930A-183	Sequence 183, App
841	25	80.6	500	1	US-08-314-601-2	Sequence 20, Appl	914	25	80.6	794	1	US-07-885-972A-2	Sequence 2, Appl
842	25	80.6	500	4	PCT-US95-13051-2	Sequence 2, Appl	915	25	80.6	794	1	US-07-885-972A-4	Sequence 4, Appl
843	25	80.6	502	2	US-09-330-970-1	Sequence 1, Appl	916	25	80.6	794	1	US-08-865-203-2	Sequence 2, Appl
844	25	80.6	505	2	US-09-620-405B-478	Sequence 478, App	917	25	80.6	794	1	US-08-745-880-2	Sequence 2, Appl
845	25	80.6	505	2	US-09-620-405B-485	Sequence 485, App	918	25	80.6	794	1	US-08-745-880-4	Sequence 4, Appl
846	25	80.6	505	2	US-09-604-287A-478	Sequence 478, App	919	25	80.6	794	1	US-08-480-382-2	Sequence 2, Appl
847	25	80.6	505	2	US-09-604-287A-485	Sequence 485, App	920	25	80.6	794	1	US-08-480-382-4	Sequence 4, Appl
848	25	80.6	505	2	US-09-634-759-478	Sequence 478, App	921	25	80.6	794	1	US-07-849-420-2	Sequence 2, Appl
849	25	80.6	505	2	US-09-634-759-485	Sequence 485, App	922	25	80.6	794	2	US-09-253-854-2	Sequence 2, Appl
850	25	80.6	505	2	US-09-590-751A-478	Sequence 478, App	923	25	80.6	794	2	US-08-955-424-2	Sequence 2, Appl
851	25	80.6	505	2	US-09-551-621A-478	Sequence 478, App	924	25	80.6	794	2	US-09-592-480-1	Sequence 1, Appl
852	25	80.6	505	2	US-10-976-622-478	Sequence 478, App	925	25	80.6	794	2	US-10-133-910-2	Sequence 2, Appl
853	25	80.6	505	2	US-10-976-622-478	Sequence 478, App	926	25	80.6	794	2	US-09-949-016-6239	Sequence 6239, Ap
854	25	80.6	505	2	US-10-976-622-485	Sequence 485, App	927	25	80.6	820	2	US-09-949-016-9924	Sequence 9924, Ap
855	25	80.6	508	2	US-09-302-540-10562	Sequence 10562, A	928	25	80.6	863	2	US-09-619-353-14	Sequence 14, Appl
856	25	80.6	509	2	US-08-857-076-46	Sequence 46, Appl	929	25	80.6	887	1	US-07-867-106-3	Sequence 3, Appl
857	25	80.6	510	2	US-09-305-658-46	Sequence 46, Appl	930	25	80.6	934	2	US-09-949-002-289	Sequence 289, App
858	25	80.6	510	2	US-09-252-991A-33009	Sequence 33009, A	931	25	80.6	970	1	US-08-673-789-7	Sequence 7, Appl
859	25	80.6	514	2	US-08-467-023-134	Sequence 134, App	932	25	80.6	973	1	US-08-162-809-10	Sequence 10, Appl
860	25	80.6	516	2	US-09-949-002-547	Sequence 547, App	933	25	80.6	981	2	US-09-949-002-513	Sequence 513, Appl
861	25	80.6	519	2	US-09-270-767-41281	Sequence 41281, A	934	25	80.6	987	1	US-08-436-04-6	Sequence 6, Appl
862	25	80.6	519	2	US-09-270-767-56497	Sequence 56497, A	935	25	80.6	987	1	US-08-436-054-6	Sequence 6, Appl
863	25	80.6	524	2	US-09-549-519-27	Sequence 27, Appl	936	25	80.6	987	4	PCT-US95-08812-6	Sequence 6, Appl
864	25	80.6	524	2	US-09-549-519-28	Sequence 28, Appl	937	25	80.6	988	1	US-08-162-809-14	Sequence 14, Appl
865	25	80.6	528	2	US-09-949-016-9678	Sequence 9678, Ap	938	25	80.6	989	2	US-09-954-987B-171	Sequence 171, App
866	25	80.6	530	2	US-09-252-991A-23666	Sequence 23666, A	939	25	80.6	990	2	US-09-949-016-7235	Sequence 7235, Ap
867	25	80.6	535	2	US-09-252-991A-28236	Sequence 28236, A	940	25	80.6	991	2	US-09-949-016-7768	Sequence 7768, Ap
868	25	80.6	540	2	US-09-252-991A-33091	Sequence 33091, A	941	25	80.6	1024	2	US-09-562-737-88	Sequence 88, Appl
869	25	80.6	561	1	US-08-559-492-12	Sequence 12, Appl	942	25	80.6	1024	2	US-09-949-016-7276	Sequence 7276, Ap
870	25	80.6	563	2	US-09-252-991A-28458	Sequence 28458, A	943	25	80.6	1049	2	US-09-999-833A-496	Sequence 496, App
871	25	80.6	567	2	US-09-252-991A-28481	Sequence 28481, A	944	25	80.6	1049	2	US-09-954-987B-170	Sequence 170, App
872	25	80.6	567	2	US-09-949-016-7250	Sequence 7250, Ap	945	25	80.6	1049	2	US-09-954-987B-172	Sequence 172, App
873	25	80.6	571	2	US-09-252-991A-28549	Sequence 28549, A	946	25	80.6	1049	2	US-10-020-444A-966	Sequence 496, App
874	25	80.6	581	2	US-09-252-991A-25414	Sequence 25414, A	947	25	80.6	1074	1	US-08-470-058-2	Sequence 2, Appl
875	25	80.6	588	2	US-10-087-167-121	Sequence 121, App	948	25	80.6	1074	2	US-09-037-188-2	Sequence 2, Appl
876	25	80.6	588	2	US-10-087-167-123	Sequence 123, App	949	25	80.6	1074	2	US-09-285-310-2	Sequence 2, Appl
877	25	80.6	589	2	US-09-252-991A-33631	Sequence 32631, A	950	25	80.6	1074	2	US-09-753-385-2	Sequence 2, Appl
878	25	80.6	591	2	US-09-949-016-10026	Sequence 10026, A	951	25	80.6	1079	2	US-09-058-489-22	Sequence 22, Appl
879	25	80.6	591	2	US-10-087-167-119	Sequence 119, App	952	25	80.6	1101	2	US-09-561-709B-5	Sequence 5, Appl
880	25	80.6	593	2	US-10-087-167-125	Sequence 125, App	953	25	80.6	1149	2	US-08-560-005-5	Sequence 5, Appl
881	25	80.6	595	2	US-09-252-991A-18995	Sequence 18995, A	954	25	80.6	1149	2	US-09-418-540-5	Sequence 5, Appl
882	25	80.6	596	2	US-09-252-991A-32193	Sequence 32193, A	955	25	80.6	1149	2	US-09-969-528-5	Sequence 5, Appl
883	25	80.6	596	2	US-09-949-016-7776	Sequence 7776, Ap	956	25	80.6	1240	2	US-09-058-489-23	Sequence 23, Appl
884	25	80.6	599	2	US-10-087-167-127	Sequence 127, App	957	25	80.6	1253	2	US-08-506-296B-14	Sequence 14, Appl
885	25	80.6	599	2	US-10-087-167-148	Sequence 148, App	958	25	80.6	1253	2	US-09-489-039A-12097	Sequence 12097, A
886	25	80.6	602	2	US-10-087-167-143	Sequence 143, App	959	25	80.6	1257	1	US-08-340-428B-49	Sequence 49, Appl
887	25	80.6	609	2	US-09-270-767-46418	Sequence 46418, A	960	25	80.6	1260	2	US-08-506-296B-21	Sequence 21, Appl
888	25	80.6	611	1	US-08-752-307B-10	Sequence 10, Appl	961	25	80.6	1276	1	US-08-222-616-24	Sequence 24, Appl
889	25	80.6	611	2	US-09-707-802-10	Sequence 10, Appl	962	25	80.6	1276	1	US-08-446-648-24	Sequence 24, Appl
890	25	80.6	615	2	US-09-991-326-10	Sequence 10, Appl	963	25	80.6	1276	4	US-09-982-610-24	Sequence 24, Appl
891	25	80.6	620	2	US-10-087-167-135	Sequence 135, App	964	25	80.6	1276	4	PCT-US95-04228-24	Sequence 24, Appl
892	25	80.6	627	2	US-10-087-167-137	Sequence 137, App	965	25	80.6	1347	2	US-09-058-489-24	Sequence 24, Appl
893	25	80.6	627	2	US-09-902-540-15743	Sequence 15743, A	966	25	80.6	1401	2	US-09-976-598-1035	Sequence 1035, Ap
894	25	80.6	633	2	US-09-889-039A-11729	Sequence 11729, A	967	25	80.6	1404	1	US-08-400-155-2	Sequence 2, Appl
895	25	80.6	634	2	US-09-489-039A-8399	Sequence 8399, Ap	968	25	80.6	1404	2	US-08-611-722A-2	Sequence 2, Appl
896	25	80.6	635	2	US-08-857-076-101	Sequence 101, App	969	25	80.6	1404	2	US-09-195-524-2	Sequence 2, Appl
897	25	80.6	645	2	US-10-104-047-2588	Sequence 2588, Ap	970	25	80.6	1410	1	US-08-470-058-4	Sequence 4, Appl
898	25	80.6	655	2	US-10-104-047-2502	Sequence 2502, Ap	971	25	80.6	1410	2	US-09-037-188-4	Sequence 4, Appl
899	25	80.6	661	2	US-09-252-991A-18225	Sequence 18225, A	972	25	80.6	1410	2	US-09-285-310-4	Sequence 4, Appl
900	25	80.6	666	2	US-09-422-869-18	Sequence 18, Appl	973	25	80.6	1410	2	US-09-753-385-4	Sequence 4, Appl
901	25	80.6	666	6	5262177-4	Patent No. 5262177	974	25	80.6	1525	2	US-09-191-647-2	Sequence 2, Appl
902	25	80.6	698	1	US-08-175-158A-2	Sequence 2, Appl	975	25	80.6	1525	2	US-09-540-245A-2	Sequence 2, Appl
903	25	80.6	698	2	US-09-439-740-2	Sequence 2, Appl	976	25	80.6	1525	2	US-09-540-153-2	Sequence 2, Appl

977 25 80.6 1525 2 US-10-289-776-2 Sequence 2, Appl1
978 25 80.6 1529 2 US-09-312-283C-396 Sequence 396, App
979 25 80.6 1529 2 US-10-188-495-67 Sequence 67, Appl
980 25 80.6 1551 2 US-09-949-016-6785 Sequence 6785, Ap
981 25 80.6 1572 2 US-09-562-702A-32 Sequence 32, Appl
982 25 80.6 1572 2 US-09-561-818A-28 Sequence 28, Appl
983 25 80.6 1572 2 US-10-037-182-20 Sequence 20, Appl
984 25 80.6 1605 2 US-09-562-702A-30 Sequence 30, Appl
985 25 80.6 1605 2 US-09-561-818A-26 Sequence 26, Appl
986 25 80.6 1605 2 US-10-037-182-18 Sequence 18, Appl
987 25 80.6 1656 2 US-09-949-016-7247 Sequence 7247, Ap
988 25 80.6 1681 2 US-09-920-653B-3 Sequence 3, Appl1
989 25 80.6 1720 2 US-08-477-451-12 Sequence 12, Appl
990 25 80.6 1761 2 US-09-561-709B-1 Sequence 1, Appl1
991 25 80.6 1792 2 US-09-561-818A-12 Sequence 12, Appl
992 25 80.6 1816 2 US-09-561-818A-10 Sequence 10, Appl
993 25 80.6 1821 2 US-09-949-016-5938 Sequence 5938, Ap
994 25 80.6 1831 2 US-08-479-722B-2 Sequence 2, Appl1
995 25 80.6 1833 2 US-09-592-685-2 Sequence 2, Appl1
996 25 80.6 1833 4 PCT-US95-02251-18 Sequence 18, Appl
997 25 80.6 2050 1 US-08-347-594A-2 Sequence 2, Appl1
998 25 80.6 2109 2 US-08-646-695-6 Sequence 6, Appl1
999 25 80.6 2109 4 PCT-US96-06053-6 Sequence 6, Appl1
1000 25 80.6 2813 2 US-09-381-261A-1 Sequence 1, Appl1

ALIGNMENTS

REGISTRATION NUMBER: 32750
REFERENCE/DOCKET NUMBER: GBRO-024/00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-7622
TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: redox sequence typical for thioredoxins
LOCATION: 1..4
US-07-820-688A-5
Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 1 CGPC 4

RESULT 1
US-07-820-688A-5
Sequence 5, Application US/07820688A
Patent No. 5328839
GENERAL INFORMATION:
APPLICANT: AHARONOWITZ, YAIR
APPLICANT: VAN DER VOORT, LUCIA H
APPLICANT: COHEN, GERALD
APPLICANT: BOVENBERG, ROELOF A. L.
APPLICANT: SCHREIBER, RACHEL
APPLICANT: ARGAMAN, ANAT
APPLICANT: AV-GAY, YOSEF
APPLICANT: NAN, HELENA M.
APPLICANT: KATTEVILDER, ALFRED
APPLICANT: PALLISSER, HARRIET
TITLE OF INVENTION: AN OXIDO REDUCTASE ENZYME SYSTEM
TITLE OF INVENTION: OBTAINABLE FROM P. CHRYSOGENUM, THE SET OF GENES ENCODING
TITLE OF INVENTION: THE SAME AND THE USE OF OXIDO REDUCTASE ENZYME SYSTEMS OR
TITLE OF INVENTION: GENES ENCODING THE SAME FOR INCREASING ANTIBIOTIC PRODUCTION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,688A
FILING DATE: 19920324
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NU91/00101
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH. D., BARBARA

RESULT 2
US-08-274-043B-5
Sequence 5, Application US/08274043B
Patent No. 5652132
GENERAL INFORMATION:
APPLICANT: Aharonowitz, Yair
APPLICANT: Van Der Voort, Lucia H. M.
APPLICANT: Cohen, Gerald
APPLICANT: Bovenberg, Roelof A. L.
APPLICANT: Schreiber, Rachel
APPLICANT: Argaman, Anat
APPLICANT: Av-Gay, Yosef
APPLICANT: Nan, Helena M.
APPLICANT: Kattevilder, Alfred
APPLICANT: Pallisa, Harriet
TITLE OF INVENTION: An oxido reductase enzyme system obtainable from
TITLE OF INVENTION: P. chrysogenum, the set of genes encoding the same and the us.
TITLE OF INVENTION: oxido reductase enzyme systems or genes encoding the same for
TITLE OF INVENTION: Increasing antibiotic production
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Barbara Rae-Venter
STREET: P.O. Box 60039
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/274,043B
FILING DATE: 12-JULY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/820,688
FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/NU91/00101
FILING DATE: 18-JUNE-1991
APPLICATION NUMBER: EPO 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-024/01US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: redox sequence typical for thioredoxins
LOCATION: 1..4
US-08-274-043B-5

Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 3
US-08-386-729A-5
Sequence 5, Application US/08386729A
Patent No. 5753435
GENERAL INFORMATION:
APPLICANT: Ananowitz, Yair
APPLICANT: Van Der Voort, Lucia H. M.
APPLICANT: Cohen, Gerald
APPLICANT: Bovenberg, Roelof A. L.
APPLICANT: Schreiber, Rachel
APPLICANT: Argaman, Anat
APPLICANT: Av-Gay, Yoseeff
APPLICANT: Nan, Helena M.
APPLICANT: Kaltefleiter, Alfred
APPLICANT: Pallisa, Harriet
TITLE OF INVENTION: An oxido reductase enzyme system
TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
TITLE OF INVENTION: production
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Well, Gotshall & Manges
STREET: 2882 Sand Hill Road, Ste. 280
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,729A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/274,043
FILING DATE: 12-JULY-1994
APPLICATION NUMBER: US 07/820,688
FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/NL91/000101
FILING DATE: 18-JUNE-1991
APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-024/02US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: redox sequence typical for thioredoxins
LOCATION: 1..4
US-08-386-729A-5

Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 4
US-08-687-276-3
Sequence 3, Application US/08687276
Patent No. 5910435
GENERAL INFORMATION:
APPLICANT: Raines, Ronald T
TITLE OF INVENTION: SYNTHETIC PROTEIN FOLDING CATALYSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,276
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93952
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-687-276-3

Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 5
US-08-883-804-2
Sequence 2, Application US/08883804
Patent No. 5985261
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: Das, Kumuda C.
TITLE OF INVENTION: USE OF THIOPROXIN-LIKE MOLECULES FOR
INDUCTION OF MMSD TO TREAT OXIDATIVE DAMAGE
TITLE OF INVENTION: INDUCTION OF MMSD TO TREAT OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,804
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-804-2
Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4
RESULT 6
US-08-504-538A-21
Sequence 21, Application US/08504538A
Patent No. 6004746
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: McCoy, John W.
APPLICANT: Jensen, Timm H.
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING
PROTEIN INTERACTIONS
TITLE OF INVENTION: PROTEIN INTERACTIONS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2214
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,538A
FILING DATE: 07/20/95
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,082
FILING DATE: 07/20/94
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/259001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-504-538A-21
Query Match 100.0%; Score 31; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4
RESULT 7
US-09-579-883A-1
Sequence 1, Application US/09579883A
Patent No. 6686443
GENERAL INFORMATION:
APPLICANT: RABENSTEIN, DALLAS
APPLICANT: SHI, TIESHENG
TITLE OF INVENTION: CHEMICAL REAGENTS FOR FORMATION OF DISULFIDE BONDS IN PEPTIDES
FILE REFERENCE: 407T-891100US
CURRENT APPLICATION NUMBER: US/09/579,883A
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent version 3.0
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-579-883A-1
Query Match 100.0%; Score 31; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4
RESULT 8
US-09-679-705-2
Sequence 2, Application US/09679705
Patent No. 6872563
GENERAL INFORMATION:
APPLICANT: BECKWITH, JONATHAN
APPLICANT: ASLUND, FREDRIK
APPLICANT: BESSETTE, PAUL H.
APPLICANT: GEORGIU, GEORGE
APPLICANT: RITZ, DANIEL
APPLICANT: LIM, JACKIE EUN-AH

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
FILE REFERENCE: HMV-052.01
CURRENT APPLICATION NUMBER: US/09/679,705
CURRENT FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/157,770
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/163,939
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/166,044
PRIOR FILING DATE: 1999-11-17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-679-705-2

Query Match 100.0%; Score 31; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 9

US-08-883-804-4
Sequence 4, Application US/08883804
Patent No. 5985261
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: Das, Kumuda C.
TITLE OF INVENTION: USE OF THIOREDOXIN-LIKE MOLECULES FOR
TITLE OF INVENTION: INDUCTION OF MMSOD TO TREAT OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rosa P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,804
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-804-4

Query Match 100.0%; Score 31; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 10

US-08-883-804-5
Sequence 5, Application US/08883804
Patent No. 5985261
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: Das, Kumuda C.
TITLE OF INVENTION: USE OF THIOREDOXIN-LIKE MOLECULES FOR
TITLE OF INVENTION: INDUCTION OF MMSOD TO TREAT OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rosa P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,804
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-804-5

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 11

US-08-627-907A-6
Sequence 6, Application US/08627907A
Patent No. 6060302
GENERAL INFORMATION:
APPLICANT: HIRANO, Naoto
APPLICANT: HIRAI, Hisamatu
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND DNA
TITLE OF INVENTION: SEQUENCE ENCODING THE SAME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,907A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-238402
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01572
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JR., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-627-907A-6

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 12
US-07-901-713A-3
Sequence 3, Application US/07901713A
Patent No. 6291205
GENERAL INFORMATION:
APPLICANT: Tuttle, Michael F.
APPLICANT: Freedman, Robert B.
APPLICANT: Markus, Henry Z.
APPLICANT: Schultz, Loren D.
APPLICANT: Montgomery, Donna L.
APPLICANT: Ellis, Ronald W.
TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF
TITLE OF INVENTION: DISULFIDE BONDED RECOMBINANT PROTEINS BY SACCAROMYCES
FILE REFERENCE: 18469
CURRENT APPLICATION NUMBER: US/07/901,713A
CURRENT FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: S. cerevisiae PDI thioredoxin active site
US-07-901-713A-3

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 13
US-08-571-985-27
Sequence 27, Application US/08571985
Patent No. 5783557
GENERAL INFORMATION:
APPLICANT: Burstein, Yigal
APPLICANT: Trainin, Nathan
APPLICANT: Rycus, Avigail
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 578157thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,985
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2163.00048
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-571-985-27

Query Match 100.0%; Score 31; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 3 CGPC 6

RESULT 14
US-09-116-766-27
Sequence 27, Application US/09116766
Patent No. 5968898
GENERAL INFORMATION:
APPLICANT: Burstein, Yigal
APPLICANT: Trainin, Nathan
APPLICANT: Rycus, Avigail
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5968898thwestern Hwy., Suite 410

CITY: Farmington Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,766
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2163.00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-116-766-27

Query Match 100.0%; Score 31; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 3 CGPC 6

RESULT 15
US-08-836-480-34
Sequence 34, Application US/08836480
Patent No. 6103697
GENERAL INFORMATION:
APPLICANT: Bergstrand, Hakan
APPLICANT: Erickson, Tomas
APPLICANT: Karabelas, Kostas
APPLICANT: Lindvall, Magnus
APPLICANT: Sarnstrand, Bengt
TITLE OF INVENTION: NEW PEPTIDES WITH IMMUNOMODULATORY EFFECTS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,480
FILING DATE: 14-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 95\403256-8
FILING DATE: 14-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 06275/036001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-480-34

Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 3 CGPC 6

RESULT 16
US-09-562-897-34
Sequence 34, Application US/09562897
Patent No. 6228374
GENERAL INFORMATION:
APPLICANT: Bergstrand, Hakan
APPLICANT: Erickson, Tomas
APPLICANT: Karabelas, Kostas
APPLICANT: Lindvall, Magnus
APPLICANT: Sarnstrand, Bengt
TITLE OF INVENTION: NEW PEPTIDES WITH IMMUNOMODULATORY EFFECTS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,897
FILING DATE: 01-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,480
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 06275/036001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-562-897-34

Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 3 CGPC 6

RESULT 17
US-08-750-142B-54
; Sequence 54, Application US/08750142B
; Patent No. 6228373
; GENERAL INFORMATION:
; APPLICANT: Bergstrand, Hakan
; APPLICANT: Eriksson, Tomas
; APPLICANT: Lindvall, Magnus
; APPLICANT: Sarnstrand, Bengt
; TITLE OF INVENTION: NEW PEPTIDES WITH
; TITLE OF INVENTION: IMMUNOMODULATORY EFFECTS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,142B
; FILING DATE: 25-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE96/00365
; FILING DATE: 22-MAR-1996
; APPLICATION NUMBER: SE9501067-4
; FILING DATE: 24-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06275/062001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-750-142B-54

Query Match 100.0%; Score 31; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 2 CGPC 5

RESULT 18
US-09-160-513-217
; Sequence 217, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marguis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-160-513-217

Query Match 100.0%; Score 31; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 4 CGPC 7

RESULT 19
US-09-230-041-31
; Sequence 31, Application US/09230041A
; Patent No. 6465179
; GENERAL INFORMATION:
; APPLICANT: THIREOS, GEORGE
; APPLICANT: KARETZOPoulos, DIMITRIS
; TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
; FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
; CURRENT APPLICATION NUMBER: US/09/230,041A
; CURRENT FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: EP97108240.9
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-09-230-041-31

Query Match 100.0%; Score 31; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 13e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 21 CGPC 24

RESULT 20
US-09-881-572A-25

; Sequence 25, Application US/09881572A
; Patent No. 6762031
; GENERAL INFORMATION:
; APPLICANT: Roth, Monica;
; APPLICANT: Bupp, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 29
; TYPE: PRF
; ORGANISM: Amphotrophic Murine Leukemia Virus
US-09-881-572A-25

Query Match 100.0%; Score 31; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 11 CGPC 14

RESULT 21
US-09-881-572A-5
; Sequence 5, Application US/09881572A
; Patent No. 6762031
; GENERAL INFORMATION:
; APPLICANT: Roth, Monica;
; APPLICANT: Bupp, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRF
; ORGANISM: amphotrophic murine leukemia virus
US-09-881-572A-5

Query Match 100.0%; Score 31; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 11 CGPC 14

RESULT 22
US-10-044-359-26
; Sequence 26, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: Heriman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: B81367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416

; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 35
; TYPE: PRF
; ORGANISM: Androctonus mauretanicus
US-10-044-359-26

Query Match 100.0%; Score 31; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 1 CGPC 4

RESULT 23
US-08-239-256-16
; Sequence 16, Application US/08239256
; Patent No. 5585345
; GENERAL INFORMATION:
; APPLICANT: BOIME, IRVING
; APPLICANT: MATZUK, MARTIN M.
; APPLICANT: KEENE, JEFFREY L.
; TITLE OF INVENTION: CTP EXTENDED FORM OF LH
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,256
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20030.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-239-256-16

Query Match 100.0%; Score 31; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 23 CGPC 26

RESULT 24
US-09-244-583-20
; Sequence 20, Application US/09244583

```
; Patent No. 6479654
; GENERAL INFORMATION:
; APPLICANT: BAIRD, ANDREW
; APPLICANT: ANDREASON, GRAI
; TITLE OF INVENTION: NOVEL FORMS OF THE ANGIOGENIC FACTOR
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR: VEGF
; FILE REFERENCE: 240/086
; CURRENT APPLICATION NUMBER: US/09/244,583
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 60/073,979
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-244-583-20
```

```
Query Match          100.0%; Score 31; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 CGPC 5
      ||||
Db      2 CGPC 5
```

```
RESULT 25
US-09-583-638-11
; Sequence 11, Application US/09583638
; Patent No. 6635421
; GENERAL INFORMATION:
; APPLICANT: KLAGSBRUN, MICHAEL
; APPLICANT: SOKER, SHAY
; APPLICANT: MIAO, HUA-QUNAN
; APPLICANT: TAKASHIMA, SEIJI
; TITLE OF INVENTION: NEUROFILINS AND USE THEREOF IN METHODS FOR
; TITLE OF INVENTION: DIAGNOSIS AND PROGNOSIS OF CANCER
; FILE REFERENCE: 701039-48800
; CURRENT APPLICATION NUMBER: US/09/583,638
; CURRENT FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US98/26127
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-583-638-11
```

```
Query Match          100.0%; Score 31; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      ||||
Db      2 CGPC 5
```

```
RESULT 26
US-09-579-420B-1
; Sequence 1, Application US/09579420B
; Patent No. 6777534
; GENERAL INFORMATION:
; APPLICANT: Klagsbrun, Michael
; APPLICANT: Soker, Shay
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
```

```
; FILE REFERENCE: 701039-047875-C
; CURRENT APPLICATION NUMBER: US/09/579,420B
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: PCT/US98/26103
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-579-420B-1
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```
Query Match          100.0%; Score 31; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      ||||
Db      2 CGPC 5
```

```
RESULT 27
US-09-579-420B-19
; Sequence 19, Application US/09579420B
; Patent No. 6777534
; GENERAL INFORMATION:
; APPLICANT: Klagsbrun, Michael
; APPLICANT: Soker, Shay
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 701039-047875-C
; CURRENT APPLICATION NUMBER: US/09/579,420B
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: PCT/US98/26103
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-579-420B-19
```

```
Query Match          100.0%; Score 31; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      ||||
Db      2 CGPC 5
```

```
RESULT 28
US-09-513-999C-7252
; Sequence 7252, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Ducleert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.RBG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
```

PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7252
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 15
OTHER INFORMATION: Xaa= * or Glu or Gly or Trp
US-09-513-999C-7252

Query Match 100.0%; Score 31; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 8 CGPC 11

RESULT 29

US-09-513-999C-5904
Sequence 5904, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5904
LENGTH: 53
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 27
OTHER INFORMATION: Xaa=Arg or Ser or Thr
US-09-513-999C-5904

Query Match 100.0%; Score 31; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 34 CGPC 37

RESULT 30

US-09-513-999C-5905
Sequence 5905, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5905
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 2
OTHER INFORMATION: Xaa=Ala or Ser
FEATURE:
NAME/KEY: UNSURE
LOCATION: 27
OTHER INFORMATION: Xaa=Arg or Ser or Thr
US-09-513-999C-5905

Query Match 100.0%; Score 31; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 34 CGPC 37

RESULT 31

US-09-902-540-11828
Sequence 11828, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11828
LENGTH: 77
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-11828

Query Match 100.0%; Score 31; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 32

US-09-630-273-2
Sequence 2, Application US/09630273
Patent No. 6521416
GENERAL INFORMATION:
APPLICANT: Birken et al, Steven
TITLE OF INVENTION: Determination Of The Amount Of h1h Beta Core Fragment
IN A Sample From A Subject And Uses Thereof
FILE REFERENCE: 54204-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/630,273
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: PCT/US99/02279
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2

/ LENGTH: 80
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-630-273-2

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 77 CGPC 80

RESULT 33
US-09-621-976-6168
/ Sequence 6168, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621.976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 6168
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-621-976-6168

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 63 CGPC 66

RESULT 34
US-09-198-452A-697
/ Sequence 697, Application US/09198452A
/ Patent No. 6559294
/ GENERAL INFORMATION:
/ APPLICANT: Grifflais, R.
/ TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
/ TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
/ FILE REFERENCE: 9710-003-999
/ CURRENT APPLICATION NUMBER: US/09/198.452A
/ CURRENT FILING DATE: 1998-11-24
/ NUMBER OF SEQ ID NOS: 6849
/ SEQ ID NO 697
/ LENGTH: 102
/ TYPE: PRT
/ ORGANISM: Chlamydia pneumoniae
US-09-198-452A-697

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 28 CGPC 31

RESULT 35
US-09-621-976-5629

/ Sequence 5629, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621.976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 5629
/ LENGTH: 102
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE: SIGNAL
/ NAME/KEY: SIGNAL
/ LOCATION: -35..-1
US-09-621-976-5629

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 35 CGPC 38

RESULT 36
US-08-241-853-27
/ Sequence 27, Application US/08241853
/ Patent No. 5693488
/ GENERAL INFORMATION:
/ APPLICANT: Fang, Kathy S.
/ APPLICANT: Hanafusa, Hidesaburo
/ TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
/ TITLE OF INVENTION: AND METHODS OF USE THEREOF
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Klauber & Jackson
/ STREET: 411 Hackensack Avenue
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/241.853
/ FILING DATE: 12-MAY-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 600-1-078
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201 487-5800
/ TELEFAX: 201 343-1684
/ TELEX: 133521
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 103 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO

US-08-241-853-27

Query Match 100.0%; Score 31; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 37

US-08-850-917-27
Sequence 27, Application US/08850917
Patent No. 5854045

GENERAL INFORMATION:

APPLICANT: Fang, Kathy S.
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA

ZIP: 07601
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/850,917

FILING DATE: 02-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/241,853

FILING DATE: 12-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-078

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 103 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-850-917-27

Query Match 100.0%; Score 31; DB 1; Length 103;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 38

US-09-583-110-3078
Sequence 3078, Application US/09583110
Patent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A

CURRENT APPLICATION NUMBER: US/09/583,110

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 3078

LENGTH: 104

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-583-110-3078

Query Match 100.0%; Score 31; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 28 CGPC 31

RESULT 39

5210073-1
Patent No. 5210073

APPLICANT: YODOI, JUNJI;UCHIDA, ATSUSHI;TAGAWA, YUTAKA

MITSUI, AKIRA;HIRAKAWA, TADASHI

TITLE OF INVENTION: METHOD FOR TREATING CANCER THERAPY

RADIATION DAMAGE OR ARTERIOSCLEROSIS USING HUMAN ADP

NUMBER OF SEQUENCES: 1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/589,616

FILING DATE: 28-SEP-1990

SEQ ID NO:1;

LENGTH: 104

5210073-1

Query Match 100.0%; Score 31; DB 6; Length 104;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 31 CGPC 34

RESULT 40

US-08-826-910-3
Sequence 3, Application US/08826910
Patent No. 5919657

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: THIOREDUXIN-LIKE PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,910
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0268 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 339649
; US-08-826-910-3

Query Match          100.0%; Score 31; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      32 CGPC 35

RESULT 41
US-08-826-910-4
; Sequence 4, Application US/08826910
; Patent No. 5919657
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: THIOREDOXIN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,910
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0268 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 453972
; US-08-826-910-4

Query Match          100.0%; Score 31; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      32 CGPC 35

RESULT 42
US-09-601-144-68
; Sequence 68, Application US/09601144
; Patent No. 6566514
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Young, Aiping H.
; APPLICANT: Lee, Yoon S.
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDOXIN
; TITLE OF INVENTION: AND THIOREDOXIN REDUCTASE GENES AND METHODS OF USING
; TITLE OF INVENTION: SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 683-1120S-A
; CURRENT APPLICATION NUMBER: US/09/601,144
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/073,196
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
; US-09-601-144-68

Query Match          100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      32 CGPC 35

RESULT 43
US-09-513-999C-8037
; Sequence 8037, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8037
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-999C-8037

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Query Match 100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 44
US-08-386-729A-10
Sequence 10, Application US/08386729A
Patent No. 5753435
GENERAL INFORMATION:
APPLICANT: Aharonowitz, Yair
APPLICANT: Van Der Voort, Lucia H. M.
APPLICANT: Cohen, Gerald
APPLICANT: Bovenberg, Roelof A. L.
APPLICANT: Schreiber, Rachel
APPLICANT: Argaman, Anat
APPLICANT: Av-Gay, Yosef
APPLICANT: Nan, Helena M.
APPLICANT: Kallewilder, Alfred
APPLICANT: Pallisa, Harriet
TITLE OF INVENTION: An oxido reductase enzyme system
TITLE OF INVENTION: obtainable from P. chrysoenum, the set of genes
encoding the same and the use of oxido reductase enzyme
TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
production
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weil, Gotshal & Manges
STREET: 2882 Sand Hill Road, Ste. 280
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08386, 729A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/274,043
FILING DATE: 12-JULY-1994
APPLICATION NUMBER: US 07/820,688
FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/NL91/000101
FILING DATE: 18-JUNE-1991
APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-024/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-386-729A-10
Query Match 100.0%; Score 31; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 32 CGPC 35

RESULT 45
US-09-383-586-13
Sequence 13, Application US/09383586
Patent No. 6242419
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevlin
APPLICANT: Orrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compounds isolated from stromal cells
TITLE OF INVENTION: and methods for their use
FILE REFERENCE: 11000.1037c1
CURRENT APPLICATION NUMBER: US/09/383,586
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 106
TYPE: PRT
ORGANISM: Mouse
US-09-383-586-13

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 33 CGPC 36

RESULT 46
US-09-823-038A-13
Sequence 13, Application US/09823038A
Patent No. 6797271
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevlin
APPLICANT: Orrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1037c3
CURRENT APPLICATION NUMBER: US/09/823,038A
CURRENT FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 106
TYPE: PRT
ORGANISM: Mouse
US-09-823-038A-13

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 33 CGPC 36

RESULT 47
US-07-745-382-22
Sequence 22, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioresdoxin and Thioresdoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cseer, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-382-22
Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 33 CGPC 36
RESULT 48
US-07-921-848-22
Sequence 22, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioresdoxin and Thioresdoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cseer, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-921-848-22
Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 33 CGPC 36
RESULT 49
US-08-165-301A-22
Sequence 22, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: G1 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-22

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
DB 33 CGPC 36

RESULT 50
US-08-165-301A-26
Sequence 26, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-26

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
DB 33 CGPC 36

RESULT 51
US-08-165-301A-28
Sequence 28, Application US/08165301A
Patent No. 5646016

GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-28

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
DB 33 CGPC 36

RESULT 52
US-08-810-436-22
Sequence 22, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-22

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 33 CGPC 36

RESULT 53
US-08-810-436-26
Sequence 26, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlaasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-26

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 33 CGPC 36

RESULT 54
US-08-810-436-28
Sequence 28, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlaasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-28

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 33 CGPC 36

RESULT 55
US-09-485-885-17

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; Sequence 17, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchetkh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-17

Query Match          100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      33 CGPC 36

RESULT 56
US-09-166-966E-10
; Sequence 10, Application US/09166366E
; Patent No. 6407208
; GENERAL INFORMATION:
; APPLICANT: CHEN, DAVID CHANHAN
; APPLICANT: HU, NITEN-TAI
; APPLICANT: CHEN, YUN-JU
; APPLICANT: HSEU, TZONG-HSIUNG
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
; FILE REFERENCE: 32350-150960
; CURRENT APPLICATION NUMBER: US/09/166,966E
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: TW 86114750
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: thioredoxin
; LOCATION: 1..109
; OTHER INFORMATION: amino acid of thioredoxin
US-09-166-966E-10

Query Match          100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      33 CGPC 36

RESULT 57
US-09-248-796A-19911
; Sequence 19911, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
```

```
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19911
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19911

Query Match          100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      36 CGPC 39

RESULT 58
PCT-US94-14179-22
; Sequence 22, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14179
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinert, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14179-22

Query Match          100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 CGPC 5
|||
Db 33 CGPC 36

RESULT 59
PCT-US94-14179-26
; Sequence 26, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: Diblasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14179
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinerdt, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
PCT-US94-14179-26
Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CGPC 5
|||
Db 33 CGPC 36
RESULT 60
PCT-US94-14179-28
; Sequence 28, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: Diblasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
PCT-US94-14179-28
Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CGPC 5
|||
Db 33 CGPC 36
RESULT 61
US-09-621-976-4028
; Sequence 4028, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4028
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -102...-1
US-09-621-976-4028
Query Match 100.0%; Score 31; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CGPC 5
|||
Db 74 CGPC 77
RESULT 62
US-09-264-419C-6
; Sequence 6, Application US/09264419C
; Patent No. 6174682
; GENERAL INFORMATION:

APPLICANT: Rhododouct, Mehran
TITLE OF INVENTION: No. 6174682e1 Thioresdoin Family Active Site Molecules and Uses
FILE REFERENCE: WNI-076
CURRENT APPLICATION NUMBER: US/09/264,419C
CURRENT FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 111
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-264-419C-6

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 111;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 34 CGPC 37

RESULT 63
US-09-134-001C-3859
Sequence 3859, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3859
LENGTH: 111
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3859

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 111;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 36 CGPC 39

RESULT 64
US-09-107-532A-6739
Sequence 6739, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6739:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...112
SEQUENCE DESCRIPTION: SEQ ID NO: 6739:
US-09-107-532A-6739

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 112;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 36 CGPC 39

RESULT 65
US-10-104-047-3199
Sequence 3199, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3199
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3199

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 113;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 37 CGPC 40

RESULT 66
US-08-918-288-71
Sequence 71, Application US/08918288
Patent No. 623890
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-918-288-71
Query Match 100.0%; Score 31; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 90 CGPC 93

RESULT 67
US-09-282-357-71
Sequence 71, Application US/09282357
Patent No. 6242580
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
City: Washington
STATE: DC

COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,357
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/918,288
FILING DATE: 25 AUG-1997
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-282-357-71
Query Match 100.0%; Score 31; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 90 CGPC 93

RESULT 68
US-09-897-425-41
Sequence 41, Application US/09897425
Patent No. 6750046
GENERAL INFORMATION:
APPLICANT: MOLONEY, MAURICE M.
APPLICANT: DALMIA, BIPIN K.
TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
TITLE OF INVENTION: PROTEINS ON OIL BODIES
FILE REFERENCE: 034547/0106
CURRENT APPLICATION NUMBER: US/09/897,425
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/210,843
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/846,021
PRIOR FILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: 08/366,783
PRIOR FILING DATE: 1994-12-30
PRIOR APPLICATION NUMBER: 08/142,418
PRIOR FILING DATE: 1993-11-16
PRIOR APPLICATION NUMBER: 07/659,835
PRIOR FILING DATE: 1991-02-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 114
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-897-425-41

Query Match 100.0%; Score 31; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
|||
Db 40 CGPC 43

RESULT 69
US-09-107-433-2930

; Sequence 2930, Application US/09107433
; Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinlelo, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 2930:

SEQUENCE CHARACTERISTICS:

LENGTH: 114 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc.feature

LOCATION: (B) LOCATION 1...114

SEQUENCE DESCRIPTION: SEQ ID NO: 2930;

US-09-107-433-2930

Query Match 100.0%; Score 31; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
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Db 38 CGPC 41

RESULT 70

US-09-786-715-11

; Sequence 11, Application US/09786715

; Patent No. 6897356
; GENERAL INFORMATION:

APPLICANT: Allen, Steve

APPLICANT: Lu, Albert

APPLICANT: Thorpe, Cathy

TITLE OF INVENTION: Thioleodoxin H Homologs

FILE REFERENCE: BB-1246

CURRENT APPLICATION NUMBER: US/09/786,715

CURRENT FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: 60/099,501

PRIOR FILING DATE: September 8, 1998

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Microsoft Office 97

SEQ ID NO 11

LENGTH: 114

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-09-786-715-11

Query Match 100.0%; Score 31; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
|||
Db 40 CGPC 43

Search completed: February 23, 2006, 00:43:45
Job time : 44.5 secs

115 Page Blank (us910)

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:42:47 ; Search time 116.5 Seconds
(without alignments)
21.519 Million cell updates/sec

Title: US-10-660-118a-2

Perfect score: 31

Sequence: 1 XCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA.Main:*

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2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubppa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/prodata/1/pubppa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	31	100.0	4	US-10-628-391-2	Sequence 2, Appl
6	31	100.0	4	US-10-776-933-149	Sequence 149, Appl
7	31	100.0	6	US-10-304-287-4	Sequence 4, Appl
8	31	100.0	6	US-10-290-072-233	Sequence 233, Appl
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24	31	100.0	28	US-10-179-382-31	Sequence 31, Appl
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84	31	100.0	73	US-10-424-599-179898	Sequence 179898, A
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103	31	100.0	80	4	US-10-373-617A-3	Sequence 3, Appl1	176	31	100.0	104	4	US-10-032-201B-152	Sequence 152, App
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105	31	100.0	80	4	US-10-361-652-2	Sequence 2, Appl1	178	31	100.0	104	4	US-10-032-201B-155	Sequence 155, App
106	31	100.0	80	6	US-11-097-143-30585	Sequence 30585, A	179	31	100.0	104	4	US-10-032-201B-158	Sequence 158, App
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115	31	100.0	84	4	US-10-408-765A-312	Sequence 312, App	188	31	100.0	104	4	US-10-451-467A-188	Sequence 188, App
116	31	100.0	84	4	US-10-425-115-310941	Sequence 310941, A	189	31	100.0	104	5	US-10-472-920-3670	Sequence 3670, App
117	31	100.0	84	4	US-10-425-115-316596	Sequence 316596, A	190	31	100.0	105	3	US-09-954-342-61	Sequence 61, Appl1
118	31	100.0	85	3	US-09-925-301-1356	Sequence 1356, App	191	31	100.0	105	4	US-10-171-311-226	Sequence 226, App
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121	31	100.0	86	4	US-10-767-701-60198	Sequence 60198, A	194	31	100.0	105	4	US-10-032-201B-94	Sequence 94, Appl1
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144	31	100.0	99	3	US-09-730-617-41	Sequence 41, Appl1	217	31	100.0	106	4	US-10-032-201B-113	Sequence 113, App
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149	31	100.0	102	4	US-10-032-201B-102	Sequence 102, App	222	31	100.0	106	4	US-10-032-201B-116	Sequence 116, App
150	31	100.0	102	4	US-10-032-201B-103	Sequence 103, App	223	31	100.0	106	4	US-10-424-599-249497	Sequence 249497, A
151	31	100.0	102	4	US-10-032-201B-104	Sequence 104, App	224	31	100.0	106	4	US-10-425-114-48446	Sequence 48446, A
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153	31	100.0	102	4	US-10-032-201B-126	Sequence 126, App	226	31	100.0	106	4	US-10-408-765A-2072	Sequence 2072, App
154	31	100.0	102	4	US-10-032-201B-128	Sequence 128, App	227	31	100.0	106	4	US-10-628-391-1	Sequence 1, Appl1
155	31	100.0	102	4	US-10-289-762-697	Sequence 697, App	228	31	100.0	106	6	US-10-425-115-365910	Sequence 365910, A
156	31	100.0	102	5	US-10-275-652-20	Sequence 20, Appl1	229	31	100.0	107	3	US-11-097-143-7479	Sequence 7479, App
157	31	100.0	102	5	US-10-501-282-3126	Sequence 3126, App	230	31	100.0	107	4	US-09-746-783-19	Sequence 19, Appl1
158	31	100.0	103	4	US-10-032-201B-96	Sequence 96, Appl1	231	31	100.0	107	4	US-10-032-201B-71	Sequence 71, Appl1
159	31	100.0	103	4	US-10-032-201B-124	Sequence 124, App	232	31	100.0	107	4	US-10-032-201B-74	Sequence 74, Appl1
160	31	100.0	103	4	US-10-032-585-7785	Sequence 7785, App	233	31	100.0	107	4	US-10-032-201B-75	Sequence 75, Appl1
161	31	100.0	103	4	US-10-660-118A-6	Sequence 6, Appl1	234	31	100.0	107	4	US-10-032-201B-109	Sequence 109, App
162	31	100.0	103	4	US-10-660-118A-7	Sequence 7, Appl1	235	31	100.0	107	4	US-10-032-201B-121	Sequence 121, App
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165	31	100.0	103	4	US-10-451-467A-614	Sequence 614, App	238	31	100.0	107	4	US-10-335-977-6753	Sequence 6753, App
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248	31	100.0	108	4	US-10-032-201B-133	Sequence 133, App	321	31	100.0	117	4	US-10-424-599-283863	Sequence 283863,
249	31	100.0	108	4	US-10-032-201B-142	Sequence 142, App	322	31	100.0	118	4	US-10-032-201B-82	Sequence 82, App
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252	31	100.0	109	3	US-09-927-876-40	Sequence 40, App	325	31	100.0	118	4	US-10-425-115-200792	Sequence 200792,
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254	31	100.0	109	4	US-10-128-714-3073	Sequence 3073, Ap	327	31	100.0	118	5	US-10-978-538-4	Sequence 4, App
255	31	100.0	109	4	US-10-128-714-8073	Sequence 8073, Ap	328	31	100.0	118	5	US-10-978-538-10	Sequence 10, App
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268	31	100.0	109	4	US-10-660-118a-4	Sequence 4, App	341	31	100.0	121	4	US-10-437-963-158010	Sequence 158010,
269	31	100.0	109	4	US-10-767-701-51831	Sequence 51831, A	342	31	100.0	121	4	US-10-425-115-283697	Sequence 283697,
270	31	100.0	109	5	US-10-899-771-17	Sequence 17, App	343	31	100.0	121	4	US-10-425-115-216847	Sequence 216847,
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280	31	100.0	110	5	US-10-450-763-53132	Sequence 53132, A	353	31	100.0	122	4	US-10-425-115-280336	Sequence 280326,
281	31	100.0	111	4	US-10-437-963-182983	Sequence 182983,	354	31	100.0	122	4	US-10-425-115-280338	Sequence 280348,
282	31	100.0	111	4	US-10-724-972A-5631	Sequence 5631, Ap	355	31	100.0	122	4	US-10-425-115-280382	Sequence 280382,
283	31	100.0	111	4	US-10-425-115-197955	Sequence 197955,	356	31	100.0	122	5	US-10-826-324-8	Sequence 4, App
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288	31	100.0	112	4	US-10-296-615-1167	Sequence 1167, Ap	361	31	100.0	123	4	US-10-425-115-283695	Sequence 283695,
289	31	100.0	112	4	US-10-767-701-33511	Sequence 33511, A	362	31	100.0	123	5	US-10-978-538-1	Sequence 8, App
290	31	100.0	112	4	US-10-425-115-201579	Sequence 201579,	363	31	100.0	124	3	US-09-738-628-6919	Sequence 6919, Ap
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292	31	100.0	113	3	US-09-963-339-8	Sequence 306849,	365	31	100.0	124	5	US-10-494-547-34	Sequence 34, App
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294	31	100.0	113	3	US-09-963-339-8	Sequence 8, App	367	31	100.0	125	4	US-10-194-885-20	Sequence 20, App
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297	31	100.0	113	4	US-10-108-260A-3146	Sequence 3146, Ap	370	31	100.0	125	4	US-10-437-963-15318	Sequence 15318,
298	31	100.0	113	4	US-10-425-115-324504	Sequence 324504,	371	31	100.0	125	4	US-10-767-701-55966	Sequence 55966, A
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303	31	100.0	114	4	US-10-032-201B-39	Sequence 39, App	376	31	100.0	126	4	US-10-741-601-389	Sequence 389, App
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305	31	100.0	114	5	US-10-617-320-2930	Sequence 2930, Ap	378	31	100.0	126	5	US-10-741-600-1162	Sequence 1162, Ap
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310	31	100.0	116	3	US-09-863-339-7	Sequence 7, App	383	31	100.0	127	4	US-10-425-114-60505	Sequence 60505, A
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312	31	100.0	116	4	US-10-145-586-49	Sequence 49, App	385	31	100.0	127	5	US-10-450-763-48663	Sequence 48663, A
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316	31	100.0	116	4	US-10-425-115-349852	Sequence 349852,	389	31	100.0	128	5	US-10-450-763-54097	Sequence 54097, A
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318	31	100.0	117	4	US-10-032-201B-98	Sequence 98, App	391	31	100.0	129	4	US-10-104-047-2145	Sequence 2145, Ap
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393	31	100.0	129	4	US-10-437-963-126907	Sequence 126907,	466	31	100.0	143	4	US-10-425-115-247348	Sequence 247348,
394	31	100.0	130	4	US-10-091-841-6	Sequence 6, App1	467	31	100.0	143	4	US-10-425-115-273032	Sequence 273032,
395	31	100.0	130	4	US-10-032-201B-136	Sequence 136, App	468	31	100.0	144	4	US-10-425-115-49225	Sequence 49225, A
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406	31	100.0	132	4	US-10-425-115-317382	Sequence 317382,	479	31	100.0	148	4	US-10-425-115-365408	Sequence 365408,
407	31	100.0	132	4	US-10-425-115-323035	Sequence 323035,	480	31	100.0	148	4	US-10-919-193B-33	Sequence 33, App1
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409	31	100.0	133	4	US-10-032-201B-80	Sequence 80, App1	482	31	100.0	149	3	US-09-738-626-6793	Sequence 6793, Ap
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413	31	100.0	133	4	US-10-767-701-43666	Sequence 43666, A	486	31	100.0	151	4	US-10-050-786-10	Sequence 10, App1
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417	31	100.0	134	4	US-10-424-599-237789	Sequence 237789,	490	31	100.0	152	4	US-10-425-114-62447	Sequence 62447, A
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427	31	100.0	137	4	US-10-424-599-259824	Sequence 259824,	500	31	100.0	161	4	US-10-437-963-133912	Sequence 133912,
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433	31	100.0	137	4	US-10-425-115-272549	Sequence 272549,	506	31	100.0	165	4	US-10-200-050-3	Sequence 3, App1
434	31	100.0	137	4	US-10-425-115-272551	Sequence 272551,	507	31	100.0	165	4	US-10-318-302-1	Sequence 1, App1
435	31	100.0	137	6	US-11-106-649-40	Sequence 40, App1	508	31	100.0	165	4	US-10-417-962-20	Sequence 20, App1
436	31	100.0	138	4	US-10-424-599-157666	Sequence 157666,	509	31	100.0	165	4	US-10-437-963-131521	Sequence 131521,
437	31	100.0	138	4	US-10-437-963-161970	Sequence 161970,	510	31	100.0	165	5	US-10-429-482-2	Sequence 2, App1
438	31	100.0	139	4	US-10-032-201B-119	Sequence 119, App	511	31	100.0	165	5	US-10-429-515-2	Sequence 2, App1
439	31	100.0	139	4	US-10-424-599-23785	Sequence 23785,	512	31	100.0	165	5	US-10-429-635-2	Sequence 2, App1
440	31	100.0	139	4	US-10-425-114-66698	Sequence 66698, A	513	31	100.0	165	5	US-10-429-653-2	Sequence 2, App1
441	31	100.0	139	6	US-11-097-143-31419	Sequence 31419, A	514	31	100.0	165	5	US-10-429-659-2	Sequence 2, App1
442	31	100.0	140	4	US-10-032-201B-64	Sequence 64, App1	515	31	100.0	165	5	US-10-429-661-2	Sequence 2, App1
443	31	100.0	140	4	US-10-032-201B-163	Sequence 163, App	516	31	100.0	165	5	US-10-429-660-2	Sequence 2, App1
444	31	100.0	140	4	US-10-425-114-60597	Sequence 60597, A	517	31	100.0	165	5	US-10-429-662-2	Sequence 2, App1
445	31	100.0	141	3	US-09-730-617-47	Sequence 47, App1	518	31	100.0	165	5	US-10-429-655-2	Sequence 2, App1
446	31	100.0	141	3	US-09-730-617-48	Sequence 48, App1	519	31	100.0	165	5	US-10-429-654-2	Sequence 2, App1
447	31	100.0	141	3	US-09-927-876-6	Sequence 6, App1	520	31	100.0	165	5	US-10-714-449-1	Sequence 1, App1
448	31	100.0	141	3	US-10-360-149-6	Sequence 6, App1	521	31	100.0	165	5	US-10-919-193B-32	Sequence 32, App1
449	31	100.0	141	4	US-10-424-599-226954	Sequence 226954,	522	31	100.0	165	5	US-10-954-311-8	Sequence 8, App1
450	31	100.0	141	4	US-10-425-114-48043	Sequence 48043, A	523	31	100.0	166	4	US-10-032-201B-147	Sequence 147, App
451	31	100.0	141	4	US-10-425-114-48133	Sequence 48133, A	524	31	100.0	166	4	US-10-032-201B-153	Sequence 153, App
452	31	100.0	141	4	US-10-425-114-48138	Sequence 48138, A	525	31	100.0	166	4	US-10-032-201B-156	Sequence 156, App
453	31	100.0	141	4	US-10-425-114-60598	Sequence 60598, A	526	31	100.0	166	4	US-10-032-201B-160	Sequence 160, App
454	31	100.0	141	4	US-10-425-114-61985	Sequence 61985, A	527	31	100.0	166	4	US-10-032-201B-165	Sequence 165, App
455	31	100.0	141	4	US-10-457-047-6	Sequence 6, App1	528	31	100.0	166	5	US-10-264-049-3110	Sequence 3110, Ap
456	31	100.0	141	5	US-10-425-115-338893	Sequence 338893,	529	31	100.0	167	3	US-09-764-860-527	Sequence 8, App1
457	31	100.0	141	5	US-10-357-819-26	Sequence 26, App1	530	31	100.0	167	4	US-10-074-095-527	Sequence 527, App
458	31	100.0	141	5	US-10-811-081-6	Sequence 6, App1	531	31	100.0	167	4	US-10-032-201B-65	Sequence 65, App1
459	31	100.0	142	4	US-10-378-029-75	Sequence 75, App1	532	31	100.0	167	4	US-10-212-878-527	Sequence 527, App
460	31	100.0	142	4	US-10-425-115-227007	Sequence 227007,	533	31	100.0	167	4	US-10-437-963-137652	Sequence 137652,
461	31	100.0	142	4	US-10-425-115-325859	Sequence 325859,	534	31	100.0	167	4	US-10-660-118A-14	Sequence 14, App1
462	31	100.0	143	3	US-09-978-360A-641	Sequence 641, App	535	31	100.0	167	4	US-10-767-701-46297	Sequence 46297, A
463	31	100.0	143	4	US-10-239-656-2	Sequence 2, App1	536	31	100.0	167	4	US-10-425-115-196292	Sequence 196292,
464	31	100.0	143	4	US-10-437-963-122996	Sequence 122996,	537	31	100.0	167	4	US-10-425-115-249938	Sequence 249938,
465	31	100.0	143	4	US-10-425-115-247344	Sequence 247344,	538	31	100.0	168	4	US-10-425-115-196290	Sequence 196290,

539	31	100.0	168	4	US-10-425-115-249786	Sequence 249786,	612	31	100.0	187	4	US-10-437-963-183458	Sequence 183458,
540	31	100.0	169	3	US-09-897-898-9	Sequence 9, Appl1	613	31	100.0	188	3	US-09-893-737-16	Sequence 16,
541	31	100.0	169	3	US-09-897-425-44	Sequence 44, Appl1	614	31	100.0	188	4	US-10-425-115-360038	Sequence 360038,
542	31	100.0	169	4	US-10-032-201B-18	Sequence 18, Appl1	615	31	100.0	188	5	US-10-970-713-16	Sequence 16, Appl1
543	31	100.0	169	4	US-10-424-599-176516	Sequence 176516,	616	31	100.0	189	4	US-10-094-746-2776	Sequence 2776, Ap
544	31	100.0	170	3	US-09-935-727-4	Sequence 4, Appl1	617	31	100.0	189	4	US-10-437-963-105917	Sequence 105917,
545	31	100.0	170	4	US-10-418-242-4	Sequence 4, Appl1	618	31	100.0	189	4	US-10-437-963-204688	Sequence 204688,
546	31	100.0	170	5	US-10-450-763-35332	Sequence 35332, A	619	31	100.0	189	5	US-10-919-193B-30	Sequence 30, Appl1
547	31	100.0	171	4	US-10-425-114-59988	Sequence 59988, A	620	31	100.0	190	3	US-09-813-398-8	Sequence 8, Appl1
548	31	100.0	171	4	US-10-425-114-63526	Sequence 63526, A	621	31	100.0	190	4	US-10-177-488-4	Sequence 4, Appl1
549	31	100.0	172	4	US-10-032-201B-66	Sequence 66, Appl1	622	31	100.0	190	4	US-10-155-492-4	Sequence 4, Appl1
550	31	100.0	172	4	US-10-032-201B-67	Sequence 67, Appl1	623	31	100.0	190	5	US-10-032-201B-57	Sequence 57, Appl1
551	31	100.0	172	4	US-10-437-963-137025	Sequence 137025,	624	31	100.0	190	4	US-10-826-324-8	Sequence 8, Appl1
552	31	100.0	172	4	US-10-660-118A-15	Sequence 15, Appl1	625	31	100.0	190	6	US-11-052-721-1	Sequence 1, Appl1
553	31	100.0	172	4	US-10-767-701-33148	Sequence 33148, A	626	31	100.0	191	3	US-09-349-954A-2	Sequence 2, Appl1
554	31	100.0	173	4	US-10-032-201B-61	Sequence 61, Appl1	627	31	100.0	191	3	US-09-932-451A-2	Sequence 2, Appl1
555	31	100.0	173	4	US-10-437-963-108195	Sequence 108195,	628	31	100.0	191	3	US-09-907-007-2	Sequence 2, Appl1
556	31	100.0	173	4	US-10-425-115-187390	Sequence 187390,	629	31	100.0	191	3	US-09-795-006A-2	Sequence 2, Appl1
557	31	100.0	173	4	US-10-425-115-187392	Sequence 187392,	630	31	100.0	191	3	US-09-870-759-122	Sequence 122, App
558	31	100.0	174	3	US-09-764-868-633	Sequence 633, App	631	31	100.0	191	4	US-09-751-708A-122	Sequence 122, App
559	31	100.0	174	4	US-10-767-701-32096	Sequence 32096, A	632	31	100.0	191	4	US-10-083-817-3	Sequence 3, Appl1
560	31	100.0	174	4	US-10-425-115-317875	Sequence 317875,	633	31	100.0	191	4	US-10-200-050-2	Sequence 2, Appl1
561	31	100.0	175	4	US-10-032-201B-69	Sequence 69, Appl1	634	31	100.0	191	4	US-10-201-386-56	Sequence 56, Appl1
562	31	100.0	175	4	US-10-032-201B-166	Sequence 166, App	635	31	100.0	191	4	US-10-268-447-6	Sequence 6, Appl1
563	31	100.0	175	4	US-10-424-599-177899	Sequence 177899,	636	31	100.0	191	4	US-10-262-538-20	Sequence 20, Appl1
564	31	100.0	175	4	US-10-424-599-282483	Sequence 282483,	637	31	100.0	191	4	US-10-277-184-2	Sequence 2, Appl1
565	31	100.0	175	4	US-10-425-114-50857	Sequence 50857, A	638	31	100.0	191	4	US-10-207-655-51	Sequence 51, Appl1
566	31	100.0	175	4	US-10-767-701-40803	Sequence 40803, A	639	31	100.0	191	4	US-10-207-655-53	Sequence 53, Appl1
567	31	100.0	175	4	US-10-425-115-256814	Sequence 256814,	640	31	100.0	191	4	US-10-032-201B-55	Sequence 55, Appl1
568	31	100.0	176	4	US-10-425-115-260475	Sequence 260475,	641	31	100.0	191	4	US-10-131-988-17	Sequence 17, Appl1
569	31	100.0	177	4	US-10-032-201B-63	Sequence 63, Appl1	642	31	100.0	191	4	US-10-170-338-227	Sequence 227, App
570	31	100.0	177	4	US-10-425-114-41212	Sequence 41212, A	643	31	100.0	191	4	US-10-246-099-32	Sequence 32, Appl1
571	31	100.0	177	4	US-10-425-115-349412	Sequence 349412,	644	31	100.0	191	4	US-10-352-155-4	Sequence 4, Appl1
572	31	100.0	178	3	US-09-764-891-3869	Sequence 3869, Ap	645	31	100.0	191	4	US-10-116-275-227	Sequence 227, App
573	31	100.0	178	4	US-10-032-201B-52	Sequence 52, Appl1	646	31	100.0	191	4	US-10-418-529-6	Sequence 6, Appl1
574	31	100.0	178	4	US-10-424-599-262936	Sequence 262936,	647	31	100.0	191	4	US-10-370-291-4	Sequence 4, Appl1
575	31	100.0	179	4	US-10-323-362-4	Sequence 4, Appl1	648	31	100.0	191	4	US-10-440-464-127	Sequence 127, App
576	31	100.0	179	4	US-10-032-201B-59	Sequence 59, Appl1	649	31	100.0	191	4	US-10-424-599-275952	Sequence 275952,
577	31	100.0	179	4	US-10-424-599-225033	Sequence 225033,	650	31	100.0	191	4	US-10-673-708-2	Sequence 2, Appl1
578	31	100.0	179	4	US-10-425-114-62266	Sequence 62266, A	651	31	100.0	191	4	US-10-474-776-661	Sequence 661, App
579	31	100.0	179	4	US-10-425-114-66811	Sequence 66811, A	652	31	100.0	191	4	US-10-792-480-56	Sequence 56, Appl1
580	31	100.0	179	4	US-10-425-115-280370	Sequence 280370,	653	31	100.0	191	4	US-10-792-461-56	Sequence 56, Appl1
581	31	100.0	179	4	US-10-425-115-305796	Sequence 305796,	654	31	100.0	191	4	US-10-793-039-34	Sequence 34, Appl1
582	31	100.0	180	4	US-10-425-114-48070	Sequence 48070, A	655	31	100.0	191	4	US-10-770-666-32	Sequence 32, Appl1
583	31	100.0	180	4	US-10-425-114-52471	Sequence 52471, A	656	31	100.0	191	4	US-10-425-115-305799	Sequence 305799,
584	31	100.0	180	4	US-10-425-114-66813	Sequence 66813, A	657	31	100.0	191	4	US-10-669-176-20	Sequence 20, Appl1
585	31	100.0	180	4	US-10-437-963-147191	Sequence 147191,	658	31	100.0	191	4	US-10-428-817A-118	Sequence 118, App
586	31	100.0	180	4	US-10-437-963-154824	Sequence 154824,	659	31	100.0	191	5	US-10-749-706-3	Sequence 12, Appl1
587	31	100.0	180	4	US-10-425-115-314784	Sequence 314784,	660	31	100.0	191	5	US-10-772-927A-12	Sequence 12, Appl1
588	31	100.0	181	4	US-10-032-201B-68	Sequence 68, Appl1	661	31	100.0	191	5	US-10-615-345-21	Sequence 21, Appl1
589	31	100.0	181	4	US-10-424-599-178291	Sequence 178291,	662	31	100.0	191	5	US-10-901-417-17	Sequence 17, Appl1
590	31	100.0	181	4	US-10-424-599-178934	Sequence 178934,	663	31	100.0	191	5	US-10-868-577A-7	Sequence 7, Appl1
591	31	100.0	181	4	US-10-424-599-279345	Sequence 279345,	664	31	100.0	191	5	US-10-868-546-18	Sequence 18, Appl1
592	31	100.0	181	4	US-10-424-599-280573	Sequence 280573,	665	31	100.0	191	5	US-10-937-758A-99	Sequence 99, Appl1
593	31	100.0	181	4	US-10-437-963-127106	Sequence 127106,	666	31	100.0	191	5	US-10-756-149-4876	Sequence 4876, Ap
594	31	100.0	181	4	US-10-437-963-204686	Sequence 204686,	667	31	100.0	191	3	US-09-852-209A-8	Sequence 8, Appl1
595	31	100.0	182	4	US-10-032-201B-54	Sequence 54, Appl1	668	31	100.0	192	4	US-10-131-600-8	Sequence 8, Appl1
596	31	100.0	182	4	US-10-032-201B-56	Sequence 56, Appl1	669	31	100.0	192	4	US-10-303-997B-8	Sequence 8, Appl1
597	31	100.0	182	4	US-10-424-599-250227	Sequence 250227,	670	31	100.0	192	4	US-10-439-337A-8	Sequence 8, Appl1
598	31	100.0	182	4	US-10-425-114-67114	Sequence 67114, A	671	31	100.0	192	4	US-10-767-701-46126	Sequence 46126, A
599	31	100.0	182	4	US-10-437-963-111424	Sequence 111424,	672	31	100.0	192	5	US-10-485-533-17	Sequence 17, Appl1
600	31	100.0	182	4	US-10-767-701-42070	Sequence 42070, A	673	31	100.0	193	4	US-10-032-201B-62	Sequence 62, Appl1
601	31	100.0	182	4	US-10-425-115-256661	Sequence 256661,	674	31	100.0	194	4	US-10-437-963-104337	Sequence 104337,
602	31	100.0	182	4	US-10-425-115-314786	Sequence 314786,	675	31	100.0	194	4	US-10-437-963-204634	Sequence 204634,
603	31	100.0	183	4	US-10-424-599-225032	Sequence 225032,	676	31	100.0	194	5	US-10-617-320-5104	Sequence 5104, Ap
604	31	100.0	183	4	US-10-767-701-46296	Sequence 46296, A	677	31	100.0	195	4	US-10-424-599-262247	Sequence 262247,
605	31	100.0	183	4	US-10-425-115-229688	Sequence 229688,	678	31	100.0	196	4	US-10-180-120-2	Sequence 2, Appl1
606	31	100.0	183	5	US-10-919-193B-31	Sequence 31, Appl1	679	31	100.0	196	4	US-10-437-963-195282	Sequence 195282,
607	31	100.0	185	4	US-10-032-201B-53	Sequence 53, Appl1	680	31	100.0	197	4	US-10-767-701-33489	Sequence 33489, A
608	31	100.0	185	5	US-10-739-930-6217	Sequence 6217, Ap	681	31	100.0	198	4	US-10-425-115-212572	Sequence 212572,
609	31	100.0	185	5	US-10-739-930-6865	Sequence 6865, Ap	682	31	100.0	201	4	US-10-425-114-42331	Sequence 42331, A
610	31	100.0	185	5	US-10-472-928-1980	Sequence 1980, Ap	683	31	100.0	204	4	US-10-425-114-47113	Sequence 47113, A
611	31	100.0	186	4	US-10-032-201B-60	Sequence 60, Appl1	684	31	100.0	206	5	US-10-872-198-103	Sequence 103, App

685	31	100.0	206	5	US-10-919-193B-29	Sequence 29, Appl	758	31	100.0	232	5	US-10-868-577A-57	Sequence 57, Appl
686	31	100.0	206	6	US-11-021-951-103	Sequence 103, App	759	31	100.0	232	5	US-10-868-549-11	Sequence 11, Appl
687	31	100.0	208	4	US-10-293-157-126	Sequence 26, Appl	760	31	100.0	232	5	US-10-980-815-7	Sequence 7, Appl
688	31	100.0	209	4	US-10-423-000-54	Sequence 54, Appl	761	31	100.0	232	5	US-10-978-107-33	Sequence 33, Appl
689	31	100.0	211	3	US-09-877-156-20	Sequence 20, Appl	762	31	100.0	232	5	US-10-971-643-2	Sequence 2, Appl
690	31	100.0	211	6	US-11-097-143-5826	Sequence 5826, Ap	763	31	100.0	232	5	US-10-992-196-7	Sequence 7, Appl
691	31	100.0	213	4	US-10-425-000-62	Sequence 62, Appl	764	31	100.0	232	5	US-10-992-195-7	Sequence 7, Appl
692	31	100.0	213	3	US-09-963-156A-1	Sequence 1, Appl	765	31	100.0	232	6	US-11-067-015-7	Sequence 7, Appl
693	31	100.0	214	4	US-10-425-000-58	Sequence 58, Appl	766	31	100.0	232	6	US-11-078-507-7	Sequence 7, Appl
694	31	100.0	214	4	US-10-425-000-66	Sequence 66, Appl	767	31	100.0	234	4	US-10-029-386-32351	Sequence 32351, A
695	31	100.0	214	4	US-10-749-832-1	Sequence 1, Appl	768	31	100.0	236	3	US-09-777-789-62	Sequence 62, Appl
696	31	100.0	215	3	US-09-244-694-3	Sequence 3, Appl	769	31	100.0	237	3	US-09-746-284-5	Sequence 5, Appl
697	31	100.0	215	3	US-10-418-529-8	Sequence 8, Appl	770	31	100.0	237	4	US-10-425-114-66489	Sequence 66489, A
698	31	100.0	215	4	US-10-370-291-6	Sequence 6, Appl	771	31	100.0	241	4	US-10-425-115-260478	Sequence 260478, A
699	31	100.0	215	4	US-10-425-000-56	Sequence 56, Appl	772	31	100.0	242	3	US-09-919-603-5	Sequence 5, Appl
700	31	100.0	215	5	US-10-615-243-15	Sequence 15, Appl	773	31	100.0	243	5	US-10-491-213-46	Sequence 46, Appl
701	31	100.0	215	5	US-10-868-577A-10	Sequence 10, Appl	774	31	100.0	247	4	US-10-369-493-9470	Sequence 9470, Ap
702	31	100.0	215	5	US-10-868-549-19	Sequence 19, Appl	775	31	100.0	247	5	US-10-450-763-59922	Sequence 59922, A
703	31	100.0	215	5	US-10-926-806-4	Sequence 4, Appl	776	31	100.0	249	4	US-10-177-293-148	Sequence 148, App
704	31	100.0	215	5	US-10-924-025A-105	Sequence 105, App	777	31	100.0	249	4	US-10-479-284-15	Sequence 15, Appl
705	31	100.0	215	5	US-10-970-698A-56	Sequence 56, Appl	778	31	100.0	249	4	US-10-755-889-130	Sequence 130, App
706	31	100.0	215	5	US-10-450-763-41147	Sequence 41147, A	779	31	100.0	249	5	US-10-450-763-53065	Sequence 53065, A
707	31	100.0	215	5	US-10-798-896-7	Sequence 7, Appl	780	31	100.0	250	3	US-09-764-868-1063	Sequence 1063, Ap
708	31	100.0	215	6	US-11-019-829-87	Sequence 87, Appl	781	31	100.0	250	3	US-09-955-999-77	Sequence 77, Appl
709	31	100.0	216	4	US-10-335-009-8	Sequence 8, Appl	782	31	100.0	251	4	US-10-437-963-128810	Sequence 128810, A
710	31	100.0	216	4	US-10-425-114-66365	Sequence 66365, A	783	31	100.0	252	4	US-10-423-156-8	Sequence 8, Appl
711	31	100.0	216	5	US-10-723-860-613	Sequence 613, App	784	31	100.0	252	4	US-10-423-156-8	Sequence 8, Appl
712	31	100.0	216	5	US-10-756-149-4881	Sequence 4881, Ap	785	31	100.0	252	4	US-10-425-115-267887	Sequence 267887, A
713	31	100.0	216	5	US-10-512-181-10	Sequence 10, Appl	786	31	100.0	259	4	US-10-437-963-135706	Sequence 135706, A
714	31	100.0	217	4	US-10-425-114-63276	Sequence 63276, A	787	31	100.0	261	4	US-10-012-542-413	Sequence 413, App
715	31	100.0	217	4	US-10-425-000-70	Sequence 70, Appl	788	31	100.0	261	4	US-10-115-123-413	Sequence 413, App
716	31	100.0	217	4	US-10-424-999-38	Sequence 38, Appl	789	31	100.0	261	4	US-10-800-834-413	Sequence 413, App
717	31	100.0	218	4	US-10-282-122A-55347	Sequence 55347, A	790	31	100.0	263	4	US-10-108-260A-2809	Sequence 2809, Ap
718	31	100.0	218	4	US-10-425-000-50	Sequence 50, Appl	791	31	100.0	263	5	US-10-732-923-13421	Sequence 13421, A
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ALIGNMENTS

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RESULT 1
US-10-286-516A-11
; Sequence 11, Application US/10286516A
; Publication No. US20030092087A1
; GENERAL INFORMATION:
; APPLICANT: McBridge, Jere W.
; APPLICANT: Walker, David H.
; TITLE OF INVENTION: Shricliffa Disulfide Bond Formation
; FILE REFERENCE: D6428
; CURRENT APPLICATION NUMBER: US/10/286, 516A
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/335, 611
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: Escherichia coli conserved cysteine
; OTHER INFORMATION: motif in active site of thiodoxin
; OTHER INFORMATION: protein
US-10-286-516A-11

Query Match          100.0%; Score 31; DB 4; Length 4;
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QY 2 CGPC 5
Db 1 CGPC 4

RESULT 2
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; Publication No. US20030109457A1
; GENERAL INFORMATION:
; APPLICANT: Atlas, Daphne
; TITLE OF INVENTION: MULTI-COMPONENT ANTIOXIDANT COMPOUNDS, PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAME AND THEIR USE FOR REDUCING OR PREVENTING OXIDATI
; FILE REFERENCE: 24890
; CURRENT APPLICATION NUMBER: US/10/234, 319A
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; CURRENT FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 21
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US-10-234-319A-1
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RESULT 3
US-10-369-094-1
; Sequence 1, Application US/10369094
; Publication No. US20030235588A1
; GENERAL INFORMATION:
; APPLICANT: Richon, Victoria M.
; APPLICANT: Marks, Paul A.
; APPLICANT: Rifkind, Richard A.
; TITLE OF INVENTION: Method of Treating TRX Mediated Diseases
; FILE REFERENCE: 3254.1005-001
; CURRENT APPLICATION NUMBER: US/10/369, 094
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/357, 383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-369-094-1
```

```
Query Match          100.0%; Score 31; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2 CGPC 5
Db 1 CGPC 4
```

```
RESULT 4
US-10-660-118A-1
; Sequence 1, Application US/10660118A
; Publication No. US20040131606A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; FILE REFERENCE: 2879-98
; CURRENT APPLICATION NUMBER: US/10/660, 118A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409, 960
; PRIOR FILING DATE: 2002-09-10
; CURRENT APPLICATION NUMBER: 60/462, 082
```

; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-10-660-118A-1

Query Match 100.0%; Score 31; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 5
US-10-628-391-2
; Sequence 2, Application US/10628391
; Publication No. US20040146526A1
; GENERAL INFORMATION:
; APPLICANT: WINDLE, Henry J.
; APPLICANT: O'TOOLE, Dermot
; APPLICANT: KELEHOR, Dermot
; APPLICANT: ABDEL-LATIF, Mohamed M.
; TITLE OF INVENTION: INHIBITION OF NF-kappaB ACTIVATION
; FILE REFERENCE: P69048USO
; CURRENT APPLICATION NUMBER: US/10/628,391
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/IB02/00011
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: the redox active peptide sequence
US-10-628-391-2

Query Match 100.0%; Score 31; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 6
US-10-776-933-149
; Sequence 149, Application US/10776933
; Publication No. US20040241717A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRIE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: MISENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF THIOREDUXIN
; FILE REFERENCE: 58614(71432)
; CURRENT APPLICATION NUMBER: US/10/776,933
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,374
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 149
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-776-933-149

Query Match 100.0%; Score 31; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 7
US-10-304-287-4
; Sequence 4, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Walsman, David M.
; APPLICANT: Kwon, Mijung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: mammalian
US-10-304-287-4

Query Match 100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 8
US-10-290-072-233
; Sequence 233, Application US/10290072
; Publication No. US2003021151A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalma, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjardais, John R.
; APPLICANT: Helfetz, Peter
; APPLICANT: Lugibuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: active site consensus sequence
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: "Xaa" at position 1 can be any amino acid, preferably a
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: "Xaa" at position 6 can be any amino acid, preferably polar amino
; OTHER INFORMATION: acids
US-10-290-072-233

Query Match          100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
DB      2 CGPC 5

RESULT 9
US-10-461-224-5
; Sequence 5, Application US/10461224
; Publication No. US20040019104A1
; GENERAL INFORMATION:
; APPLICANT: Edright, Richard H.
; TITLE OF INVENTION: Reagents and Procedures for High Specificity Labeling
; FILE REFERENCE: 744-34
; CURRENT APPLICATION NUMBER: US/10/461,224
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/388,699
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Target sequence.
US-10-461-224-5

Query Match          100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
DB      2 CGPC 5

RESULT 10
US-10-660-118A-2
; Sequence 2, Application US/10660118A
; Publication No. US20040131606A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; FILE REFERENCE: 2879-98
; CURRENT APPLICATION NUMBER: US/10/660,118A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082

; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-10-660-118A-3

Query Match          100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
DB      2 CGPC 5

RESULT 11
US-10-660-118A-3
; Sequence 3, Application US/10660118A
; Publication No. US20040131606A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; FILE REFERENCE: 2879-98
; CURRENT APPLICATION NUMBER: US/10/660,118A
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-10-660-118A-3

Query Match          100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
DB      2 CGPC 5

RESULT 12
US-10-735-577-4
; Sequence 4, Application US/10735577
; Publication No. US20040142897A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David W.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metasta
; FILE REFERENCE: ME03-009
; CURRENT APPLICATION NUMBER: US/10/735,577
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/433,140
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 6
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; TYPE: PRT
; ORGANISM: mammalian
US-10-735-577-4

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 13
US-10-461-224-10
; Sequence 10, Application US/10461224
; Publication No. US20040019104A1
; GENERAL INFORMATION:
; APPLICANT: EdBright, Richard H.
; TITLE OF INVENTION: Reagents and Procedures for High Specificity Labeling
; FILE REFERENCE: 744-34
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/388,699
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Target sequence.
US-10-461-224-10

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 14
US-10-954-951-11
; Sequence 11, Application US/10954951
; Publication No. US20050136449A1
; GENERAL INFORMATION:
; APPLICANT: Hanson, George
; APPLICANT: Kudlicki, Wieslaw Antoni
; APPLICANT: Kepertipola, Shrinanthi
; TITLE OF INVENTION: Compositions and Methods for Synthesizing, Purifying and
; FILE REFERENCE: 0942.6650001
; CURRENT APPLICATION NUMBER: US/10/954,951
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/508,142
; PRIOR FILING DATE: 2003-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: C terminal of Cam Ortho expressed in PRESETB
US-10-954-951-11

Query Match
Best Local Similarity 100.0%; Score 31; DB 5; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 15
US-09-572-404B-918
; Sequence 918, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 918
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in LHB at 105-114 and may interact with Sequence
US-09-572-404B-918

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 6 CGPC 9

RESULT 16
US-09-572-404B-970
; Sequence 970, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 970
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in LHB at 105-114 and may interact with Sequence
US-09-572-404B-970

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 6 CGPC 9

RESULT 17
US-10-615-343-2
; Sequence 2, Application US/10615343
; Publication No. US20050009110A1
; GENERAL INFORMATION:
; APPLICANT: CHANG, XIAO-JIA
; TITLE OF INVENTION: METHODS OF PRODUCING ANTIBODIES FOR DIAGNOSTICS AND THERAPEUTICS
```

FILE REFERENCE: IGA-003.01
CURRENT APPLICATION NUMBER: US/10/615,343
CURRENT FILING DATE: 2003-07-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-615-343-2

Query Match 100.0%; Score 31; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 9 CGPC 12

RESULT 18

US-10-044-844-217
Sequence 217, Application US/10044844
Publication No. US2004009904A1
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
Margulis, David M.
Jones, David S.
Yu, Lin
TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND
METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED PATHOLOGIES
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,844
FILING DATE: 10-Jan-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 25231-20061.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-10-044-844-217

Query Match 100.0%; Score 31; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 4 CGPC 7

RESULT 19

US-10-846-079-217
Sequence 217, Application US/10846079
Publication No. US20050208480A1
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
Margulis, David M.
Jones, David S.
Yu, Lin

TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND
METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED PATHOLOGIES
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/846,079
FILING DATE: 13-May-2004
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 25231-20061.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-10-846-079-217

Query Match 100.0%; Score 31; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 4 CGPC 7

RESULT 20

US-09-963-339-10
Sequence 10, Application US/09963339
Publication No. US20030049700A1
GENERAL INFORMATION:
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-090001
CURRENT APPLICATION NUMBER: US/09/963,339
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/235,049
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10

Query Match 100.0%; Score 31; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-09-963-339-10

Query Match 100.0%; Score 31; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 9 CGPC 12

RESULT 21
US-10-145-586-59
Sequence 59, Application US/10145586
Publication No. US20030138890A1
GENERAL INFORMATION:
APPLICANT: Alexandra Glucksmann, Maria
APPLICANT: Sillos-Santiago, Immaculada
APPLICANT: M. Galvin, Katherine
APPLICANT: Weich, Nadine
APPLICANT: Curtis, Rory A.J.
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS, HUMAN LEUCINE-RICH
TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
FILE REFERENCE: 10448-188001
CURRENT APPLICATION NUMBER: US/10/145,586
CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-586-59

Query Match 100.0%; Score 31; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 9 CGPC 12

RESULT 22
US-10-050-882-98
Sequence 98, Application US/10050882
Publication No. US20030104400A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 27 Human secreted proteins
FILE REFERENCE: P2038P1
CURRENT APPLICATION NUMBER: US/10/050,882
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 09/661,453
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/US00/06783
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/125,055
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 98
LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
US-10-050-882-98

Query Match 100.0%; Score 31; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 19 CGPC 22

RESULT 23
US-10-963-903-98
Sequence 98, Application US/10963903
Publication No. US20050239099A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 27 Human secreted proteins
FILE REFERENCE: P2038P1C2
CURRENT APPLICATION NUMBER: US/10/963,903
CURRENT FILING DATE: 2004-10-14
PRIOR APPLICATION NUMBER: US 10/050,882
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 09/661,453
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/US00/06783
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: US 60/125,055
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 98
LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
US-10-963-903-98

Query Match 100.0%; Score 31; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 19 CGPC 22

RESULT 24
US-10-179-382-31
Sequence 31, Application US/10179382
Publication No. US2003016235A1
GENERAL INFORMATION:
APPLICANT: THIREOS, GEORGE
APPLICANT: KAFETZPOULOS, DIMITRIS
TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
CURRENT APPLICATION NUMBER: US/10/179,382
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US/09/230,041
PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 28
TYPE: PRT
ORGANISM: Rhizobium leguminosarum
US-10-179-382-31

Query Match 100.0%; Score 31; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 21 CGPC 24

```
RESULT 25
US-09-881-572A-25
; Sequence 25, Application US/09881572A
; Patent No. US20020164583A1
; GENERAL INFORMATION:
; APPLICANT: Roche, Monica;
; APPLICANT: Bupp, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 25
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Amphotrophic Murine Leukemia Virus
US-09-881-572A-25

Query Match          100.0%; Score 31; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        |||||
Db      11 CGPC 14

RESULT 26
US-09-881-572A-5
; Sequence 5, Application US/09881572A
; Patent No. US20020164583A1
; GENERAL INFORMATION:
; APPLICANT: Roche, Monica;
; APPLICANT: Bupp, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: amphotrophic murine leukemia virus
US-09-881-572A-5

Query Match          100.0%; Score 31; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        |||||
Db      11 CGPC 14

RESULT 27
US-09-864-761-40069
; Sequence 40069, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
```

```
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/532,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40069
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003681.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4
; OTHER INFORMATION: EST HUMAN HIT: BF446535.1, EVALU6 6.00e-12
; OTHER INFORMATION: SWISSPROT HIT: Q02597, EVALU6 1.70e+00
US-09-864-761-40069

Query Match          100.0%; Score 31; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        |||||
Db      8 CGPC 11

RESULT 28
US-10-424-599-160512
; Sequence 160512, Application US/10424599
```

```
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovacic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 160512
LENGTH: 32
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_115960C.1.pep
US-10-424-599-160512
```

```
Query Match          100.0%; Score 31; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 CGPC 5
      ||||
Db      23 CGPC 26
```

```
RESULT 29
US-10-044-359-26
Sequence 26, Application US/10044359
Publication No. US20020160454A1
GENERAL INFORMATION:
APPLICANT: Heriman, Rafael
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BR1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 35
TYPE: PRT
ORGANISM: Androctonus mauretanicus
US-10-044-359-26
```

```
Query Match          100.0%; Score 31; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 CGPC 5
      ||||
Db      1 CGPC 4
```

```
RESULT 30
US-09-801-260-5
Sequence 5, Application US/09801260
Patent No. US20020034801A1
GENERAL INFORMATION:
APPLICANT: Cutlis, Roy A.J.
TITLE OF INVENTION: 22105, A NOVEL HUMAN THIOREDOXIN FAMILY
FILE REFERENCE: 10448-022001
CURRENT APPLICATION NUMBER: US/09/801,260
CURRENT FILING DATE: 2001-03-06
```

```
PRIOR APPLICATION NUMBER: US 60/187,447
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus sequence
US-09-801-260-5
```

```
Query Match          100.0%; Score 31; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 CGPC 5
      ||||
Db      33 CGPC 36
```

```
RESULT 31
US-10-145-586-44
Sequence 44, Application US/10145586
Publication No. US20030138890A1
GENERAL INFORMATION:
APPLICANT: Alexandra Glucksmann, Maria
APPLICANT: Siles-Santiago, Imaculada
APPLICANT: M. Galvin, Katherine
APPLICANT: Welch, Nadine
APPLICANT: Curtis, Roy A.J.
APPLICANT: Bandaru, Rajasekhar
APPLICANT: Kapeller-Liberman, Rosana
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS
TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LECTIVE-RICH
FILE REFERENCE: 10448-188001
CURRENT APPLICATION NUMBER: US/10/145,586
CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 95
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus sequence
US-10-145-586-44
```

```
Query Match          100.0%; Score 31; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 CGPC 5
      ||||
Db      33 CGPC 36
```

```
RESULT 32
US-10-450-763-51435
Sequence 51435, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
```

```
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 51435
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-450-763-51435

Query Match          100.0%; Score 31; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
        1 CGPC 4

Db      1 CGPC 4

RESULT 33
US-09-864-761-35367
/ Sequence 35367, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
/ FILE REFERENCE: Aecmlca-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 35367
/ LENGTH: 43
```

```
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC011297.1
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
/ OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
/ OTHER INFORMATION: EST HUMAN HIT: AM65671.1, EVALUE 3.00e-03
/ OTHER INFORMATION: SWISSPROT HIT: Q14990, EVALUE 4.00e-04
US-09-864-761-35367

Query Match          100.0%; Score 31; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
        1 CGPC 20

Db      17 CGPC 20

RESULT 34
US-10-293-157-20
/ Sequence 20, Application US/10293157
/ Publication No. US20030144200A1
/ GENERAL INFORMATION:
/ APPLICANT: BAIRD, ANDREW
/ APPLICANT: ANDREASON, GRAI
/ TITLE OF INVENTION: NOVEL FORMS OF THE ANGIOGENIC FACTOR
/ TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR: VEGF
/ FILE REFERENCE: 240/086
/ CURRENT APPLICATION NUMBER: US/10/293,157
/ PRIOR FILING DATE: 2002-11-12
/ PRIOR APPLICATION NUMBER: US/09/244,583
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: 60/073,979
/ PRIOR FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 20
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-293-157-20

Query Match          100.0%; Score 31; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
        2 CGPC 5

Db      2 CGPC 5

RESULT 35
US-10-424-599-255327
/ Sequence 255327, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
```

/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 255327
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_72582C.1.pap
US-10-424-599-255327

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
18 CGPC 21

RESULT 36
US-09-832-355A-3
/ Sequence 3, Application US/09832355A
/ Publication No. US20030027751A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovesdi, Imre
/ APPLICANT: Kessler, Paul
/ TITLE OF INVENTION: VEGF FUSION PROTEINS
/ FILE REFERENCE: 205654
/ CURRENT APPLICATION NUMBER: US/09/832,355A
/ CURRENT FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 126
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-832-355A-3

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
2 CGPC 5

RESULT 37
US-10-104-440-11
/ Sequence 11, Application US/10104440
/ Publication No. US20020132774A1
/ GENERAL INFORMATION:
/ APPLICANT: KLAGSBRUN, Michael
/ APPLICANT: SOKER, Shay
/ APPLICANT: MIAO, Hua Quan
/ TITLE OF INVENTION: ANTAGONISTS OF NEUROPILIN RECEPTOR FUNCTION AND USE
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 48802 C
/ CURRENT APPLICATION NUMBER: US/10/104,440
/ CURRENT FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: 09/580,803
/ PRIOR FILING DATE: 2000-05-30
/ PRIOR APPLICATION NUMBER: 60/069,155
/ PRIOR FILING DATE: 1997-12-09
/ PRIOR APPLICATION NUMBER: 60/069,687
/ PRIOR FILING DATE: 1997-12-29
/ PRIOR APPLICATION NUMBER: 60/078,541
/ PRIOR FILING DATE: 1998-03-19
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 11
/ LENGTH: 44
/ TYPE: PRT

/ ORGANISM: human
US-10-104-440-11

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
2 CGPC 5

RESULT 38
US-10-104-610-15
/ Sequence 15, Application US/10104610
/ Publication No. US20030104532A1
/ GENERAL INFORMATION:
/ APPLICANT: KLAGSBRUN, Michael
/ APPLICANT: SOKER, Shay
/ APPLICANT: GAGNON, Michael L.
/ TITLE OF INVENTION: SOLUBLE INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH
/ TITLE OF INVENTION: AND USE THEREOF
/ FILE REFERENCE: 48801 C
/ CURRENT APPLICATION NUMBER: US/10/104,610
/ CURRENT FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: 09/580,989
/ PRIOR FILING DATE: 2000-05-30
/ PRIOR APPLICATION NUMBER: 60/069,155
/ PRIOR FILING DATE: 1997-12-09
/ PRIOR APPLICATION NUMBER: 60/069,687
/ PRIOR FILING DATE: 1997-12-12
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: human
US-10-104-610-15

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
2 CGPC 5

RESULT 39
US-10-424-599-252212
/ Sequence 252212, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 252212
/ LENGTH: 45
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(45)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_6976C.1.pep
US-10-424-599-252212

Query Match 100.0%; Score 31; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 15 CGPC 18

RESULT 40

US-10-425-115-210616
Sequence 210616, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 210616
LENGTH: 47
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_12367C.1.pep
US-10-425-115-210616

Query Match 100.0%; Score 31; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 18 CGPC 21

RESULT 41

US-10-425-115-321622
Sequence 321622, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 321622
LENGTH: 47
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(47)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_56384C.1.pep
US-10-425-115-321622

Query Match 100.0%; Score 31; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 42

US-11-097-143-37521
Sequence 37521, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37521
LENGTH: 47
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-37521

Query Match 100.0%; Score 31; DB 6; Length 47;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 43

US-10-425-115-334172
Sequence 334172, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 334172
LENGTH: 49
TYPE: PRT
ORGANISM: Zea mays
FEATURE:

Query Match 100.0%; Score 31; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 6e+02;

```

; NAME/KEY: unsure
; LOCATION: (1).(49)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_6787C.1.pdp
US-10-425-115-334172

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 10 CGPC 13

RESULT 44
US-09-801-260-4
; Sequence 4, Application US/09801260
; Patent No. US20020034801A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: 22105, A NOVEL HUMAN THIOREDOXIN FAMILY
; FILE REFERENCE: 10448-022001
; CURRENT APPLICATION NUMBER: US/09/801,260
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,447
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-801-260-4

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 21 CGPC 24

RESULT 45
US-10-145-586-43
; Sequence 43, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos-Santiago, Imaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Welch, Nadine
; APPLICANT: Curtis, Roy A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Lieberman, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-145-586-43

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 21 CGPC 24

RESULT 46
US-10-437-963-164055
; Sequence 164055, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 164055
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62993C.1.pdp
US-10-437-963-164055

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 5 CGPC 8

RESULT 47
US-10-424-599-166951
; Sequence 166951, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 166951
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_121771C.1.pdp
US-10-424-599-166951

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 53;
```

Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 33 CGPC 36

RESULT 48

US-09-864-761-42458
; Sequence 42458, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42458
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011510.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EST HUMAN HIT: BE148597.1, EVALUE 2.00e-24
; OTHER INFORMATION: SWISSPROT HIT: P03204, EVALUE 3.50e+00
US-09-864-761-42458

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 9 CGPC 12

RESULT 49

US-10-318-302-2
; Sequence 2, Application US/10318302
; Publication No. US20030171556A1
; GENERAL INFORMATION:
; APPLICANT: POSCO
; APPLICANT: POSTECH FOUNDATION
; APPLICANT: Chae, Chi-Bom
; APPLICANT: Gho, Yong Song
; APPLICANT: Yang, Seung-Pil
; APPLICANT: Kwon, Byung Oh
; APPLICANT: Bae, Dong-Goo
; APPLICANT: Haeng, Sewook
; TITLE OF INVENTION: BETA-AMYLOID BINDING FACTORS AND INHIBITORS THEREOF
; FILE REFERENCE: 10011-00001
; CURRENT APPLICATION NUMBER: US/10/318,302
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-302-2

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 7 CGPC 10

RESULT 50
US-10-425-115-307743
; Sequence 307743, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovall, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 307743
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_43730C.1.pep
US-10-425-115-307743
Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 40 CGPC 43

RESULT 51
US-10-868-577A-28
; Sequence 28; Application US/10868577A
; Publication No. US2005032697A1
; GENERAL INFORMATION:
; APPLICANT: Alitalia et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-28

Query Match 100.0%; Score 31; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 7 CGPC 10

RESULT 52
US-11-097-143-26469
; Sequence 26469; Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26469
; LENGTH: 55
; TYPE: PRT
; ORGANISM: DROSOPHILA

US-11-097-143-26469

Query Match 100.0%; Score 31; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 3 CGPC 6

RESULT 53
US-10-425-115-219153
; Sequence 219153; Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 219153
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: MRT4577_131459C.1.pap
US-10-425-115-219153

Query Match 100.0%; Score 31; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 45 CGPC 48

RESULT 54
US-11-097-143-26490
; Sequence 26490; Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26490
; LENGTH: 56
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26490

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 55
US-10-029-386-28568
; Sequence 28568; Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28568
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P00203, EVALUATE 1.20e+00
US-10-029-386-28568

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 6 CGPC 9

RESULT 56
US-10-425-115-353222
; Sequence 353222; Application US/10425115
; Publication No. US2004021272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 353222
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Zea mays
```

```

; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_85311C.1.pep
US-10-425-115-353222

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 29 CGPC 32

RESULT 57
US-10-424-599-185374
; Sequence 185374; Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 185374
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_138407C.1.pep
US-10-424-599-185374

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 58;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 38 CGPC 41

RESULT 58
US-10-437-963-202381
; Sequence 202381; Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 202381
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_97667C.1.pep
US-10-437-963-202381

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 58;
```

Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 17 CGPC 20

RESULT 59

US-10-424-599-176362
; Sequence 176362, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 176362
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130272C.1.pep
US-10-424-599-176362

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 41 CGPC 44

RESULT 60

US-09-864-408A-7494
; Sequence 7494, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7494
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-7494

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 4 CGPC 7

RESULT 61
US-11-097-143-10200
; Sequence 10200, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10200
; LENGTH: 60
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-10200

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
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Db 41 CGPC 44

RESULT 62

US-10-424-599-278438
; Sequence 278438, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278438
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93452C.1.pep
US-10-424-599-278438

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 28 CGPC 31

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RESULT 63
US-10-423-115-233772
; Sequence 233772, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233772
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144792C.1.pep
US-10-425-115-233772

Query Match          100.0%; Score 31; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      40 CGPC 43

RESULT 64
US-11-097-143-26472
; Sequence 26472, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26472
; LENGTH: 63
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26472

Query Match          100.0%; Score 31; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
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Db      17 CGPC 20

RESULT 65
US-10-425-115-336734
; Sequence 336734, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 336734
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(64)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70240C.1.pep
US-10-425-115-336734

Query Match          100.0%; Score 31; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      40 CGPC 43

RESULT 66
US-10-424-599-180203
; Sequence 180203, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180203
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(65)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_133738C.1.pep
US-10-424-599-180203

Query Match          100.0%; Score 31; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 CGPC 5
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Db 28 CGPC 31

RESULT 67
US-10-437-963-152827
; Sequence 152827, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152827
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5283C.1.pcp
US-10-437-963-152827

Query Match 100.0%; Score 31; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 21 CGPC 24

RESULT 68
US-10-425-115-256158
; Sequence 256158, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256158
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165207C.1.pcp
US-10-425-115-256158

Query Match 100.0%; Score 31; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 10 CGPC 13

RESULT 69
US-11-097-143-32565
; Sequence 32565, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: C1000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32565
; LENGTH: 67
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32565

Query Match 100.0%; Score 31; DB 6; Length 67;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 8 CGPC 11

RESULT 70
US-10-243-552-978
; Sequence 978, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Ma, Yunding
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 807A
; CURRENT APPLICATION NUMBER: US/10/243,552
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404

; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: pc_fl_genes Version 5.0
; SEQ ID NO 978
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-552-978

Query Match 100.0%; Score 31; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 7,8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 53 CGPC 56

Search completed: February 23, 2006, 00:47:46
Job time : 128.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:44:02 : Search time 11.5 Seconds
(without alignments)
7.767 Million cell updates/sec

Title: US-10-660-118a-2
Perfect score: 31
Sequence: 1 XGSPCX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 1000 summaries

Database : Published Applications AA.New:*
1: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppa/FCI_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	31	100.0	4	US-11-144-301A-8	Sequence 8, App11
3	31	100.0	4	US-11-223-405-1	Sequence 1, App11
4	31	100.0	4	US-11-223-547-1	Sequence 1, App11
5	31	100.0	4	US-11-058-926-2	Sequence 2, App11
6	31	100.0	6	US-11-090-916-2	Sequence 2, App11
7	31	100.0	7	US-11-090-916-3	Sequence 3, App11
8	31	100.0	7	US-11-131-744-2	Sequence 2, App11
9	31	100.0	84	US-10-467-657-5372	Sequence 5372, App
10	31	100.0	91	US-11-131-744-1	Sequence 1, App11
11	31	100.0	103	US-11-074-176-286	Sequence 286, App1
12	31	100.0	103	US-11-090-916-6	Sequence 9, App11
13	31	100.0	103	US-11-090-916-7	Sequence 7, App11
14	31	100.0	104	US-11-090-916-5	Sequence 5, App11
15	31	100.0	105	US-10-821-234-1371	Sequence 1371, App
16	31	100.0	105	US-11-090-916-8	Sequence 8, App11
17	31	100.0	105	US-11-090-916-9	Sequence 10, App11
18	31	100.0	105	US-11-090-916-10	Sequence 10, App11
19	31	100.0	105	US-11-090-916-11	Sequence 11, App11
20	31	100.0	105	US-11-090-916-12	Sequence 12, App11
21	31	100.0	105	US-11-106-796-13	Sequence 13, App11
22	31	100.0	105	US-11-144-301A-9	Sequence 9, App11
23	31	100.0	105	US-11-144-301A-9	Sequence 10, App11
24	31	100.0	105	US-11-032-773-943	Sequence 943, App
25	31	100.0	107	US-10-689-742-19	Sequence 19, App1

26	31	100.0	107	US-11-098-686-10612	Sequence 10612, A
27	31	100.0	109	US-11-090-916-4	Sequence 4, App11
28	31	100.0	113	US-11-072-512-3199	Sequence 3199, App
29	31	100.0	122	US-11-195-459-12	Sequence 12, App1
30	31	100.0	122	US-11-195-459-16	Sequence 16, App1
31	31	100.0	122	US-11-195-459-19	Sequence 19, App1
32	31	100.0	123	US-11-195-459-10	Sequence 10, App1
33	31	100.0	126	US-10-995-561-703	Sequence 703, App
34	31	100.0	127	US-11-106-796-10	Sequence 10, App1
35	31	100.0	127	US-11-106-796-11	Sequence 11, App1
36	31	100.0	127	US-11-106-796-12	Sequence 12, App1
37	31	100.0	129	US-10-467-657-4354	Sequence 4354, App
38	31	100.0	129	US-11-072-512-2145	Sequence 2145, App
39	31	100.0	134	US-11-090-916-13	Sequence 13, App1
40	31	100.0	134	US-11-195-459-8	Sequence 8, App11
41	31	100.0	143	US-09-978-360A-641	Sequence 641, App
42	31	100.0	167	US-11-090-916-14	Sequence 14, App1
43	31	100.0	172	US-11-090-916-15	Sequence 15, App1
44	31	100.0	177	US-11-131-744-3	Sequence 3, App11
45	31	100.0	183	US-10-467-962B-6	Sequence 6, App11
46	31	100.0	189	US-10-995-561-643	Sequence 643, App
47	31	100.0	191	US-10-995-561-642	Sequence 642, App
48	31	100.0	191	US-11-064-774A-2	Sequence 2, App11
49	31	100.0	191	US-11-075-400-2	Sequence 4, App11
50	31	100.0	191	US-11-226-005-4	Sequence 2, App11
51	31	100.0	191	US-11-129-076-9	Sequence 9, App11
52	31	100.0	191	US-11-145-494-2	Sequence 2, App11
53	31	100.0	191	US-11-075-047A-81	Sequence 81, App1
54	31	100.0	197	US-11-098-686-11017	Sequence 11017, A
55	31	100.0	209	US-10-467-657-8494	Sequence 8494, App
56	31	100.0	215	US-10-995-561-640	Sequence 640, App
57	31	100.0	215	US-10-995-561-645	Sequence 645, App
58	31	100.0	215	US-10-995-561-646	Sequence 646, App
59	31	100.0	215	US-11-149-462-3	Sequence 3, App11
60	31	100.0	216	US-11-106-399-8	Sequence 8, App11
61	31	100.0	224	US-11-072-512-3343	Sequence 3343, App
62	31	100.0	232	US-10-995-561-641	Sequence 641, App
63	31	100.0	232	US-10-995-561-644	Sequence 644, App
64	31	100.0	232	US-11-153-880-7	Sequence 7, App11
65	31	100.0	232	US-11-064-774A-147	Sequence 147, App
66	31	100.0	232	US-11-211-724-5	Sequence 5, App11
67	31	100.0	232	US-11-233-119-7	Sequence 7, App11
68	31	100.0	232	US-11-075-047A-91	Sequence 91, App1
69	31	100.0	273	US-11-131-744-6	Sequence 6, App11
70	31	100.0	282	US-11-186-284-85	Sequence 85, App1
71	31	100.0	294	US-11-055-822-480	Sequence 480, App
72	31	100.0	294	US-11-055-822-880	Sequence 880, App
73	31	100.0	300	US-11-154-257-2	Sequence 2, App11
74	31	100.0	325	US-09-978-360A-406	Sequence 406, App
75	31	100.0	354	US-11-054-281-58	Sequence 58, App1
76	31	100.0	373	US-11-186-284-16	Sequence 16, App1
77	31	100.0	373	US-11-054-281-59	Sequence 59, App1
78	31	100.0	380	US-11-090-439-52	Sequence 52, App1
79	31	100.0	380	US-11-090-439-54	Sequence 54, App1
80	31	100.0	380	US-11-054-281-60	Sequence 60, App1
81	31	100.0	430	US-11-072-512-2204	Sequence 2204, App
82	31	100.0	440	US-11-131-744-7	Sequence 7, App11
83	31	100.0	447	US-10-967-527A-14	Sequence 14, App1
84	31	100.0	448	US-10-967-527A-16	Sequence 16, App1
85	31	100.0	448	US-11-182-016-24	Sequence 24, App1
86	31	100.0	450	US-11-186-284-14	Sequence 14, App1
87	31	100.0	502	US-10-966-483-23	Sequence 23, App1
88	31	100.0	502	US-11-021-441-7	Sequence 7, App11
89	31	100.0	509	US-11-124-367A-447	Sequence 447, App
90	31	100.0	539	US-11-043-788-464	Sequence 464, App
91	31	100.0	549	US-11-043-788-467	Sequence 467, App
92	31	100.0	549	US-11-043-788-468	Sequence 468, App
93	31	100.0	563	US-10-966-483-25	Sequence 25, App1
94	31	100.0	563	US-11-021-441-9	Sequence 9, App11
95	31	100.0	572	US-10-763-712A-10	Sequence 10, App1
96	31	100.0	572	US-10-763-712A-11	Sequence 11, App1
97	31	100.0	572	US-10-763-712A-37	Sequence 37, App1
98	31	100.0	572	US-10-763-712A-109	Sequence 109, App

99	31	100.0	572	6	US-10-763-712A-110	Sequence 110, App	172	25	80.6	355	6	US-10-967-527A-22	Sequence 22, Appl
100	31	100.0	574	6	US-10-763-712A-11	Sequence 1, Appl1	173	25	80.6	355	7	US-11-182-946-14	Sequence 14, Appl1
101	31	100.0	574	6	US-10-763-712A-6	Sequence 6, Appl1	174	25	80.6	380	7	US-11-144-236-1	Sequence 1, Appl1
102	31	100.0	574	6	US-10-763-712A-102	Sequence 102, App	175	25	80.6	386	6	US-10-131-826A-340	Sequence 340, App
103	31	100.0	574	6	US-10-966-483-31	Sequence 31, Appl1	176	25	80.6	386	7	US-11-183-878-2	Sequence 2, Appl1
104	31	100.0	574	6	US-11-021-441-15	Sequence 15, Appl1	177	25	80.6	386	7	US-11-099-135-1	Sequence 1, Appl1
105	31	100.0	581	6	US-10-966-483-27	Sequence 27, Appl1	178	25	80.6	398	7	US-10-072-512-2769	Sequence 2769, App
106	31	100.0	581	6	US-10-966-483-29	Sequence 29, Appl1	179	25	80.6	400	6	US-10-948-053-4	Sequence 4, Appl1
107	31	100.0	581	7	US-11-021-441-11	Sequence 11, Appl1	180	25	80.6	400	6	US-10-948-053-5	Sequence 5, Appl1
108	31	100.0	581	7	US-11-021-441-13	Sequence 13, Appl1	181	25	80.6	401	6	US-10-949-720-419	Sequence 419, App
109	31	100.0	654	6	US-10-510-947-6	Sequence 6, Appl1	182	25	80.6	401	6	US-10-510-876-2	Sequence 2, Appl1
110	31	100.0	654	6	US-10-055-877-255	Sequence 255, App	183	25	80.6	401	6	US-10-510-876-4	Sequence 4, Appl1
111	31	100.0	660	6	US-10-055-877-254	Sequence 254, App	184	25	80.6	401	6	US-10-948-053-8	Sequence 8, Appl1
112	31	100.0	747	6	US-10-131-826A-426	Sequence 426, App	185	25	80.6	406	6	US-10-948-053-7	Sequence 7, Appl1
113	31	100.0	755	7	US-11-067-121-6	Sequence 6, Appl1	186	25	80.6	406	6	US-10-948-053-6	Sequence 6, Appl1
114	31	100.0	757	7	US-11-067-121-16	Sequence 16, Appl1	187	25	80.6	406	7	US-11-098-686-10564	Sequence 10564, A
115	31	100.0	757	7	US-11-186-284-41	Sequence 41, Appl1	188	25	80.6	407	6	US-10-948-053-3	Sequence 3, Appl1
116	31	100.0	780	6	US-10-878-556A-197	Sequence 197, App	189	25	80.6	431	6	US-10-949-720-410	Sequence 410, App
117	31	100.0	884	7	US-11-098-686-11426	Sequence 11426, A	190	25	80.6	466	7	US-11-127-877-41	Sequence 41, Appl1
118	31	100.0	885	6	US-10-467-657-2302	Sequence 2302, App	191	25	80.6	502	7	US-11-226-701-4	Sequence 4, Appl1
119	31	100.0	905	7	US-11-072-512-22728	Sequence 2728, App	192	25	80.6	514	6	US-10-498-026-97	Sequence 97, Appl1
120	31	100.0	954	6	US-10-467-9628-31	Sequence 31, Appl1	193	25	80.6	514	6	US-10-498-026-98	Sequence 98, Appl1
121	31	100.0	961	6	US-10-831-997-4	Sequence 4, Appl1	194	25	80.6	522	6	US-10-949-720-425	Sequence 425, App
122	31	100.0	976	6	US-10-966-483-2	Sequence 2, Appl1	195	25	80.6	537	6	US-10-949-720-424	Sequence 424, App
123	31	100.0	976	6	US-10-511-273-1	Sequence 1, Appl1	196	25	80.6	537	7	US-11-144-236-6	Sequence 6, Appl1
124	31	100.0	976	7	US-11-233-796-2	Sequence 2, Appl1	197	25	80.6	555	6	US-10-949-720-387	Sequence 387, App
125	31	100.0	976	7	US-11-072-175-138	Sequence 138, App	198	25	80.6	570	6	US-10-949-720-386	Sequence 386, App
126	31	100.0	1035	6	US-10-966-483-20	Sequence 20, Appl1	199	25	80.6	570	6	US-10-949-720-412	Sequence 412, App
127	31	100.0	1035	7	US-11-021-441-4	Sequence 4, Appl1	200	25	80.6	645	7	US-11-072-512-2588	Sequence 2588, App
128	31	100.0	1075	7	US-11-174-150-34	Sequence 34, Appl1	201	25	80.6	655	7	US-11-072-512-2502	Sequence 2502, App
129	31	100.0	1114	6	US-11-174-150-35	Sequence 35, Appl1	202	25	80.6	698	7	US-11-177-506-46	Sequence 46, Appl1
130	31	100.0	1857	6	US-10-055-877-252	Sequence 252, Appl1	203	25	80.6	771	6	US-10-949-720-389	Sequence 389, App
131	31	100.0	2084	6	US-10-055-877-73	Sequence 73, Appl1	204	25	80.6	794	7	US-11-218-986-2	Sequence 2, Appl1
132	31	100.0	2098	6	US-10-055-877-253	Sequence 253, App	205	25	80.6	820	6	US-10-821-234-1176	Sequence 1176, App
133	31	100.0	2109	6	US-10-055-877-251	Sequence 251, App	206	25	80.6	985	7	US-11-113-424-61	Sequence 61, Appl1
134	25	80.6	47	7	US-11-116-746-8	Sequence 8, Appl1	207	25	80.6	987	6	US-10-949-720-395	Sequence 395, App
135	25	80.6	58	6	US-10-467-657-7330	Sequence 7390, App	208	25	80.6	990	6	US-10-821-234-1201	Sequence 1201, App
136	25	80.6	88	7	US-10-467-657-8627	Sequence 8627, App	209	25	80.6	1049	6	US-10-131-826A-358	Sequence 358, App
137	25	80.6	88	7	US-11-018-868-8	Sequence 8, Appl1	210	25	80.6	1187	6	US-10-821-234-955	Sequence 955, App
138	25	80.6	106	7	US-11-072-512-2975	Sequence 2975, App	211	25	80.6	2143	6	US-10-453-372-1188	Sequence 1188, App
139	25	80.6	114	6	US-10-986-501-190	Sequence 190, Appl1	212	25	80.6	2764	6	US-10-995-561-691	Sequence 691, App
140	25	80.6	117	7	US-11-103-957-74	Sequence 74, Appl1	213	25	80.6	2813	6	US-10-995-561-688	Sequence 688, App
141	25	80.6	120	6	US-10-793-626-2214	Sequence 2214, App	214	25	80.6	2919	6	US-10-821-234-1133	Sequence 1133, App
142	25	80.6	132	7	US-11-072-512-3215	Sequence 3215, App	215	25	80.6	3335	7	US-11-019-711-47	Sequence 47, Appl1
143	25	80.6	161	7	US-11-154-257-3	Sequence 3, Appl1	216	25	80.6	3712	7	US-11-019-711-48	Sequence 48, Appl1
144	25	80.6	167	7	US-11-072-512-3290	Sequence 3290, App	217	25	80.6	3712	7	US-11-019-711-51	Sequence 51, Appl1
145	25	80.6	170	6	US-10-467-657-104	Sequence 104, App	218	25	80.6	4374	7	US-11-128-572-2	Sequence 2, Appl1
146	25	80.6	204	7	US-10-467-657-8078	Sequence 8078, App	219	25	80.6	4961	6	US-10-453-372-1142	Sequence 1142, App
147	25	80.6	204	7	US-11-080-991-8	Sequence 8, Appl1	220	25	80.6	4961	6	US-10-453-372-1132	Sequence 1132, App
148	25	80.6	211	7	US-11-072-512-3219	Sequence 3219, App	221	24	77.4	46	7	US-11-188-552-70	Sequence 70, Appl1
149	25	80.6	228	6	US-10-793-626-1862	Sequence 1862, App	222	24	77.4	50	7	US-11-188-552-69	Sequence 69, Appl1
150	25	80.6	229	5	US-09-978-360A-753	Sequence 753, App	223	24	77.4	50	7	US-11-174-845-2	Sequence 2, Appl1
151	25	80.6	229	6	US-10-131-826A-522	Sequence 522, App	224	24	77.4	50	7	US-11-174-851-2	Sequence 2, Appl1
152	25	80.6	241	6	US-10-467-657-4474	Sequence 4474, App	225	24	77.4	115	6	US-10-467-657-2032	Sequence 2032, App
153	25	80.6	246	7	US-11-072-512-2232	Sequence 2232, App	226	24	77.4	131	6	US-10-518-955-4	Sequence 2, Appl1
154	25	80.6	246	7	US-11-072-512-2243	Sequence 2243, App	227	24	77.4	132	6	US-10-518-955-2	Sequence 4, Appl1
155	25	80.6	247	7	US-11-072-512-2790	Sequence 2790, App	228	24	77.4	134	6	US-10-498-026-37	Sequence 37, Appl1
156	25	80.6	255	6	US-10-170-997-2	Sequence 2, Appl1	229	24	77.4	146	7	US-11-226-657-80	Sequence 80, Appl1
157	25	80.6	255	7	US-11-182-946-11	Sequence 11, Appl1	230	24	77.4	260	7	US-11-182-946-8	Sequence 8, Appl1
158	25	80.6	255	7	US-11-108-257-2	Sequence 2, Appl1	231	24	77.4	331	7	US-11-185-878-3	Sequence 3, Appl1
159	25	80.6	259	6	US-10-131-826A-300	Sequence 300, App	232	24	77.4	334	6	US-10-514-057-6	Sequence 6, Appl1
160	25	80.6	259	6	US-10-821-234-1561	Sequence 1561, App	233	24	77.4	335	7	US-11-182-946-7	Sequence 7, Appl1
161	25	80.6	259	7	US-11-182-946-2	Sequence 2, Appl1	234	24	77.4	393	7	US-11-100-352-3	Sequence 3, Appl1
162	25	80.6	259	7	US-11-132-746-1	Sequence 1, Appl1	235	24	77.4	393	7	US-11-103-957-55	Sequence 55, Appl1
163	25	80.6	277	7	US-11-132-285-3	Sequence 3, Appl1	236	24	77.4	393	7	US-11-018-868-24	Sequence 24, Appl1
164	25	80.6	277	7	US-11-182-946-12	Sequence 12, Appl1	237	24	77.4	622	6	US-10-453-372-1186	Sequence 1186, App
165	25	80.6	280	6	US-10-131-826A-458	Sequence 458, App	238	24	77.4	669	7	US-11-076-187-3	Sequence 203, App
166	25	80.6	280	6	US-10-689-742-160	Sequence 160, App	239	24	77.4	710	7	US-11-169-041-203	Sequence 89, Appl1
167	25	80.6	299	7	US-11-116-746-3	Sequence 3, Appl1	240	24	77.4	843	7	US-11-129-104-89	Sequence 1186, App
168	25	80.6	336	6	US-10-467-657-5848	Sequence 5848, App	241	24	77.4	1544	6	US-10-453-372-1186	Sequence 1186, App
169	25	80.6	349	7	US-11-182-946-13	Sequence 13, Appl1	242	24	77.4	1565	6	US-10-453-372-1180	Sequence 1180, App
170	25	80.6	350	7	US-11-132-285-41	Sequence 41, Appl1	243	24	77.4	1566	6	US-10-453-372-1150	Sequence 1190, App
171	25	80.6	353	7	US-11-072-512-2052	Sequence 2052, App	244	24	77.4	2053	6	US-10-453-372-1174	Sequence 1174, App

245	23	74.2	4	7	US-11-029-003-90	Sequence 90, Appl	318	23	74.2	52	7	US-11-233-683-34	Sequence 34, Appl
246	23	74.2	5	6	US-11-058-926-3	Sequence 3, Appl1	319	23	74.2	53	6	US-10-914-391A-7	Sequence 7, Appl1
247	23	74.2	5	7	US-10-895-064-153	Sequence 153, Appl	320	23	74.2	54	6	US-10-467-657-2264	Sequence 2264, Ap
248	23	74.2	5	7	US-11-129-741-153	Sequence 153, App	321	23	74.2	55	7	US-11-000-463-303	Sequence 303, App
249	23	74.2	5	7	US-11-129-741-3086	Sequence 3086, Ap	322	23	74.2	55	7	US-11-000-463-775	Sequence 775, App
250	23	74.2	6	7	US-11-029-003-88	Sequence 88, Appl	323	23	74.2	56	7	US-11-042-814-6	Sequence 6, Appl1
251	23	74.2	7	7	US-11-029-003-87	Sequence 87, Appl	324	23	74.2	58	6	US-10-914-391A-4	Sequence 4, Appl1
252	23	74.2	7	7	US-11-029-003-89	Sequence 89, Appl	325	23	74.2	63	7	US-11-174-996A-93	Sequence 93, Appl
253	23	74.2	8	7	US-11-142-327-5	Sequence 5, Appl1	326	23	74.2	64	7	US-11-174-996A-89	Sequence 89, Appl
254	23	74.2	9	7	US-11-040-159-122	Sequence 122, App	327	23	74.2	67	7	US-11-172-536-7	Sequence 7, Appl1
255	23	74.2	10	6	US-10-929-988-48	Sequence 48, Appl	328	23	74.2	66	7	US-11-022-232B-20	Sequence 20, Appl
256	23	74.2	10	6	US-11-192-219-44	Sequence 44, Appl	329	23	74.2	68	6	US-11-123-836-164	Sequence 164, App
257	23	74.2	12	6	US-10-901-576-2	Sequence 2, Appl1	330	23	74.2	72	7	US-11-123-836-164	Sequence 14, Appl
258	23	74.2	15	6	US-10-925-366A-11	Sequence 11, Appl	331	23	74.2	72	7	US-11-198-847-121	Sequence 221, App
259	23	74.2	15	6	US-10-909-769-31	Sequence 31, Appl	332	23	74.2	72	7	US-11-198-847-121	Sequence 55, Appl
260	23	74.2	15	7	US-11-198-847-336	Sequence 336, App	333	23	74.2	74	7	US-11-174-996A-55	Sequence 55, Appl
261	23	74.2	15	7	US-11-198-847-337	Sequence 337, App	334	23	74.2	74	7	US-11-174-996A-77	Sequence 77, Appl
262	23	74.2	16	6	US-10-929-988-301	Sequence 301, App	335	23	74.2	75	6	US-10-478-345-10	Sequence 10, Appl
263	23	74.2	16	7	US-11-142-327-1	Sequence 1, Appl1	336	23	74.2	75	6	US-10-478-345-14	Sequence 14, Appl
264	23	74.2	16	7	US-11-142-327-2	Sequence 2, Appl1	337	23	74.2	75	7	US-11-174-996A-73	Sequence 73, Appl
265	23	74.2	16	7	US-11-142-327-3	Sequence 3, Appl1	338	23	74.2	75	7	US-11-174-996A-75	Sequence 75, Appl
266	23	74.2	16	7	US-11-142-327-4	Sequence 4, Appl1	339	23	74.2	75	7	US-11-174-996A-83	Sequence 83, Appl
267	23	74.2	17	7	US-11-198-847-334	Sequence 334, App	340	23	74.2	75	7	US-11-174-996A-87	Sequence 87, Appl
268	23	74.2	17	7	US-11-198-847-335	Sequence 335, App	341	23	74.2	75	7	US-11-174-996A-91	Sequence 91, Appl
269	23	74.2	19	7	US-11-198-847-235	Sequence 235, App	342	23	74.2	75	7	US-11-174-996A-95	Sequence 95, Appl
270	23	74.2	19	7	US-11-198-847-236	Sequence 236, App	343	23	74.2	75	7	US-11-174-996A-97	Sequence 97, Appl
271	23	74.2	21	7	US-11-233-683-28	Sequence 28, App	344	23	74.2	77	7	US-11-174-996A-53	Sequence 53, Appl
272	23	74.2	24	6	US-10-895-861-26	Sequence 26, Appl	345	23	74.2	77	7	US-10-467-657-3504	Sequence 3504, Ap
273	23	74.2	27	6	US-10-895-861-73	Sequence 73, Appl	346	23	74.2	80	6	US-10-467-657-3504	Sequence 150, App
274	23	74.2	27	6	US-10-895-861-83	Sequence 83, Appl	347	23	74.2	81	6	US-10-131-826A-150	Sequence 150, App
275	23	74.2	28	7	US-11-120-501-31	Sequence 31, Appl	348	23	74.2	84	5	US-09-978-360A-716	Sequence 716, Appl
276	23	74.2	29	6	US-10-986-501-269	Sequence 269, App	349	23	74.2	91	7	US-11-042-814-7	Sequence 7, Appl1
277	23	74.2	32	6	US-10-895-064-976	Sequence 976, App	350	23	74.2	92	6	US-10-821-230-1505	Sequence 1505, Ap
278	23	74.2	32	7	US-11-129-741-976	Sequence 976, App	351	23	74.2	93	7	US-11-230-180-12	Sequence 12, Appl
279	23	74.2	32	7	US-11-129-741-3972	Sequence 3972, Ap	352	23	74.2	96	6	US-10-467-657-4198	Sequence 4198, Ap
280	23	74.2	34	6	US-10-532-480-13	Sequence 13, Appl	353	23	74.2	97	6	US-10-467-657-4214	Sequence 4214, Ap
281	23	74.2	35	7	US-11-233-683-49	Sequence 49, Appl	354	23	74.2	97	7	US-11-054-281-299	Sequence 299, App
282	23	74.2	35	7	US-11-233-683-50	Sequence 50, Appl	355	23	74.2	98	7	US-11-172-536-8	Sequence 8, Appl1
283	23	74.2	35	7	US-11-233-683-53	Sequence 53, Appl	356	23	74.2	102	6	US-10-467-657-796	Sequence 796, App
284	23	74.2	35	7	US-11-233-683-54	Sequence 54, Appl	357	23	74.2	105	6	US-10-453-372-1178	Sequence 1178, Ap
285	23	74.2	35	7	US-11-233-683-55	Sequence 55, Appl	358	23	74.2	106	7	US-11-073-222-6	Sequence 2, Appl1
286	23	74.2	39	6	US-10-895-064-295	Sequence 295, App	359	23	74.2	106	7	US-11-072-512-2828	Sequence 2828, Ap
287	23	74.2	39	7	US-11-129-741-295	Sequence 295, App	360	23	74.2	107	6	US-11-253-881-6	Sequence 6, Appl1
288	23	74.2	39	7	US-11-129-741-3227	Sequence 3227, Ap	361	23	74.2	107	6	US-10-467-657-6644	Sequence 6644, Appl
289	23	74.2	40	6	US-10-979-871-4	Sequence 4, Appl1	362	23	74.2	112	7	US-11-129-741-4223	Sequence 4223, Ap
290	23	74.2	40	6	US-10-979-871-5	Sequence 5, Appl1	363	23	74.2	115	7	US-11-155-288-11	Sequence 11, Appl
291	23	74.2	40	6	US-10-979-871-6	Sequence 6, Appl1	364	23	74.2	116	7	US-11-072-512-2094	Sequence 2094, Ap
292	23	74.2	40	6	US-10-979-871-7	Sequence 7, Appl1	365	23	74.2	124	5	US-09-995-498-84	Sequence 84, Appl
293	23	74.2	40	6	US-10-979-871-8	Sequence 8, Appl1	366	23	74.2	124	7	US-11-119-098-2	Sequence 2, Appl1
294	23	74.2	40	6	US-10-979-871-9	Sequence 9, Appl1	367	23	74.2	127	6	US-10-763-712A-82	Sequence 82, Appl
295	23	74.2	40	6	US-10-979-871-10	Sequence 10, Appl	368	23	74.2	127	6	US-11-072-512-3790	Sequence 3790, Ap
296	23	74.2	40	6	US-10-979-871-11	Sequence 11, Appl	369	23	74.2	127	7	US-11-195-459-2	Sequence 2, Appl1
297	23	74.2	40	6	US-10-979-871-12	Sequence 12, Appl	370	23	74.2	128	7	US-11-195-459-4	Sequence 4, Appl1
298	23	74.2	40	6	US-10-979-871-13	Sequence 13, Appl	371	23	74.2	128	7	US-11-183-205-14	Sequence 14, Appl
299	23	74.2	40	6	US-10-895-861-32	Sequence 32, Appl	372	23	74.2	130	7	US-11-008-727-8	Sequence 8, Appl1
300	23	74.2	41	7	US-11-326-657-206	Sequence 206, App	373	23	74.2	130	7	US-11-135-855-27	Sequence 27, Appl
301	23	74.2	41	7	US-11-233-683-30	Sequence 30, Appl	374	23	74.2	130	7	US-11-073-222-5	Sequence 5, Appl1
302	23	74.2	41	7	US-11-233-683-35	Sequence 35, Appl	375	23	74.2	130	7	US-11-072-512-2940	Sequence 2940, Ap
303	23	74.2	41	7	US-11-233-683-36	Sequence 36, Appl	376	23	74.2	130	7	US-11-253-881-5	Sequence 5, Appl1
304	23	74.2	41	7	US-11-233-683-37	Sequence 37, Appl	377	23	74.2	137	6	US-10-821-234-1242	Sequence 1242, Appl
305	23	74.2	41	7	US-11-233-683-44	Sequence 44, Appl	378	23	74.2	138	7	US-11-008-727-2	Sequence 2, Appl1
306	23	74.2	41	7	US-11-233-683-47	Sequence 47, Appl	379	23	74.2	142	7	US-11-182-908-22	Sequence 22, Appl
307	23	74.2	42	6	US-10-895-861-42	Sequence 42, Appl	380	23	74.2	145	6	US-10-821-234-1231	Sequence 1231, Ap
308	23	74.2	42	6	US-10-895-861-44	Sequence 44, Appl	381	23	74.2	146	7	US-11-226-657-63	Sequence 63, Appl
309	23	74.2	45	7	US-11-123-896-165	Sequence 165, App	382	23	74.2	149	7	US-11-226-657-205	Sequence 205, App
310	23	74.2	47	7	US-11-000-463-756	Sequence 756, App	383	23	74.2	150	7	US-11-036-797-35	Sequence 35, Appl
311	23	74.2	48	6	US-10-895-861-39	Sequence 39, Appl	384	23	74.2	156	6	US-10-821-233-1397	Sequence 1397, Ap
312	23	74.2	48	6	US-10-895-861-56	Sequence 56, Appl	385	23	74.2	156	7	US-11-132-839-9	Sequence 9, Appl1
313	23	74.2	49	6	US-10-895-861-57	Sequence 57, Appl	386	23	74.2	157	6	US-10-793-626-1720	Sequence 1720, Ap
314	23	74.2	51	6	US-10-967-527A-15	Sequence 15, Appl	387	23	74.2	159	7	US-11-132-285-7	Sequence 7, Appl1
315	23	74.2	51	6	US-10-895-861-49	Sequence 49, Appl	388	23	74.2	160	6	US-10-924-074-10	Sequence 10, Appl
316	23	74.2	52	6	US-10-914-391A-9	Sequence 9, Appl1	389	23	74.2	163	6	US-10-510-386-126	Sequence 126, App
317	23	74.2	52	7	US-11-233-683-29	Sequence 29, Appl	390	23	74.2	165	7	US-11-069-856-23	Sequence 23, Appl

391	23	74.2	166	7	US-11-226-657-204	Sequence 204, App	464	23	74.2	240	7	US-11-218-234-23	Sequence 23, Appl
392	23	74.2	174	7	US-11-072-512-2144	Sequence 2144, Ap	465	23	74.2	243	6	US-11-098-686-10149	Sequence 10149, A
393	23	74.2	178	5	US-09-810-501-71	Sequence 71, Appl	466	23	74.2	244	7	US-10-924-074-2	Sequence 2, Appl1
394	23	74.2	182	5	US-09-978-660A-717	Sequence 717, App	467	23	74.2	245	7	US-11-029-003-20	Sequence 20, Appl
395	23	74.2	182	6	US-10-131-826A-174	Sequence 174, App	468	23	74.2	247	7	US-11-072-512-1998	Sequence 1998, Ap
396	23	74.2	183	5	US-09-978-660A-680	Sequence 680, App	469	23	74.2	249	7	US-11-010-239-107	Sequence 107, App
397	23	74.2	183	5	US-09-810-501-77	Sequence 77, Appl	470	23	74.2	250	7	US-11-242-294-35	Sequence 35, Appl1
398	23	74.2	183	6	US-10-821-234-1485	Sequence 1485, Ap	471	23	74.2	251	7	US-11-242-294-6	Sequence 6, Appl1
399	23	74.2	183	6	US-10-467-657-6906	Sequence 6906, Ap	472	23	74.2	251	7	US-11-242-294-29	Sequence 29, Appl
400	23	74.2	183	7	US-11-186-284-111	Sequence 111, App	473	23	74.2	251	7	US-11-242-294-31	Sequence 31, Appl
401	23	74.2	183	7	US-11-186-284-113	Sequence 113, App	474	23	74.2	251	7	US-11-242-294-33	Sequence 33, Appl
402	23	74.2	184	7	US-11-072-512-2477	Sequence 2477, Ap	475	23	74.2	251	7	US-11-242-294-37	Sequence 37, Appl
403	23	74.2	185	6	US-10-967-527A-10	Sequence 10, Appl	476	23	74.2	251	7	US-11-242-294-39	Sequence 39, Appl
404	23	74.2	186	6	US-10-467-657-470	Sequence 470, App	477	23	74.2	254	5	US-09-810-501-69	Sequence 69, Appl
405	23	74.2	187	6	US-11-024-959-304	Sequence 304, App	478	23	74.2	255	6	US-10-660-499A-2	Sequence 2, Appl1
406	23	74.2	188	7	US-11-024-959-307	Sequence 307, App	479	23	74.2	255	7	US-11-057-923-5	Sequence 5, Appl1
407	23	74.2	188	7	US-11-072-512-2380	Sequence 2380, Ap	480	23	74.2	256	7	US-11-029-003-14	Sequence 14, Appl
408	23	74.2	191	6	US-10-924-074-4	Sequence 4, Appl1	481	23	74.2	258	6	US-10-467-657-4130	Sequence 4130, Ap
409	23	74.2	191	6	US-10-055-877-42	Sequence 42, Appl	482	23	74.2	259	6	US-10-763-712A-116	Sequence 116, App
410	23	74.2	195	7	US-11-132-839-11	Sequence 11, Appl	483	23	74.2	259	7	US-11-057-923-6	Sequence 6, Appl1
411	23	74.2	195	7	US-11-182-908-19	Sequence 19, Appl	484	23	74.2	259	7	US-11-098-686-11421	Sequence 11421, A
412	23	74.2	200	6	US-10-454-437-246	Sequence 246, App	485	23	74.2	262	6	US-10-498-026-46	Sequence 46, Appl
413	23	74.2	201	7	US-11-072-512-3518	Sequence 3518, Ap	486	23	74.2	263	6	US-10-498-026-31	Sequence 31, Appl
414	23	74.2	203	7	US-11-132-839-10	Sequence 10, Appl	487	23	74.2	263	6	US-10-498-026-45	Sequence 45, Appl
415	23	74.2	203	7	US-11-069-856-1	Sequence 1, Appl1	488	23	74.2	263	7	US-11-033-039-193	Sequence 193, App
416	23	74.2	207	7	US-11-072-512-2278	Sequence 2278, Ap	489	23	74.2	263	7	US-11-072-512-3558	Sequence 3558, Ap
417	23	74.2	207	7	US-11-072-512-2607	Sequence 2607, Ap	490	23	74.2	264	6	US-10-778-636-3	Sequence 3, Appl1
418	23	74.2	210	5	US-09-995-493-204	Sequence 204, App	491	23	74.2	264	6	US-10-778-636-4	Sequence 4, Appl1
419	23	74.2	211	6	US-10-821-234-1372	Sequence 1372, Ap	492	23	74.2	265	6	US-10-689-742-188	Sequence 188, App
420	23	74.2	211	6	US-10-498-026-107	Sequence 107, App	493	23	74.2	266	5	US-09-995-493-6	Sequence 6, Appl1
421	23	74.2	211	6	US-10-498-026-108	Sequence 108, App	494	23	74.2	267	6	US-10-841-956A-4	Sequence 4, Appl1
422	23	74.2	211	6	US-10-498-026-109	Sequence 109, App	495	23	74.2	269	6	US-10-841-956A-8	Sequence 8, Appl1
423	23	74.2	211	7	US-11-132-839-12	Sequence 12, Appl	496	23	74.2	269	7	US-11-072-512-3305	Sequence 3305, Ap
424	23	74.2	212	6	US-10-498-026-110	Sequence 110, App	497	23	74.2	270	6	US-10-841-956A-5	Sequence 5, Appl1
425	23	74.2	216	6	US-10-821-234-1033	Sequence 1033, Ap	498	23	74.2	270	7	US-11-008-727-24	Sequence 24, Appl
426	23	74.2	220	6	US-10-995-561-976	Sequence 576, App	499	23	74.2	277	6	US-10-924-074-24	Sequence 24, Appl
427	23	74.2	220	6	US-10-670-009-3	Sequence 3, Appl1	500	23	74.2	277	7	US-11-182-924-10	Sequence 10, Appl
428	23	74.2	222	6	US-10-746-909-2	Sequence 2, Appl1	501	23	74.2	277	7	US-11-127-046-2	Sequence 2, Appl1
429	23	74.2	223	6	US-10-746-909-3	Sequence 3, Appl1	502	23	74.2	277	7	US-11-169-041-196	Sequence 196, App
430	23	74.2	224	6	US-10-131-826A-86	Sequence 86, Appl	503	23	74.2	280	6	US-10-511-538-41	Sequence 41, Appl
431	23	74.2	225	6	US-10-670-009-5	Sequence 5, Appl1	504	23	74.2	280	7	US-11-098-686-10511	Sequence 10511, A
432	23	74.2	225	7	US-11-092-953-9	Sequence 9, Appl1	505	23	74.2	281	6	US-10-841-956A-7	Sequence 7, Appl1
433	23	74.2	225	7	US-11-128-937-9	Sequence 9, Appl1	506	23	74.2	282	6	US-10-841-956A-6	Sequence 6, Appl1
434	23	74.2	226	7	US-11-132-285-5	Sequence 5, Appl1	507	23	74.2	282	7	US-11-183-205-40	Sequence 40, Appl1
435	23	74.2	227	6	US-10-467-657-2624	Sequence 2624, Ap	508	23	74.2	283	6	US-10-987-663-4	Sequence 4, Appl1
436	23	74.2	227	6	US-10-670-009-4	Sequence 4, Appl1	509	23	74.2	283	6	US-10-821-234-1560	Sequence 1560, Ap
437	23	74.2	227	6	US-10-670-009-7	Sequence 7, Appl1	510	23	74.2	292	7	US-11-055-822-940	Sequence 940, App
438	23	74.2	227	6	US-10-841-956A-17	Sequence 17, Appl	511	23	74.2	293	6	US-10-131-826A-422	Sequence 422, App
439	23	74.2	227	7	US-11-008-727-14	Sequence 14, Appl	512	23	74.2	293	6	US-10-841-956A-9	Sequence 9, Appl1
440	23	74.2	227	7	US-11-201-825-67	Sequence 67, Appl	513	23	74.2	296	6	US-10-954-468-9	Sequence 9, Appl1
441	23	74.2	228	6	US-10-670-009-2	Sequence 2, Appl1	514	23	74.2	297	6	US-10-967-527A-17	Sequence 17, Appl
442	23	74.2	228	6	US-10-841-956A-16	Sequence 16, Appl	515	23	74.2	299	7	US-11-098-686-11010	Sequence 11010, A
443	23	74.2	229	6	US-10-924-074-8	Sequence 8, Appl1	516	23	74.2	301	6	US-10-979-871-2	Sequence 2, Appl1
444	23	74.2	229	7	US-11-072-512-3781	Sequence 3781, Ap	517	23	74.2	307	7	US-11-024-959-291	Sequence 291, App
445	23	74.2	231	7	US-11-132-285-61	Sequence 61, Appl	518	23	74.2	308	7	US-11-072-512-3715	Sequence 3715, Ap
446	23	74.2	232	6	US-10-821-234-1023	Sequence 1023, Ap	519	23	74.2	310	6	US-10-714-887-42	Sequence 42, Appl
447	23	74.2	232	6	US-10-636-320-4	Sequence 4, Appl1	520	23	74.2	310	6	US-10-485-517-409	Sequence 409, App
448	23	74.2	232	6	US-10-948-053-1	Sequence 1, Appl1	521	23	74.2	314	6	US-10-689-742-116	Sequence 116, App
449	23	74.2	232	7	US-11-128-059-66	Sequence 66, Appl	522	23	74.2	316	7	US-11-072-512-2079	Sequence 2079, Ap
450	23	74.2	232	7	US-11-227-940-7	Sequence 7, Appl1	523	23	74.2	318	6	US-10-821-234-1117	Sequence 1117, Ap
451	23	74.2	232	7	US-11-201-825-66	Sequence 66, Appl	524	23	74.2	318	7	US-11-021-305-168	Sequence 168, App
452	23	74.2	233	6	US-10-923-327-18	Sequence 18, Appl	525	23	74.2	319	6	US-10-498-026-21	Sequence 21, Appl
453	23	74.2	233	6	US-10-923-327-19	Sequence 19, Appl	526	23	74.2	320	6	US-10-498-026-13	Sequence 13, Appl
454	23	74.2	233	7	US-11-150-533-45	Sequence 45, Appl	527	23	74.2	320	7	US-11-102-883-20	Sequence 20, Appl
455	23	74.2	235	7	US-11-126-126-16	Sequence 16, Appl	528	23	74.2	320	7	US-11-152-811-3	Sequence 3, Appl1
456	23	74.2	236	6	US-10-763-712A-115	Sequence 115, App	529	23	74.2	320	7	US-11-183-205-50	Sequence 50, Appl
457	23	74.2	236	7	US-11-008-727-4	Sequence 4, Appl1	530	23	74.2	321	6	US-10-478-345-8	Sequence 8, Appl1
458	23	74.2	237	6	US-10-924-074-6	Sequence 6, Appl1	531	23	74.2	321	7	US-11-072-512-2235	Sequence 2235, Ap
459	23	74.2	238	6	US-10-841-956A-20	Sequence 20, Appl	532	23	74.2	325	6	US-10-467-657-3026	Sequence 3026, Ap
460	23	74.2	238	7	US-11-008-727-26	Sequence 26, Appl	533	23	74.2	326	6	US-10-999-866-36	Sequence 36, Appl
461	23	74.2	238	7	US-11-029-003-4	Sequence 4, Appl1	534	23	74.2	326	6	US-10-493-909-22	Sequence 22, Appl
462	23	74.2	238	7	US-11-098-686-11045	Sequence 11045, A	535	23	74.2	326	7	US-11-144-248-28	Sequence 28, Appl
463	23	74.2	240	7	US-11-089-803-23	Sequence 23, Appl	536	23	74.2	326	7	US-11-061-821-36	Sequence 36, Appl

537	23	74.2	326	7	US-11-102-621-2	Sequence 2, Appl1	610	23	74.2	330	6	US-10-982-440-68	Sequence 68, Appl1
538	23	74.2	326	7	US-11-102-621-10	Sequence 10, Appl1	611	23	74.2	330	7	US-11-022-289-1	Sequence 11, Appl1
539	23	74.2	326	7	US-11-102-621-11	Sequence 11, Appl1	612	23	74.2	330	7	US-11-022-289-11	Sequence 11, Appl1
540	23	74.2	326	7	US-11-102-621-12	Sequence 12, Appl1	613	23	74.2	330	7	US-11-075-351-1	Sequence 1, Appl1
541	23	74.2	326	7	US-11-102-621-13	Sequence 13, Appl1	614	23	74.2	330	7	US-11-165-141-15	Sequence 15, Appl1
542	23	74.2	326	7	US-11-102-621-14	Sequence 14, Appl1	615	23	74.2	330	7	US-11-102-621-3	Sequence 3, Appl1
543	23	74.2	326	7	US-11-102-621-15	Sequence 15, Appl1	616	23	74.2	330	7	US-11-102-621-7	Sequence 7, Appl1
544	23	74.2	326	7	US-11-102-621-16	Sequence 16, Appl1	617	23	74.2	330	7	US-11-102-621-67	Sequence 67, Appl1
545	23	74.2	326	7	US-11-102-621-17	Sequence 17, Appl1	618	23	74.2	330	7	US-11-102-621-68	Sequence 68, Appl1
546	23	74.2	326	7	US-11-102-621-18	Sequence 18, Appl1	619	23	74.2	330	7	US-11-102-621-69	Sequence 69, Appl1
547	23	74.2	326	7	US-11-102-621-19	Sequence 19, Appl1	620	23	74.2	330	7	US-11-102-621-70	Sequence 70, Appl1
548	23	74.2	326	7	US-11-102-621-20	Sequence 20, Appl1	621	23	74.2	330	7	US-11-102-621-71	Sequence 71, Appl1
549	23	74.2	326	7	US-11-102-621-21	Sequence 21, Appl1	622	23	74.2	330	7	US-11-102-621-75	Sequence 75, Appl1
550	23	74.2	326	7	US-11-102-621-22	Sequence 22, Appl1	623	23	74.2	330	7	US-11-102-621-76	Sequence 76, Appl1
551	23	74.2	326	7	US-11-102-621-23	Sequence 23, Appl1	624	23	74.2	330	7	US-11-005-726-164	Sequence 164, Appl1
552	23	74.2	326	7	US-11-102-621-24	Sequence 24, Appl1	625	23	74.2	330	7	US-11-124-620-1	Sequence 1, Appl1
553	23	74.2	326	7	US-11-102-621-25	Sequence 25, Appl1	626	23	74.2	330	7	US-11-233-683-1	Sequence 1, Appl1
554	23	74.2	326	7	US-11-102-621-26	Sequence 26, Appl1	627	23	74.2	330	7	US-11-201-825-55	Sequence 55, Appl1
555	23	74.2	326	7	US-11-102-621-27	Sequence 27, Appl1	628	23	74.2	331	6	US-10-995-561-977	Sequence 977, Appl1
556	23	74.2	326	7	US-11-102-621-28	Sequence 28, Appl1	629	23	74.2	331	6	US-10-995-561-978	Sequence 978, Appl1
557	23	74.2	326	7	US-11-102-621-29	Sequence 29, Appl1	630	23	74.2	331	6	US-11-185-877-8	Sequence 8, Appl1
558	23	74.2	326	7	US-11-102-621-30	Sequence 30, Appl1	631	23	74.2	332	6	US-10-949-720-405	Sequence 405, Appl1
559	23	74.2	326	7	US-11-102-621-31	Sequence 31, Appl1	632	23	74.2	332	7	US-11-242-294-62	Sequence 62, Appl1
560	23	74.2	326	7	US-11-102-621-32	Sequence 32, Appl1	633	23	74.2	333	6	US-10-131-826A-132	Sequence 132, Appl1
561	23	74.2	326	7	US-11-102-621-33	Sequence 33, Appl1	634	23	74.2	333	6	US-10-821-234-1672	Sequence 1672, Appl1
562	23	74.2	326	7	US-11-102-621-34	Sequence 34, Appl1	635	23	74.2	333	6	US-11-185-877-9	Sequence 9, Appl1
563	23	74.2	326	7	US-11-102-621-35	Sequence 35, Appl1	636	23	74.2	334	6	US-10-131-826A-12	Sequence 12, Appl1
564	23	74.2	326	7	US-11-102-621-36	Sequence 36, Appl1	637	23	74.2	334	7	US-11-072-512-2440	Sequence 2440, Appl1
565	23	74.2	326	7	US-11-102-621-37	Sequence 37, Appl1	638	23	74.2	335	6	US-10-995-561-866	Sequence 866, Appl1
566	23	74.2	326	7	US-11-102-621-38	Sequence 38, Appl1	639	23	74.2	335	6	US-11-024-251-35	Sequence 35, Appl1
567	23	74.2	326	7	US-11-102-621-39	Sequence 39, Appl1	640	23	74.2	335	7	US-11-185-877-10	Sequence 10, Appl1
568	23	74.2	326	7	US-11-102-621-40	Sequence 40, Appl1	641	23	74.2	336	6	US-10-793-628-1858	Sequence 1858, Appl1
569	23	74.2	326	7	US-11-102-621-41	Sequence 41, Appl1	642	23	74.2	336	6	US-10-467-665-4390	Sequence 4390, Appl1
570	23	74.2	326	7	US-11-102-621-42	Sequence 42, Appl1	643	23	74.2	339	6	US-10-878-565A-18	Sequence 18, Appl1
571	23	74.2	326	7	US-11-102-621-43	Sequence 43, Appl1	644	23	74.2	339	6	US-10-999-866-35	Sequence 35, Appl1
572	23	74.2	326	7	US-11-102-621-44	Sequence 44, Appl1	645	23	74.2	339	6	US-10-995-561-661	Sequence 661, Appl1
573	23	74.2	326	7	US-11-102-621-45	Sequence 45, Appl1	646	23	74.2	339	6	US-10-995-561-662	Sequence 662, Appl1
574	23	74.2	326	7	US-11-102-621-46	Sequence 46, Appl1	647	23	74.2	339	6	US-10-995-561-664	Sequence 664, Appl1
575	23	74.2	326	7	US-11-102-621-47	Sequence 47, Appl1	648	23	74.2	339	6	US-10-995-561-665	Sequence 665, Appl1
576	23	74.2	326	7	US-11-102-621-48	Sequence 48, Appl1	649	23	74.2	339	6	US-10-995-561-666	Sequence 666, Appl1
577	23	74.2	326	7	US-11-102-621-49	Sequence 49, Appl1	650	23	74.2	339	6	US-10-995-561-667	Sequence 667, Appl1
578	23	74.2	326	7	US-11-102-621-50	Sequence 50, Appl1	651	23	74.2	339	7	US-11-061-821-35	Sequence 35, Appl1
579	23	74.2	326	7	US-11-102-621-51	Sequence 51, Appl1	652	23	74.2	339	7	US-11-186-284-43	Sequence 43, Appl1
580	23	74.2	326	7	US-11-102-621-52	Sequence 52, Appl1	653	23	74.2	339	7	US-11-185-877-11	Sequence 11, Appl1
581	23	74.2	326	7	US-11-102-621-53	Sequence 53, Appl1	654	23	74.2	339	7	US-11-177-648-81	Sequence 81, Appl1
582	23	74.2	326	7	US-11-102-621-54	Sequence 54, Appl1	655	23	74.2	342	7	US-11-098-686-10943	Sequence 10943, Appl1
583	23	74.2	326	7	US-11-102-621-55	Sequence 55, Appl1	656	23	74.2	344	6	US-10-821-234-923	Sequence 923, Appl1
584	23	74.2	326	7	US-11-102-621-56	Sequence 56, Appl1	657	23	74.2	344	7	US-11-242-294-52	Sequence 52, Appl1
585	23	74.2	326	7	US-11-102-621-57	Sequence 57, Appl1	658	23	74.2	344	7	US-11-098-686-10460	Sequence 10460, Appl1
586	23	74.2	326	7	US-11-102-621-58	Sequence 58, Appl1	659	23	74.2	346	7	US-11-077-386-24	Sequence 24, Appl1
587	23	74.2	326	7	US-11-102-621-59	Sequence 59, Appl1	660	23	74.2	347	7	US-11-224-624-136	Sequence 136, Appl1
588	23	74.2	326	7	US-11-102-621-60	Sequence 60, Appl1	661	23	74.2	347	7	US-11-098-686-10337	Sequence 10337, Appl1
589	23	74.2	326	7	US-11-102-621-61	Sequence 61, Appl1	662	23	74.2	348	7	US-11-242-294-54	Sequence 54, Appl1
590	23	74.2	326	7	US-11-102-621-62	Sequence 62, Appl1	663	23	74.2	349	7	US-11-098-686-10281	Sequence 10281, Appl1
591	23	74.2	326	7	US-11-102-621-63	Sequence 63, Appl1	664	23	74.2	350	6	US-10-063-703-8	Sequence 8, Appl1
592	23	74.2	326	7	US-11-102-621-64	Sequence 64, Appl1	665	23	74.2	350	7	US-11-102-621-8	Sequence 8, Appl1
593	23	74.2	326	7	US-11-102-621-65	Sequence 65, Appl1	666	23	74.2	350	7	US-11-108-528-54	Sequence 54, Appl1
594	23	74.2	326	7	US-11-102-621-66	Sequence 66, Appl1	667	23	74.2	350	7	US-11-119-351-4	Sequence 4, Appl1
595	23	74.2	326	7	US-11-102-621-72	Sequence 72, Appl1	668	23	74.2	350	7	US-11-072-512-2500	Sequence 2500, Appl1
596	23	74.2	326	7	US-11-102-621-73	Sequence 73, Appl1	669	23	74.2	351	7	US-11-108-528-52	Sequence 52, Appl1
597	23	74.2	326	7	US-11-102-621-74	Sequence 74, Appl1	670	23	74.2	351	7	US-11-102-683-28	Sequence 28, Appl1
598	23	74.2	326	7	US-11-144-222-28	Sequence 28, Appl1	671	23	74.2	353	6	US-10-131-826A-396	Sequence 396, Appl1
599	23	74.2	326	7	US-11-182-343-28	Sequence 28, Appl1	672	23	74.2	353	6	US-10-478-345-2	Sequence 2, Appl1
600	23	74.2	326	7	US-11-124-620-2	Sequence 2, Appl1	673	23	74.2	354	6	US-10-467-657-6058	Sequence 6058, Appl1
601	23	74.2	326	7	US-11-433-683-2	Sequence 2, Appl1	674	23	74.2	354	7	US-11-108-528-50	Sequence 50, Appl1
602	23	74.2	327	7	US-11-452-811-5	Sequence 5, Appl1	675	23	74.2	354	7	US-11-072-512-3151	Sequence 3151, Appl1
603	23	74.2	327	7	US-11-072-512-2508	Sequence 2508, Appl1	676	23	74.2	355	7	US-11-072-512-3566	Sequence 3566, Appl1
604	23	74.2	328	7	US-11-169-041-227	Sequence 227, Appl1	677	23	74.2	356	7	US-11-072-512-3444	Sequence 3444, Appl1
605	23	74.2	328	7	US-11-072-175-232	Sequence 232, Appl1	678	23	74.2	357	6	US-10-478-345-6	Sequence 6, Appl1
606	23	74.2	329	7	US-11-185-877-2	Sequence 2, Appl1	679	23	74.2	357	7	US-11-072-512-3308	Sequence 3308, Appl1
607	23	74.2	329	7	US-11-185-877-7	Sequence 7, Appl1	680	23	74.2	357	7	US-11-242-294-36	Sequence 36, Appl1
608	23	74.2	330	6	US-10-886-383-6	Sequence 6, Appl1	681	23	74.2	359	6	US-10-763-712A-74	Sequence 74, Appl1
609	23	74.2	330	6	US-10-493-909-20	Sequence 20, Appl1	682	23	74.2	359	7	US-11-105-172-2	Sequence 2, Appl1

683	23	74.2	360	6	US-10-467-657-7666	Sequence 7666, Ap	756	23	74.2	435	7	US-11-077-386-19	Sequence 19, Appl
684	23	74.2	360	7	US-11-112-240-1	Sequence 1, Appl1	757	23	74.2	436	7	US-11-042-814-4	Sequence 40, Appl1
685	23	74.2	360	7	US-11-112-304A-1	Sequence 1, Appl1	758	23	74.2	437	7	US-11-183-136-40	Sequence 40, Appl1
686	23	74.2	352	7	US-11-102-883-8	Sequence 8, Appl1	759	23	74.2	439	6	US-10-763-712A-39	Sequence 39, Appl
687	23	74.2	352	7	US-11-072-512-2384	Sequence 2384, Ap	760	23	74.2	442	7	US-11-102-621-124	Sequence 124, App
688	23	74.2	365	7	US-11-087-177-5	Sequence 5, Appl1	761	23	74.2	442	7	US-11-102-621-125	Sequence 125, App
689	23	74.2	366	7	US-11-075-351-38	Sequence 38, Appl	762	23	74.2	442	7	US-11-102-621-126	Sequence 126, App
690	23	74.2	369	6	US-10-763-712A-42	Sequence 42, Appl	763	23	74.2	442	7	US-11-102-621-127	Sequence 127, App
691	23	74.2	369	6	US-10-763-712A-43	Sequence 43, Appl	764	23	74.2	444	7	US-11-102-621-128	Sequence 128, App
692	23	74.2	369	6	US-10-763-712A-45	Sequence 45, Appl	765	23	74.2	444	7	US-11-172-320-6	Sequence 6, Appl1
693	23	74.2	369	6	US-10-763-712A-106	Sequence 106, App	766	23	74.2	444	7	US-11-173-969-6	Sequence 6, Appl1
694	23	74.2	374	7	US-11-075-351-42	Sequence 42, Appl	767	23	74.2	444	7	US-11-004-590-232	Sequence 232, App
695	23	74.2	376	6	US-10-523-503-52	Sequence 52, Appl	768	23	74.2	444	7	US-11-004-590-233	Sequence 233, App
696	23	74.2	378	7	US-11-201-825-60	Sequence 60, Appl	769	23	74.2	446	7	US-11-102-621-119	Sequence 119, App
697	23	74.2	379	6	US-10-763-712A-40	Sequence 40, Appl	770	23	74.2	446	7	US-11-102-621-120	Sequence 120, App
698	23	74.2	379	7	US-11-012-522-7	Sequence 7, Appl1	771	23	74.2	446	7	US-11-102-621-121	Sequence 121, App
699	23	74.2	379	7	US-11-054-281-45	Sequence 45, Appl	772	23	74.2	446	7	US-11-102-621-122	Sequence 122, App
700	23	74.2	381	6	US-10-641-678-74	Sequence 74, Appl	773	23	74.2	446	7	US-11-102-621-123	Sequence 123, App
701	23	74.2	381	6	US-10-453-372-224	Sequence 224, App	774	23	74.2	446	7	US-11-102-621-136	Sequence 136, App
702	23	74.2	381	7	US-11-054-281-2	Sequence 2, Appl	775	23	74.2	446	7	US-11-102-621-137	Sequence 137, App
703	23	74.2	381	7	US-11-054-281-41	Sequence 41, Appl	776	23	74.2	446	7	US-11-102-621-138	Sequence 138, App
704	23	74.2	381	7	US-11-054-281-42	Sequence 42, Appl	777	23	74.2	446	7	US-11-102-621-139	Sequence 139, App
705	23	74.2	381	7	US-11-054-281-43	Sequence 43, Appl	778	23	74.2	446	7	US-11-102-621-140	Sequence 140, App
706	23	74.2	381	7	US-11-054-281-44	Sequence 44, Appl	779	23	74.2	447	7	US-11-102-621-131	Sequence 130, App
707	23	74.2	381	7	US-11-169-041-152	Sequence 152, App	780	23	74.2	447	7	US-11-102-621-130	Sequence 131, App
708	23	74.2	384	7	US-11-075-351-12	Sequence 12, Appl	781	23	74.2	447	7	US-11-102-621-132	Sequence 132, App
709	23	74.2	384	7	US-11-075-351-32	Sequence 32, Appl	782	23	74.2	447	7	US-11-102-621-133	Sequence 133, App
710	23	74.2	391	7	US-11-105-172-4	Sequence 4, Appl1	783	23	74.2	447	7	US-11-004-590-230	Sequence 230, App
711	23	74.2	391	7	US-11-242-294-50	Sequence 50, Appl	784	23	74.2	447	7	US-11-004-590-231	Sequence 231, App
712	23	74.2	397	7	US-11-192-219-47	Sequence 47, Appl	785	23	74.2	447	7	US-11-004-590-231	Sequence 231, App
713	23	74.2	397	7	US-11-192-219-47	Sequence 47, Appl	786	23	74.2	448	7	US-11-158-505-8	Sequence 8, Appl1
714	23	74.2	398	7	US-11-024-959-336	Sequence 336, App	787	23	74.2	448	7	US-11-158-505-16	Sequence 16, Appl
715	23	74.2	400	7	US-11-077-386-18	Sequence 18, Appl	788	23	74.2	448	7	US-11-158-505-32	Sequence 32, Appl
716	23	74.2	401	7	US-11-072-175-224	Sequence 26, Appl	789	23	74.2	448	7	US-11-182-908-16	Sequence 24, Appl
717	23	74.2	402	7	US-11-024-251-31	Sequence 31, Appl	790	23	74.2	448	7	US-11-182-908-16	Sequence 16, Appl
718	23	74.2	404	7	US-11-075-351-23	Sequence 23, Appl	791	23	74.2	448	7	US-11-183-205-36	Sequence 56, Appl
719	23	74.2	404	7	US-11-075-351-25	Sequence 25, Appl	792	23	74.2	449	6	US-10-763-712A-21	Sequence 21, Appl
720	23	74.2	404	7	US-11-098-686-11329	Sequence 11329, A	793	23	74.2	449	6	US-10-763-712A-104	Sequence 104, App
721	23	74.2	406	6	US-10-467-657-4964	Sequence 4964, Ap	794	23	74.2	449	7	US-11-080-587-6	Sequence 6, Appl1
722	23	74.2	406	7	US-11-072-512-3010	Sequence 3010, Ap	795	23	74.2	449	7	US-11-154-337-15	Sequence 15, Appl
723	23	74.2	410	6	US-10-821-234-952	Sequence 952, App	796	23	74.2	449	7	US-11-154-337-17	Sequence 17, Appl
724	23	74.2	410	6	US-10-763-712A-85	Sequence 85, Appl	797	23	74.2	449	7	US-11-182-908-14	Sequence 14, Appl
725	23	74.2	411	7	US-11-075-351-47	Sequence 47, Appl	798	23	74.2	449	7	US-11-182-908-32	Sequence 32, Appl
726	23	74.2	413	6	US-10-821-234-989	Sequence 989, App	799	23	74.2	449	7	US-11-177-506-32	Sequence 24, Appl
727	23	74.2	414	6	US-10-131-826A-418	Sequence 418, App	800	23	74.2	450	7	US-11-025-512-12	Sequence 12, Appl
728	23	74.2	415	7	US-11-182-946-6	Sequence 6, Appl1	801	23	74.2	450	7	US-11-077-386-20	Sequence 20, Appl
729	23	74.2	415	7	US-11-029-003-12	Sequence 12, Appl	802	23	74.2	450	7	US-11-005-726-161	Sequence 161, App
730	23	74.2	417	7	US-11-072-175-733	Sequence 233, App	803	23	74.2	450	7	US-11-049-536-701	Sequence 701, App
731	23	74.2	418	6	US-10-512-325-3	Sequence 3, Appl1	804	23	74.2	451	6	US-10-923-327-7	Sequence 9, Appl1
732	23	74.2	418	7	US-11-196-919-2	Sequence 2, Appl1	805	23	74.2	451	6	US-10-923-327-9	Sequence 11, Appl
733	23	74.2	419	7	US-11-113-302-2	Sequence 2, Appl1	806	23	74.2	451	6	US-10-923-327-11	Sequence 22, Appl
734	23	74.2	419	7	US-11-113-302-4	Sequence 4, Appl1	807	23	74.2	451	7	US-11-120-338-22	Sequence 22, Appl
735	23	74.2	419	7	US-11-113-302-53	Sequence 23, Appl	808	23	74.2	451	7	US-11-120-338-25	Sequence 25, Appl
736	23	74.2	420	6	US-10-131-826A-290	Sequence 290, App	809	23	74.2	451	7	US-11-128-900-70	Sequence 70, Appl
737	23	74.2	421	6	US-10-763-712A-2	Sequence 2, Appl1	810	23	74.2	451	7	US-11-158-505-33	Sequence 33, Appl
738	23	74.2	421	6	US-10-763-712A-7	Sequence 7, Appl1	811	23	74.2	451	7	US-11-124-620-5	Sequence 5, Appl1
739	23	74.2	421	6	US-10-763-712A-13	Sequence 13, Appl	812	23	74.2	451	7	US-11-124-620-7	Sequence 7, Appl1
740	23	74.2	421	6	US-10-763-712A-15	Sequence 15, Appl	813	23	74.2	451	7	US-11-143-077-22	Sequence 22, Appl
741	23	74.2	421	6	US-10-763-712A-41	Sequence 41, Appl	814	23	74.2	452	7	US-11-016-503-6	Sequence 6, Appl1
742	23	74.2	421	6	US-10-763-712A-103	Sequence 103, App	815	23	74.2	452	7	US-11-120-338-14	Sequence 14, Appl
743	23	74.2	421	6	US-10-453-372-220	Sequence 220, App	816	23	74.2	452	7	US-11-120-338-15	Sequence 15, Appl
744	23	74.2	423	7	US-11-080-248-4	Sequence 4, Appl1	817	23	74.2	452	7	US-11-107-028-17	Sequence 17, Appl
745	23	74.2	423	7	US-11-029-003-10	Sequence 10, Appl	818	23	74.2	452	7	US-11-107-028-32	Sequence 32, Appl
746	23	74.2	427	6	US-10-513-639-20	Sequence 20, Appl	819	23	74.2	452	7	US-11-107-028-33	Sequence 33, Appl
747	23	74.2	427	7	US-11-182-946-5	Sequence 5, Appl1	820	23	74.2	452	7	US-11-107-028-43	Sequence 43, Appl
748	23	74.2	427	7	US-11-185-878-4	Sequence 4, Appl1	821	23	74.2	452	7	US-11-107-028-45	Sequence 45, Appl
749	23	74.2	428	7	US-11-029-503-24	Sequence 24, Appl	822	23	74.2	452	7	US-11-107-028-46	Sequence 46, Appl
750	23	74.2	428	7	US-11-072-512-3675	Sequence 3675, Ap	823	23	74.2	452	7	US-11-107-028-47	Sequence 47, Appl
751	23	74.2	430	7	US-11-016-503-17	Sequence 17, Appl	824	23	74.2	452	7	US-11-106-820-26	Sequence 26, Appl
752	23	74.2	430	7	US-11-029-003-22	Sequence 22, Appl	825	23	74.2	452	7	US-11-106-820-30	Sequence 30, Appl
753	23	74.2	430	7	US-11-042-814-2	Sequence 2, Appl1	826	23	74.2	452	7	US-11-106-820-30	Sequence 30, Appl
754	23	74.2	433	6	US-10-467-657-5876	Sequence 6876, Ap	827	23	74.2	452	7	US-11-106-820-45	Sequence 45, Appl
755	23	74.2	433	6	US-10-877-346-77	Sequence 77, Appl	828	23	74.2	452	7	US-11-143-077-14	Sequence 14, Appl

829	23	74.2	452	7	US-11-143-077-15	Sequence 15, Appl	902	23	74.2	470	7	US-11-144-222-49	Sequence 49, Appl
830	23	74.2	455	7	US-11-143-077-17	Sequence 17, Appl	903	23	74.2	470	7	US-11-086-289-18	Sequence 18, Appl
831	23	74.2	452	7	US-11-016-503-14	Sequence 14, Appl	904	23	74.2	470	7	US-11-121-438-35	Sequence 35, Appl
832	23	74.2	455	7	US-11-089-803-4	Sequence 4, Appl	905	23	74.2	470	7	US-11-182-343-45	Sequence 45, Appl
833	23	74.2	455	7	US-11-218-234-4	Sequence 4, Appl	906	23	74.2	470	7	US-11-182-343-46	Sequence 46, Appl
834	23	74.2	456	5	US-09-978-360A-53	Sequence 523, App	907	23	74.2	470	7	US-11-182-343-49	Sequence 49, Appl
835	23	74.2	456	6	US-10-763-712A-44	Sequence 44, Appl	908	23	74.2	470	7	US-11-041-095-22	Sequence 22, Appl
836	23	74.2	457	6	US-10-951-236-10	Sequence 10, Appl	909	23	74.2	470	7	US-11-072-512-3730	Sequence 3730, Ap
837	23	74.2	458	6	US-10-763-712A-32	Sequence 32, Appl	910	23	74.2	471	7	US-11-086-289-6	Sequence 6, Appl
838	23	74.2	458	7	US-11-016-503-12	Sequence 12, Appl	911	23	74.2	471	7	US-11-106-820-25	Sequence 25, Appl
839	23	74.2	458	7	US-11-016-503-16	Sequence 16, Appl	912	23	74.2	471	7	US-11-106-820-27	Sequence 27, Appl
840	23	74.2	458	7	US-11-089-803-2	Sequence 2, Appl	913	23	74.2	471	7	US-11-190-364-22	Sequence 23, Appl
841	23	74.2	458	7	US-11-089-803-6	Sequence 6, Appl	914	23	74.2	471	7	US-11-190-364-23	Sequence 23, Appl
842	23	74.2	458	7	US-11-149-738-2	Sequence 2, Appl	915	23	74.2	471	7	US-11-147-780-22	Sequence 22, Appl
843	23	74.2	458	7	US-11-155-269-2	Sequence 2, Appl	916	23	74.2	471	7	US-11-147-780-23	Sequence 23, Appl
844	23	74.2	458	7	US-11-193-746-2	Sequence 2, Appl	917	23	74.2	472	7	US-11-086-289-2	Sequence 2, Appl
845	23	74.2	458	7	US-11-218-234-2	Sequence 2, Appl	918	23	74.2	472	7	US-11-086-289-10	Sequence 10, Appl
846	23	74.2	458	7	US-11-218-234-6	Sequence 6, Appl	919	23	74.2	473	7	US-11-144-224-50	Sequence 50, Appl
847	23	74.2	459	6	US-10-949-720-390	Sequence 390, App	920	23	74.2	473	7	US-11-165-141-23	Sequence 23, Appl
848	23	74.2	459	6	US-10-763-712A-70	Sequence 70, Appl	921	23	74.2	473	7	US-11-144-222-50	Sequence 50, Appl
849	23	74.2	460	6	US-10-995-561-857	Sequence 857, App	922	23	74.2	473	7	US-11-182-343-50	Sequence 50, Appl
850	23	74.2	461	7	US-11-132-285-6	Sequence 6, Appl	923	23	74.2	474	6	US-10-763-712A-47	Sequence 47, Appl
851	23	74.2	461	7	US-11-182-946-4	Sequence 4, Appl	924	23	74.2	474	6	US-11-000-463-284	Sequence 284, App
852	23	74.2	461	7	US-11-183-205-32	Sequence 32, Appl	925	23	74.2	475	7	US-11-041-095-16	Sequence 16, Appl
853	23	74.2	462	7	US-11-016-503-8	Sequence 8, Appl	926	23	74.2	476	7	US-11-008-727-22	Sequence 22, Appl
854	23	74.2	462	7	US-11-177-648-9	Sequence 9, Appl	927	23	74.2	476	7	US-11-139-499-4	Sequence 4, Appl
855	23	74.2	462	7	US-11-177-648-26	Sequence 26, Appl	928	23	74.2	476	7	US-11-139-499-12	Sequence 12, Appl
856	23	74.2	462	7	US-11-177-648-27	Sequence 27, Appl	929	23	74.2	477	7	US-11-000-463-355	Sequence 355, App
857	23	74.2	462	7	US-11-177-648-28	Sequence 28, Appl	930	23	74.2	478	7	US-11-139-499-8	Sequence 8, Appl
858	23	74.2	462	7	US-11-177-648-29	Sequence 29, Appl	931	23	74.2	478	7	US-11-072-512-3812	Sequence 3812, Ap
859	23	74.2	462	7	US-11-177-648-30	Sequence 30, Appl	932	23	74.2	482	6	US-10-821-234-972	Sequence 972, App
860	23	74.2	462	7	US-11-177-648-31	Sequence 31, Appl	933	23	74.2	484	6	US-10-467-657-5472	Sequence 5472, Ap
861	23	74.2	462	7	US-11-177-648-32	Sequence 32, Appl	934	23	74.2	484	6	US-10-763-712A-12	Sequence 12, Appl
862	23	74.2	462	7	US-11-177-648-33	Sequence 33, Appl	935	23	74.2	487	7	US-11-147-047-50	Sequence 50, Appl
863	23	74.2	462	7	US-11-177-648-79	Sequence 79, Appl	936	23	74.2	487	7	US-11-072-512-2868	Sequence 2868, Ap
864	23	74.2	462	7	US-11-177-648-92	Sequence 92, Appl	937	23	74.2	487	7	US-11-072-512-3083	Sequence 3083, Ap
865	23	74.2	462	7	US-11-177-648-93	Sequence 93, Appl	938	23	74.2	488	6	US-10-821-234-972	Sequence 1000, Ap
866	23	74.2	462	7	US-11-177-648-94	Sequence 94, Appl	939	23	74.2	489	6	US-10-835-475-11	Sequence 11, Appl
867	23	74.2	462	7	US-11-177-648-95	Sequence 95, Appl	940	23	74.2	489	7	US-11-072-512-2922	Sequence 2922, Ap
868	23	74.2	462	7	US-11-177-648-96	Sequence 96, Appl	941	23	74.2	489	7	US-11-072-512-3329	Sequence 3329, Ap
869	23	74.2	462	7	US-11-177-648-97	Sequence 97, Appl	942	23	74.2	490	6	US-10-763-712A-65	Sequence 65, Appl
870	23	74.2	462	7	US-11-177-648-98	Sequence 98, Appl	943	23	74.2	490	7	US-11-072-512-2640	Sequence 2640, Ap
871	23	74.2	463	6	US-10-821-234-1094	Sequence 1094, Ap	944	23	74.2	491	6	US-10-954-466-54	Sequence 54, Appl
872	23	74.2	463	7	US-11-128-900-1	Sequence 1, Appl	945	23	74.2	492	6	US-10-467-657-8422	Sequence 8422, Ap
873	23	74.2	463	7	US-11-128-900-4	Sequence 4, Appl	946	23	74.2	494	6	US-10-763-712A-71	Sequence 71, Appl
874	23	74.2	463	7	US-11-128-900-63	Sequence 63, Appl	947	23	74.2	494	6	US-10-763-712A-111	Sequence 111, App
875	23	74.2	463	7	US-11-128-900-64	Sequence 64, Appl	948	23	74.2	496	7	US-11-165-697-50	Sequence 50, Appl
876	23	74.2	463	6	US-11-128-900-68	Sequence 68, Appl	949	23	74.2	496	7	US-11-240-406-6	Sequence 6, Appl
877	23	74.2	464	6	US-10-763-712A-46	Sequence 46, Appl	950	23	74.2	498	7	US-11-072-512-2548	Sequence 2548, Ap
878	23	74.2	464	7	US-11-128-900-2	Sequence 2, Appl	951	23	74.2	502	7	US-11-054-281-140	Sequence 140, App
879	23	74.2	464	7	US-11-128-900-66	Sequence 66, Appl	952	23	74.2	504	6	US-10-999-789-2	Sequence 2, Appl
880	23	74.2	467	6	US-10-763-712A-19	Sequence 19, Appl	953	23	74.2	509	7	US-11-008-727-16	Sequence 16, Appl
881	23	74.2	467	7	US-11-158-505-5	Sequence 5, Appl	954	23	74.2	512	7	US-11-072-512-2978	Sequence 2978, Ap
882	23	74.2	467	7	US-11-158-505-7	Sequence 7, Appl	955	23	74.2	514	6	US-10-835-475-2	Sequence 2, Appl
883	23	74.2	467	7	US-11-158-505-13	Sequence 13, Appl	956	23	74.2	515	6	US-10-821-234-1211	Sequence 1211, Ap
884	23	74.2	467	7	US-11-158-505-15	Sequence 15, Appl	957	23	74.2	515	6	US-10-954-466-33	Sequence 33, Appl
885	23	74.2	467	7	US-11-158-505-21	Sequence 21, Appl	958	23	74.2	516	6	US-10-954-466-32	Sequence 32, Appl
886	23	74.2	467	7	US-11-158-505-23	Sequence 23, Appl	959	23	74.2	517	6	US-10-954-466-16	Sequence 16, Appl
887	23	74.2	467	7	US-11-158-505-29	Sequence 29, Appl	960	23	74.2	518	6	US-10-954-466-31	Sequence 31, Appl
888	23	74.2	467	7	US-11-158-505-31	Sequence 31, Appl	961	23	74.2	519	6	US-10-954-466-30	Sequence 30, Appl
889	23	74.2	467	7	US-11-158-505-72	Sequence 72, Appl	962	23	74.2	519	6	US-11-033-039-442	Sequence 442, App
890	23	74.2	467	7	US-11-182-908-18	Sequence 18, Appl	963	23	74.2	520	6	US-10-467-657-1992	Sequence 1992, Ap
891	23	74.2	468	6	US-10-763-712A-3	Sequence 3, Appl	964	23	74.2	520	6	US-10-954-466-13	Sequence 13, Appl
892	23	74.2	468	6	US-10-763-712A-20	Sequence 20, Appl	965	23	74.2	523	6	US-10-453-372-1006	Sequence 1006, Ap
893	23	74.2	468	6	US-10-763-712A-100	Sequence 100, App	966	23	74.2	523	6	US-10-453-372-1008	Sequence 1008, Ap
894	23	74.2	468	7	US-11-086-289-14	Sequence 14, Appl	967	23	74.2	523	7	US-11-072-512-2046	Sequence 2046, Ap
895	23	74.2	468	7	US-11-086-289-22	Sequence 22, Appl	968	23	74.2	524	7	US-11-041-095-58	Sequence 58, Appl
896	23	74.2	470	7	US-11-144-248-45	Sequence 45, Appl	969	23	74.2	525	7	US-11-102-120-13	Sequence 13, Appl
897	23	74.2	470	7	US-11-144-248-46	Sequence 46, Appl	970	23	74.2	526	7	US-11-041-095-10	Sequence 10, Appl
898	23	74.2	470	7	US-11-144-248-49	Sequence 49, Appl	971	23	74.2	526	7	US-11-072-512-3582	Sequence 3582, Ap
899	23	74.2	470	7	US-11-008-727-20	Sequence 20, Appl	972	23	74.2	528	7	US-11-024-955-343	Sequence 343, App
900	23	74.2	470	7	US-11-144-222-45	Sequence 45, Appl	973	23	74.2	530	6	US-10-995-805-4	Sequence 4, Appl
901	23	74.2	470	7	US-11-144-222-46	Sequence 46, Appl	974	23	74.2	530	7	US-11-183-136-44	Sequence 44, Appl

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975      23      74.2      530 7 US-11-098-686-11263      Sequence 11263, A
976      23      74.2      530 7 US-11-124-367A-314      Sequence 314, App
977      23      74.2      531 7 US-11-008-727-18      Sequence 18, Appl
978      23      74.2      534 7 US-11-077-386-25      Sequence 25, Appl
979      23      74.2      539 7 US-11-183-136-38      Sequence 38, Appl
980      23      74.2      541 7 US-11-072-512-2161      Sequence 2161, Ap
981      23      74.2      542 7 US-11-098-686-11331      Sequence 11331, A
982      23      74.2      544 6 US-10-980-688-40      Sequence 40, Appl
983      23      74.2      545 6 US-10-453-372-222      Sequence 222, App
984      23      74.2      548 7 US-11-022-289-3      Sequence 3, Appl1
985      23      74.2      551 7 US-11-022-289-7      Sequence 7, Appl1
986      23      74.2      551 7 US-11-022-289-8      Sequence 8, Appl1
987      23      74.2      552 6 US-10-453-372-234      Sequence 234, App
988      23      74.2      552 6 US-10-453-372-236      Sequence 236, App
989      23      74.2      552 6 US-10-453-372-238      Sequence 238, App
990      23      74.2      552 6 US-10-453-372-240      Sequence 240, App
991      23      74.2      552 6 US-10-453-372-242      Sequence 242, App
992      23      74.2      552 6 US-10-453-372-244      Sequence 244, App
993      23      74.2      552 6 US-10-453-372-246      Sequence 246, App
994      23      74.2      552 6 US-10-453-372-248      Sequence 248, App
995      23      74.2      552 6 US-10-453-372-250      Sequence 250, App
996      23      74.2      552 7 US-11-072-512-3426      Sequence 3426, Ap
997      23      74.2      553 7 US-11-103-957-43      Sequence 43, Appl
998      23      74.2      553 7 US-11-018-868-30      Sequence 30, Appl
999      23      74.2      554 6 US-10-763-712A-33      Sequence 33, Appl
1000     23      74.2      555 6 US-10-763-712A-30      Sequence 30, Appl
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ALIGNMENTS

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RESULT 1
; US-11-090-916-1
; Sequence 1, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-11-090-916-1
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Query Match      100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 CGPC 5
Db      1 CGPC 4
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RESULT 2

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US-11-144-301A-8
; Sequence 8, Application US/11144301A
; Publication No. US20050288227A1
; GENERAL INFORMATION:
; APPLICANT: Marks, Paul A.
; APPLICANT: Johanna, Ungerecht
; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
; FILE REFERENCE: 28517-501 UTIL
; CURRENT APPLICATION NUMBER: US/11/144,301A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,089
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 10/369,094
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-144-301A-8
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Query Match      100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 CGPC 5
Db      1 CGPC 4
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RESULT 3
; US-11-223-405-1
; Sequence 1, Application US/11223405
; Publication No. US20060009526A1
; GENERAL INFORMATION:
; APPLICANT: Richon, Victoria M.
; APPLICANT: Marks, Paul A.
; APPLICANT: Rifkind, Richard A.
; APPLICANT: Butler, Lisa M.
; TITLE OF INVENTION: Method of Treating TRX Mediated Diseases
; FILE REFERENCE: 3254.1005-001
; CURRENT APPLICATION NUMBER: US/11/223,405
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/369,094
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/357,383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-223-405-1
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Query Match      100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 CGPC 5
Db      1 CGPC 4
```

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RESULT 4
; US-11-223-547-1
; Sequence 1, Application US/11223547
; Publication No. US20060009527A1
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/ GENERAL INFORMATION:
/ APPLICANT: Richon, Victoria M.
/ APPLICANT: Marks, Paul A.
/ APPLICANT: Riekind, Richard A.
/ APPLICANT: Butler, Lisa M.
/ TITLE OF INVENTION: Method of Treating TRX Mediated Diseases
/ FILE REFERENCE: 3254.1005-001
/ CURRENT APPLICATION NUMBER: US/11/223,547
/ CURRENT FILING DATE: 2005-09-09
/ PRIOR APPLICATION NUMBER: US/10/369,094
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: U.S. 60/357,383
/ PRIOR FILING DATE: 2002-02-15
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-223-547-1
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Query Match          100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 CGPC 5
        ||||
DB       1 CGPC 4
```

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RESULT 5
US-11-058-926-2
/ Sequence 2, Application US/11058926
/ Publication No. US20060030022A1
/ GENERAL INFORMATION:
/ APPLICANT: BECKWITH, JONATHAN
/ APPLICANT: ASLUND, FREDRIK
/ APPLICANT: BESETTE, PAUL H.
/ APPLICANT: GEORGIOU, GEORGE
/ APPLICANT: RITZ, DANIEL
/ APPLICANT: LIM, JACKIE EUN-AH
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
/ FILE REFERENCE: HMV-052.01
/ CURRENT APPLICATION NUMBER: US/11/058,926
/ CURRENT FILING DATE: 2005-02-16
/ PRIOR APPLICATION NUMBER: US/09/679,705
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: 60/157,770
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/163,939
/ PRIOR FILING DATE: 1999-11-08
/ PRIOR APPLICATION NUMBER: 60/166,044
/ PRIOR FILING DATE: 1999-11-17
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-058-926-2
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Query Match          100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 CGPC 5
        ||||
DB       1 CGPC 4
```

```
RESULT 6
US-11-090-916-2
/ Sequence 2, Application US/11090916
/ Publication No. US20050260140A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ APPLICANT: del Val, Greg
/ APPLICANT: Lee, Rees
/ TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
/ FILE REFERENCE: 2879-98-1
/ CURRENT APPLICATION NUMBER: US/11/090,916
/ CURRENT FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: 10/660,118
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/556,516
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/650,865
/ PRIOR FILING DATE: 2005-02-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 2
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide motif
/ NAME/KEY: misc feature
/ LOCATION: (1)..(6)
/ OTHER INFORMATION: Xaa = any amino acid
US-11-090-916-2
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Query Match          100.0%; Score 31; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 CGPC 5
        ||||
DB       2 CGPC 5
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```
RESULT 7
US-11-090-916-3
/ Sequence 3, Application US/11090916
/ Publication No. US20050260140A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ APPLICANT: del Val, Greg
/ APPLICANT: Lee, Rees
/ TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
/ FILE REFERENCE: 2879-98-1
/ CURRENT APPLICATION NUMBER: US/11/090,916
/ CURRENT FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: 10/660,118
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/556,516
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/650,865
/ PRIOR FILING DATE: 2005-02-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 3
/ LENGTH: 6
/ TYPE: PRT
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ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide motif
US-11-090-916-3

Query Match 100.0%; Score 31; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 8
US-11-131-744-2
Sequence 2, Application US/11131744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHOD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 2
LENGTH: 75
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-2

Query Match 100.0%; Score 31; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 33 CGPC 36

RESULT 9
US-10-467-657-5372
Sequence 5372, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MISIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMan99, version 1.04
SEQ ID NO 5372
LENGTH: 84
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5372

Query Match 100.0%; Score 31; DB 6; Length 84;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 34 CGPC 37

RESULT 10
US-11-131-744-1
Sequence 1, Application US/11131744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHOD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 91
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-1

Query Match 100.0%; Score 31; DB 7; Length 91;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 11
US-11-074-176-286
Sequence 286, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Kjaerhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia

APPLICANT: Perill, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
FILE REFERENCE: 5051-694
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 286
LENGTH: 103
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
US-11-074-176-286

Query Match 100.0%; Score 31; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 28 CGPC 31

RESULT 12

US-11-090-916-6
Sequence 6, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 103
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-11-090-916-6

Query Match 100.0%; Score 31; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 28 CGPC 31

RESULT 13

US-11-090-916-7
Sequence 7, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof

FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 103
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-11-090-916-7

Query Match 100.0%; Score 31; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 30 CGPC 33

RESULT 14

US-11-090-916-5
Sequence 5, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 104
TYPE: PRT
ORGANISM: Porphyromonas gingivalis
US-11-090-916-5

Query Match 100.0%; Score 31; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 29 CGPC 32

RESULT 15

US-10-821-234-1371
Sequence 1371, Application US/10821234
Publication No. US20050255114A1

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; GENERAL INFORMATION:
; APPLICANT: Labach, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1371
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1371
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Query Match          100.0%; Score 31; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 CGPC 5
        ||||
Db      32 CGPC 35
```

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RESULT 16
US-11-090-916-8
; Sequence 8, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-090-916-8
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Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 CGPC 5
        ||||
Db      32 CGPC 35
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RESULT 17
US-11-090-916-9
; Sequence 9, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
```

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; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-090-916-9
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      32 CGPC 35
```

```
RESULT 18
US-11-090-916-10
; Sequence 10, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-090-916-10
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      32 CGPC 35
```

```
RESULT 19
```

US-11-090-916-11
; Sequence 11, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: Lee, Rees
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Blastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-090-916-11

Query Match 100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 20
US-11-090-916-12
; Sequence 12, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: Lee, Rees
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Blastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-916-12

Query Match 100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 32 CGPC 35
RESULT 21
US-11-106-796-13
; Sequence 13, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SITOVSKI, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UWO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-796-13

Query Match 100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 22
US-11-144-301A-9
; Sequence 9, Application US/11144301A
; Publication No. US2005028827A1
; GENERAL INFORMATION:
; APPLICANT: Marks, Paul A.
; APPLICANT: Johanna, Ungerechte
; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
; FILE REFERENCE: 28517-501 UTIL
; CURRENT APPLICATION NUMBER: US/11/144,301A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,089
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 10/369,094
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-301A-9

Query Match 100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 23
US-11-144-301A-10
; Sequence 10, Application US/11144301A
; Publication No. US2005028827A1
; GENERAL INFORMATION:

```

; APPLICANT: Marks, Paul A.
; APPLICANT: Johanna, Understedt
; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
; FILE REFERENCE: 28517-501 UTIL
; CURRENT APPLICATION NUMBER: US/11/144,301A
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,089
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 10/369,094
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-301A-10
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       32 CGPC 35
```

```

RESULT 24
US-11-032-773-943
; Sequence 943, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 943
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank BAA04881
; DATABASE ENTRY DATE: 2002-12-25
US-11-032-773-943
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       32 CGPC 35
```

```

RESULT 25
US-10-689-742-19
; Sequence 19, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racie, Lisa A
```

```

; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-19
```

```
Query Match          100.0%; Score 31; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       32 CGPC 35
```

```

RESULT 26
US-11-098-686-10612
; Sequence 10612, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10612
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10612
```

```
Query Match          100.0%; Score 31; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       30 CGPC 33
```

```

RESULT 27
US-11-090-916-4
; Sequence 4, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
```

PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/550,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 109
TYPE: PRT
ORGANISM: Pseudomonas syringae
US-11-090-916-4

Query Match 100.0%; Score 31; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 34 CGPC 37

RESULT 28
US-11-072-512-3199

Sequence 3199, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3199
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3199

Query Match 100.0%; Score 31; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 37 CGPC 40

RESULT 29
US-11-195-459-12

Sequence 12, Application US/11195459
Publication No. US20050278803A1
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent
APPLICANT: Hastings, Craig
APPLICANT: Meeley, Robert
APPLICANT: Hankke, Sabine
APPLICANT: Jung, Rudolf
APPLICANT: Everard, John
APPLICANT: Allen, Stephen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS
FILE REFERENCE: 5718-119 (035718/241421)
CURRENT APPLICATION NUMBER: US/11/195,459
CURRENT FILING DATE: 2005-08-02
PRIOR APPLICATION NUMBER: US/10/005,429
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/250,703
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 122
TYPE: PRT
ORGANISM: Zea mays
US-11-195-459-12

Query Match 100.0%; Score 31; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 40 CGPC 43

RESULT 30
US-11-195-459-16

Sequence 16, Application US/11195459
Publication No. US20050278803A1
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent
APPLICANT: Hastings, Craig
APPLICANT: Meeley, Robert
APPLICANT: Hankke, Sabine
APPLICANT: Jung, Rudolf
APPLICANT: Everard, John
APPLICANT: Allen, Stephen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS
FILE REFERENCE: 5718-119 (035718/241421)
CURRENT APPLICATION NUMBER: US/11/195,459
CURRENT FILING DATE: 2005-08-02
PRIOR APPLICATION NUMBER: US/10/005,429
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/250,703
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 122
TYPE: PRT
ORGANISM: Hordeum vulgare
US-11-195-459-16

Query Match 100.0%; Score 31; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 46 CGPC 49

```
RESULT 31
US-11-195-459-19
; Sequence 19, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Meeley, Robert
; APPLICANT: Hanke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; PRIOR FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c, g,
US-11-195-459-19
```

```
Query Match          100.0%; Score 31; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       40 CGPC 43
```

```
RESULT 32
US-11-195-459-10
; Sequence 10, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Meeley, Robert
; APPLICANT: Hanke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Zea mays
US-11-195-459-10
```

```
Query Match          100.0%; Score 31; DB 7; Length 123;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       41 CGPC 44
```

```
RESULT 33
US-10-995-561-703
; Sequence 703, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CI001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 703
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-703
```

```
Query Match          100.0%; Score 31; DB 6; Length 126;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       63 CGPC 66
```

```
RESULT 34
US-11-106-796-10
; Sequence 10, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UVM0:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-796-10
```

```
Query Match          100.0%; Score 31; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       32 CGPC 35
```

```
RESULT 35
US-11-106-796-11
; Sequence 11, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
```

```

; FILE REFERENCE: UWMO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-796-11

Query Match
Best Local Similarity 100.0%; Score 31; DB 7; Length 127;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 36
US-11-106-796-12
; Sequence 12, Application US/11/106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UWMO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 127
; TYPE: PRT
; ORGANISM: RAT
US-11-106-796-12

Query Match
Best Local Similarity 100.0%; Score 31; DB 7; Length 127;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 37
US-10-467-657-4354
; Sequence 4354, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMin99, version 1.04
; SEQ ID NO 4354
; LENGTH: 129
; TYPE: PRT
```

```

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4354

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 129;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 53 CGPC 56

RESULT 38
US-11-072-512-2145
; Sequence 2145, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUDOKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTAKO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARA, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2145
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2145

Query Match
Best Local Similarity 100.0%; Score 31; DB 7; Length 129;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 74 CGPC 77

RESULT 39
US-11-090-916-13
; Sequence 13, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
```

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; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-090-916-13
```

```

Query Match          100.0%; Score 31; DB 7; Length 134;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      60 CGPC 63
```

```

RESULT 40
US-11-195-459-8
; Sequence 8, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Mealey, Robert
; APPLICANT: Hanke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; PRIOR FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Zea mays
US-11-195-459-8
```

```

Query Match          100.0%; Score 31; DB 7; Length 134;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      55 CGPC 58
```

```

RESULT 41
US-09-978-360A-641
; Sequence 641, Application US/0978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dunas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueterec, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
```

```

; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.USA.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 641
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41...-1
US-09-978-360A-641
```

```

Query Match          100.0%; Score 31; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      133 CGPC 136
```

```

RESULT 42
US-11-090-916-14
; Sequence 14, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
```

US-11-090-916-14

Query Match 100.0%; Score 31; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 89 CGPC 92

RESULT 43

US-11-090-916-15

; Sequence 15, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Reese
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 15
; TYPE: PRT
; LENGTH: 172
; ORGANISM: Oryza sativa
US-11-090-916-15

Query Match 100.0%; Score 31; DB 7; Length 172;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 95 CGPC 98

RESULT 44

US-11-131-744-3

; Sequence 3, Application US/11131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHBOB R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADGHI, MEHRNOOSH
; APPLICANT: LIANG, XIQUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26

; PRIOR APPLICATION NUMBER: 60/621,686

; PRIOR FILING DATE: 2004-10-26

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Patentin Ver. 3.3

; SEQ ID NO 3

; LENGTH: 177

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-11-131-744-3

Query Match 100.0%; Score 31; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 45

US-10-467-962B-6

; Sequence 6, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunmar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patentin Vers. 2.0
; SEQ ID NO 6
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-6

Query Match 100.0%; Score 31; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 106 CGPC 109

RESULT 46

US-10-995-561-643

; Sequence 643, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 643
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-643

Query Match 100.0%; Score 31; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 143 CGPC 146

RESULT 47
US-10-995-561-642
; Sequence 642, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-642

Query Match 100.0%; Score 31; DB 6; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 143 CGPC 146

RESULT 48
US-11-064-774A-2
; Sequence 2, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Aitalo et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH
; TITLE OF INVENTION: FACTOR DNAs AND PROTEINS
; FILE REFERENCE: 28967/35977B2
; CURRENT APPLICATION NUMBER: US/11/064,774A
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-774A-2

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 143 CGPC 146

RESULT 49
US-11-075-400-2
; Sequence 2, Application US/11075400
; Publication No. US20050282233A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, et al.
; TITLE OF INVENTION: MULTIVALENT ANTIBODY MATERIALS AND METHODS FORVEGF/PDGF FAMILY OF
; TITLE OF INVENTION: GROWTH FACTORS
; FILE REFERENCE: 28967/39820B
; CURRENT APPLICATION NUMBER: US/11/075,400
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,511
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/586,662
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-400-2

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 143 CGPC 146

RESULT 50
US-11-226-005-4
; Sequence 4, Application US/11226005
; Publication No. US20060014252A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D. et al.
; TITLE OF INVENTION: Flk-1 Binding Protein
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/226,005
; FILING DATE: 14-Sep-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,868
; FILING DATE: 05-NOV-1996
; APPLICATION NUMBER: 08/554,374
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
IMMEDIATE SOURCE:
CLONE: Hu VEGF
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-226-005-4

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 143 CGPC 146

RESULT 51
US-11-129-076-9
; Sequence 9, Application US/11129076
; Publication No. US20060019891A1
; GENERAL INFORMATION:
; APPLICANT: Edelman, Jay A.
; APPLICANT: Kaymarden, Munirva
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Protection of Cardiac Myocardium
; FILE REFERENCE: 1676.009US1
; CURRENT APPLICATION NUMBER: US/11/129,076
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-129-076-9

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 143 CGPC 146

RESULT 52
US-11-145-494-2
; Sequence 2, Application US/11145494
; Publication No. US20060024785A1
; GENERAL INFORMATION:
; APPLICANT: Keyt, Bruce A.
; APPLICANT: Nguyen, Francis H.
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING VARIANTS OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: CELL GROWTH FACTOR
; FILE REFERENCE: A-62326-2
; CURRENT APPLICATION NUMBER: US/11/145,494
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US/09/346,069
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 08/567,200
; PRIOR FILING DATE: 1995-12-05
; PRIOR APPLICATION NUMBER: 60/002,827
; PRIOR FILING DATE: 1995-08-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Bovine
US-11-145-494-2

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 143 CGPC 146

RESULT 53
US-11-075-047A-81
; Sequence 81, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
; APPLICANT: ALITALO, et al.
; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
; FILE REFERENCE: 28967/39700A
; CURRENT APPLICATION NUMBER: US/11/075,047A
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,907
; PRIOR FILING DATE: 2004-03-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-047A-81

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 143 CGPC 146

RESULT 54
US-11-098-686-11017
; Sequence 11017, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11017
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11017

Query Match 100.0%; Score 31; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 10 CGPC 13

RESULT 55
US-10-467-657-8494
; Sequence 8494, Application US/10467657

```
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CITRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 8494
/ LENGTH: 209
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8494

Query Match          100.0%; Score 31; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      102 CGPC 105

RESULT 56
US-10-995-561-640
/ Sequence 640, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 640
/ LENGTH: 209
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-640

Query Match          100.0%; Score 31; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      161 CGPC 164

RESULT 57
US-10-995-561-645
/ Sequence 645, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
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/ SEQ ID NO 645
/ LENGTH: 215
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-645

Query Match          100.0%; Score 31; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      167 CGPC 170

RESULT 58
US-10-995-561-646
/ Sequence 646, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 646
/ LENGTH: 215
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-646

Query Match          100.0%; Score 31; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      167 CGPC 170

RESULT 59
US-11-149-462-3
/ Sequence 3, Application US/11149462
/ Publication No. US20060002978A1
/ GENERAL INFORMATION:
/ APPLICANT: Shea, Lonnie D.
/ APPLICANT: Shea, Lonnie L.
/ APPLICANT: Whitteley, Kevin
/ APPLICANT: Yang, Yang
/ APPLICANT: Rives, Christopher
/ APPLICANT: Rovedo, Mark
/ APPLICANT: Iskandar, Bernans
/ TITLE OF INVENTION: Biodegradable Scaffolds and Uses Thereof
/ FILE REFERENCE: 1720-1-011N
/ CURRENT APPLICATION NUMBER: US/11/149,462
/ CURRENT FILING DATE: 2005-06-09
/ PRIOR APPLICATION NUMBER: 60/578,785
/ PRIOR FILING DATE: 2004-06-10
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 215
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-149-462-3

Query Match          100.0%; Score 31; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 CGPC 5
Db 167 CGPC 170

RESULT 60

US-11-106-399-8
; Sequence 8, Application US/11106399
; Publication No. US2006002892A1
; GENERAL INFORMATION:
; APPLICANT: MATHEW, FORUNNELLOOR A.
; APPLICANT: BOLES, KENT S.
; TITLE OF INVENTION: LIT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/106,399
; CURRENT FILING DATE: 2005-04-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-399-8

Query Match 100.0%; Score 31; DB 7; Length 216;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 96 CGPC 99

RESULT 61

US-11-072-512-3343
; Sequence 3343, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASHIO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3343
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3343

Query Match 100.0%; Score 31; DB 7; Length 224;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 28 CGPC 31

RESULT 62

US-10-995-561-641
; Sequence 641, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-641

Query Match 100.0%; Score 31; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 184 CGPC 187

RESULT 63

US-10-995-561-644
; Sequence 644, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 644
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-644

Query Match 100.0%; Score 31; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 184 CGPC 187

RESULT 64

US-11-153-880-7
; Sequence 7, Application US/11153880
; Publication No. US20050256050A1
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN

```
/ APPLICANT: ROSEN, CRAIG A.
/ APPLICANT: CAO, LIANG
/ TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
/ STREET: 1100 NEW YORK AVENUE
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/153,880
/ FILING DATE: 16-Jun-2005
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/219,442
/ FILING DATE: 23-DEC-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/999,811
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/465,968
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MARKOWICZ, KAREN R.
/ REGISTRATION NUMBER: 36/351
/ REFERENCE/DOCKET NUMBER: 1488.1000004
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)371-2600
/ TELEFAX: (202)371-2540
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 232 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: Not Relevant
/ MOLECULE TYPE: protein
/ US-11-153-880-7

Query Match          100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      184 CGPC 187

RESULT 65
US-11-064-774A-147
/ Sequence 147, Application US/11064774A
/ Publication No. US20050267024A1
/ GENERAL INFORMATION:
/ APPLICANT: Altalo et al.
/ TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH
/ FILE REFERENCE: 28967/3597B2
/ CURRENT APPLICATION NUMBER: US/11/064,774A
/ PRIOR FILING DATE: 2005-02-24
/ PRIOR APPLICATION NUMBER: 09/795,006
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: US 60/205,331
/ PRIOR FILING DATE: 2000-05-18
/ PRIOR APPLICATION NUMBER: US 60/185,205
/ PRIOR FILING DATE: 2000-02-25
/ NUMBER OF SEQ ID NOS: 1212
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/ SOFTWARE: Patent In Ver. 3.2
/ SEQ ID NO 147
/ LENGTH: 232
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-064-774A-147

Query Match          100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      184 CGPC 187

RESULT 66
US-11-211-724-5
/ Sequence 5, Application US/11211724
/ Publication No. US20050287143A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
/ FILE REFERENCE: PF112P1
/ CURRENT APPLICATION NUMBER: US/11/211,724
/ PRIOR FILING DATE: 2005-08-26
/ PRIOR APPLICATION NUMBER: US/08/465,968
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: 08/207,550
/ PRIOR FILING DATE: 1994-03-08
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 232
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-211-724-5

Query Match          100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      184 CGPC 187

RESULT 67
US-11-233-119-7
/ Sequence 7, Application US/11233119
/ Publication No. US20060025331A1
/ GENERAL INFORMATION:
/ APPLICANT: HU, JING-SHAN et al.
/ TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
/ FILE REFERENCE: PF112PAD1
/ CURRENT APPLICATION NUMBER: US/11/233,119
/ PRIOR FILING DATE: 2005-09-23
/ PRIOR APPLICATION NUMBER: 09/107,997
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: 09/042,105
/ PRIOR FILING DATE: 1998-03-13
/ PRIOR APPLICATION NUMBER: 09/999,811
/ PRIOR FILING DATE: 1997-12-24
/ PRIOR APPLICATION NUMBER: 08/465,968
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: 08/207,550
/ PRIOR FILING DATE: 1994-03-08
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: Patent In version 3.0
/ SEQ ID NO 7
/ LENGTH: 232
/ TYPE: PRT
/ ORGANISM: homo sapiens
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US-11-233-119-7

Query Match 100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
1111
DB 184 CGPC 187

RESULT 68

US-11-075-047A-91
; Sequence 91, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
; APPLICANT: ALITALO, et al.
; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
; FILE REFERENCE: 28967/39700A
; CURRENT APPLICATION NUMBER: US/11/075,047A
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,907
; PRIOR FILING DATE: 2004-03-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-047A-91

Query Match 100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
1111
DB 184 CGPC 187

RESULT 69

US-11-131-744-6
; Sequence 6, Application US/11131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHOD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADEGHI, MEHRMOOSH
; APPLICANT: LIANG, XIYUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: 60/621,686
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: protein sequence
US-11-131-744-6

Query Match 100.0%; Score 31; DB 7; Length 273;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
1111
DB 32 CGPC 35

RESULT 70

US-11-186-284-85
; Sequence 85, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-85

Query Match 100.0%; Score 31; DB 7; Length 282;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
1111
DB 32 CGPC 35

Search completed: February 23, 2006, 00:48:08
Job time : 16.5 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:31:07 ; Search time 142 Seconds
(without alignments)
18.565 Million cell updates/sec

Title: US-10-660-118a-3

Perfect score: 47

Sequence: 1 WGSPPCK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq 21:*

- 1: geneseqp1980s:**
- 2: geneseqp1990s:**
- 3: geneseqp2000s:**
- 4: geneseqp2001s:**
- 5: geneseqp2002s:**
- 6: geneseqp2003as:**
- 7: geneseqp2003bs:**
- 8: geneseqp2004s:**
- 9: geneseqp2005s:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
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2	47	100.0	6	5 ABP54936	Active si
3	47	100.0	6	6 ADA08451	Mammalian
4	47	100.0	6	8 ADM32929	Amino aci
5	47	100.0	6	8 ADP87509	Thioredox
6	47	100.0	6	8 ADP67423	Thioredox
7	47	100.0	6	8 ADP97008	Thioredox
8	47	100.0	12	2 AAM45003	Immunomod
9	47	100.0	12	2 AAY09429	Immunomod
10	47	100.0	52	4 AAU08670	Thioredox
11	47	100.0	80	2 AAR42822	RECEP 84.
12	47	100.0	84	2 AAR42821	RECEP 84.
13	47	100.0	84	7 ADJ68506	Human hea
14	47	100.0	91	5 ABP60794	Human hea
15	47	100.0	95	4 AAB49948	Thiocapsa
16	47	100.0	102	5 ABP60779	A. oryzae
17	47	100.0	102	5 ABP60755	Mycoplasma
18	47	100.0	102	5 ABP60756	Mytilus
19	47	100.0	102	5 ABP60753	Chlamydia
20	47	100.0	102	5 ABP60777	Chlamydia
21	47	100.0	102	6 ADB09186	Mycoplasma
22	47	100.0	103	5 ABP60747	Bacillus
23	47	100.0	103	5 ABG93246	C. albica
24	47	100.0	103	5 ABG93156	S. cerevi

25	47	100.0	103	5 ABG93328	Abg93328 C. albica
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27	47	100.0	103	6 ABR41607	Abri41607 Human DIT
28	47	100.0	103	8 ADK90669	Adk90669 Baker's Y
29	47	100.0	103	8 ADM32933	Adm32933 Amino aci
30	47	100.0	104	2 AAR42820	Aar42820 RECEP 104
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32	47	100.0	104	2 AAR72389	Aar72389 Recombina
33	47	100.0	104	5 AAG80708	Ag80708 S. cerevi
34	47	100.0	104	5 ABP60827	Abp60827 Staphyloc
35	47	100.0	104	5 ABP60803	Abp60803 Homo sepi
36	47	100.0	104	5 ABP60797	Abp60797 Bos tauru
37	47	100.0	104	5 ABP60812	Abp60812 Ovis arie
38	47	100.0	104	5 ABP60805	Abp60805 Mus muscu
39	47	100.0	104	5 ABP60806	Abp60806 Mus muscu
40	47	100.0	104	5 ABP60809	Abp60809 Oryctolag
41	47	100.0	104	5 ABP60810	Abp60810 Rattus no
42	47	100.0	104	5 ABP60801	Abp60801 Gallus ga
43	47	100.0	104	5 ABG93115	Abg93115 S. cerevi
44	47	100.0	104	8 ADK90667	Adk90667 Baker's Y
45	47	100.0	104	8 ADO59801	Ado59801 B. subtil
46	47	100.0	104	8 ADS88157	Ad88157 Human pro
47	47	100.0	105	1 AAP92141	Aap92141 Recombina
48	47	100.0	105	2 AAR42819	Aar42819 RECEP/thio
49	47	100.0	105	2 AAR37700	Aar37700 ADF. 11/1
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51	47	100.0	105	2 AAR72390	Aar72390 Recombina
52	47	100.0	105	2 AAM69567	Aam69567 Human thl
53	47	100.0	105	2 AAY25908	Aay25908 Human thl
54	47	100.0	105	3 AAG03956	Aag03956 Human sec
55	47	100.0	105	5 ABP60700	Abp60700 Human thl
56	47	100.0	105	5 ABP60757	Abp60757 Corynebac
57	47	100.0	105	5 ABG93363	Abg93363 Human Bax
58	47	100.0	105	6 ABO07225	Ab007225 Human p53
59	47	100.0	105	6 ABR92158	Abri92158 Human cer
60	47	100.0	105	7 ADF67269	Adf67269 Thioredox
61	47	100.0	105	7 ADF30728	Adf30728 Rat angio
62	47	100.0	105	7 ADJ70213	Adj70213 Human hea
63	47	100.0	105	8 ADJ47593	Adj47593 Wild-type
64	47	100.0	105	8 ADI82895	Adi82895 Human PRO
65	47	100.0	105	8 ADM32938	Adm32938 Amino aci
66	47	100.0	105	8 ADM32935	Adm32935 Amino aci
67	47	100.0	105	8 ADM32936	Adm32936 Amino aci
68	47	100.0	105	8 ADM32937	Adm32937 Amino aci
69	47	100.0	105	8 ADM32934	Adm32934 Amino aci
70	47	100.0	105	8 ADO19655	Ado19655 Human PRO
71	47	100.0	105	8 ADP54775	Adp54775 Human PRO
72	47	100.0	105	8 ADR49671	Adr49671 Murine th
73	47	100.0	105	8 ADP24148	Adp24148 PRO polyP
74	47	100.0	105	8 ADP08493	Adp08493 Wild-type
75	47	100.0	105	8 ADU06404	Adu06404 Novel bro
76	47	100.0	105	9 ADY19738	Ady19738 PRO polyP
77	47	100.0	105	9 ADY16038	Ady16038 PRO polyP
78	47	100.0	105	9 ADW97622	Adw97622 Human thl
79	47	100.0	105	9 AEB30735	Aeb30735 Therapeut
80	47	100.0	106	4 ABB60239	Abb60239 Drosophill
81	47	100.0	106	5 AAO22592	Aao22592 106-mer H
82	47	100.0	106	5 ABE60783	Abp60783 Penicilli
83	47	100.0	106	5 ABE60827	Abp60827 Manduca s
84	47	100.0	106	5 ABE60778	Abp60778 Streptomy
85	47	100.0	106	5 ABE60774	Abp60774 Helicobac
86	47	100.0	107	4 ABB60478	Abb60478 Drosophill
87	47	100.0	107	5 ABB60802	Abp60802 Drosophill
88	47	100.0	107	5 ABE60772	Abp60772 Haemophil
89	47	100.0	107	5 ABE60760	Abp60760 Chromatiu
90	47	100.0	107	6 ABM71327	Abm71327 Staphyloc
91	47	100.0	108	5 ABG70953	Abg70953 Escherich
92	47	100.0	108	5 ABG70952	Abg70952 Escherich
93	47	100.0	108	5 ABE60784	Abp60784 Pseudomon
94	47	100.0	108	5 ABE60768	Abp60768 Escherich
95	47	100.0	108	5 ABE60793	Abp60793 Thioabaci
96	47	100.0	108	7 ABM73822	Abm73822 DNA clone
97	47	100.0	109	2 AAR15646	Aar15646 Thioredox

98	47	100.0	109	2	AAR75767	Aar75767	His-patch	171	47	100.0	166	2	AAW59886	Aaw59886	Amino aci
99	47	100.0	109	2	AAR75769	Aar75769	E. coli t	172	47	100.0	166	2	AAW49006	Aaw49006	Human thi
100	47	100.0	109	2	AAR75768	Aar75768	Histidine	173	47	100.0	166	5	ABP41978	Abp41978	Human ova
101	47	100.0	109	2	AAI25383	Aay25383	Plasmid p	174	47	100.0	166	5	ABP60804	Abp60804	Homo sapi
102	47	100.0	109	3	AAI02639	Aay02639	Thioredox	175	47	100.0	166	5	ABP60798	Abp60798	Bos tauri
103	47	100.0	109	3	AAAB3553	Aab23553	Thioredox	176	47	100.0	166	5	ABP60807	Abp60807	Mus muscu
104	47	100.0	109	5	ABAB7949	Aab7949	Thioredox	177	47	100.0	166	7	ADBE2952	Aade2952	Rattus no
105	47	100.0	109	5	ABP60698	Abp60698	Escherich	178	47	100.0	167	4	AAAB8523	Aab8523	Thioredox
106	47	100.0	109	5	ABP60744	Abp60744	Aspergill	179	47	100.0	167	4	AAAB8525	Aab8525	Thioredox
107	47	100.0	109	6	ABJ26015	Abj26015	Aspergill	180	47	100.0	170	3	AAAG09381	Aag09381	Arabidops
108	47	100.0	109	6	ABJ25415	Abj25415	Aspergill	181	47	100.0	170	3	AAAG75114	Aag75114	Thioredox
109	47	100.0	109	6	ADOS9277	Ados9277	E. coli t	182	47	100.0	170	8	AD033544	Ado33544	Thioredox
110	47	100.0	109	8	ADJ57878	Adj57878	E. coli t	183	47	100.0	170	8	AD033539	Ado33539	Thioredox
111	47	100.0	109	8	ADMS2930	Adms2930	Amino aci	184	47	100.0	170	9	ADZ66909	Adz66909	Tx-DP-TM
112	47	100.0	109	8	ADOS9803	Ados9803	E. coli m	185	47	100.0	170	9	ADZ66912	Adz66912	Tx-DP-TM
113	47	100.0	109	9	ADZ66900	Adz66900	Thioredox	186	47	100.0	170	9	ADZ66915	Adz66915	Tx-DP-TM
114	47	100.0	109	9	ABE68327	Ab68327	E. coli t	187	47	100.0	170	9	ADZ66906	Adz66906	Tx-DP-TM
115	47	100.0	109	9	ABE68327	Ab68327	E. coli t	188	47	100.0	170	9	ADZ66906	Adz66906	Tx-DP-TM
116	47	100.0	111	4	ABBS9805	Abbs9805	Drosophil	189	47	100.0	171	3	AAAG73357	Aag73357	Arabidops
117	47	100.0	111	5	ABP39014	Abp39014	Staphyloc	190	47	100.0	171	3	AAAG52358	Aag52358	Arabidops
118	47	100.0	111	5	ABB77457	Abb77457	Fungi str	191	47	100.0	172	1	AAAP94809	Aap94809	Human int
119	47	100.0	111	8	ADSO6336	Adso6336	Staphyloc	192	47	100.0	173	7	ABM86658	Abm86658	Rice abio
120	47	100.0	112	5	ABP60738	Abp60738	Chlamydom	193	47	100.0	177	3	ADCI4129	Adci4129	Chimeric
121	47	100.0	112	5	ABP60780	Abp60780	Mycobacte	194	47	100.0	177	3	ABP60714	Abp60714	Brassicic
122	47	100.0	115	5	ABP60781	Abp60781	Mycobacte	195	47	100.0	178	3	AAAG19366	Aag19366	Arabidops
123	47	100.0	115	5	ABP60799	Abp60799	Caenorhab	196	47	100.0	178	5	ABP60703	Abp60703	Arabidops
124	47	100.0	116	7	ABM85632	Abm85632	Mouse pro	197	47	100.0	178	8	ADN74765	Adn74765	Thale cre
125	47	100.0	117	5	ABP60749	Abp60749	Borrelia	198	47	100.0	179	3	AAAG30359	Aag30359	Arabidops
126	47	100.0	118	5	ABP60733	Abp60733	Nicotiana	199	47	100.0	179	5	ABP60710	Abp60710	Arabidops
127	47	100.0	120	5	ADP70794	Adp70794	Minicell	200	47	100.0	179	7	ADG46659	Adg46659	Arabidops
128	47	100.0	120	7	ADP70792	Adp70792	Minicell	201	47	100.0	181	5	AAAG09380	Aag09380	Arabidops
129	47	100.0	120	7	ADP70791	Adp70791	Minicell	202	47	100.0	181	5	ABP60719	Abp60719	Spinacia
130	47	100.0	120	7	ADP70793	Adp70793	Minicell	203	47	100.0	182	3	AAAG52357	Aag52357	Arabidops
131	47	100.0	122	7	ADPFO4112	Adfo4112	Bacterial	204	47	100.0	182	3	AAAG27356	Aag27356	Arabidops
132	47	100.0	124	4	AAAG3165	Aag3165	C. glutami	205	47	100.0	182	5	ABP60707	Abp60707	Brassicic
133	47	100.0	124	7	ABO61500	Abo61500	Klebsiell	206	47	100.0	182	5	ABP60705	Abp60705	Brassicic
134	47	100.0	124	7	ABO61500	Abo61500	Klebsiell	207	47	100.0	182	8	ADN74793	Adn74793	Thale cre
135	47	100.0	125	7	ABM85633	Abm85633	Human pro	208	47	100.0	183	8	ADY72703	Ady72703	Tx-Conot
136	47	100.0	127	4	ABG18304	Abg18304	Novel hum	209	47	100.0	184	3	AAAG38661	Aag38661	Plant pol
137	47	100.0	127	5	ABP60782	Abp60782	Neurospor	210	47	100.0	185	5	ABP60704	Abp60704	Arabidops
138	47	100.0	129	6	ABP78912	Abp78912	N. gonorr	211	47	100.0	185	6	ABU01415	Abu01415	S. pneumo
139	47	100.0	129	6	ABD69961	Abd69961	C. neofor	212	47	100.0	185	8	ADK48707	Adk48707	Streptoco
140	47	100.0	130	5	ABP60787	Abp60787	Rickettsi	213	47	100.0	185	8	ADT56788	Adt56788	Plant pol
141	47	100.0	132	7	ADCC3012	Adcc3012	Human nov	214	47	100.0	185	8	ADT56140	Adt56140	Plant pol
142	47	100.0	133	7	ADP70773	Adp70773	Minicell	215	47	100.0	186	3	AAAG1897	Aag1897	Arabidops
143	47	100.0	134	3	ADCI4128	Adci4128	Human thi	216	47	100.0	186	5	ABP60711	Abp60711	Arabidops
144	47	100.0	137	2	AAW55082	Aaw55082	Streptoco	217	47	100.0	187	7	ABM90060	Abm90060	Rice abio
145	47	100.0	137	5	ABP54576	Abp54576	S. pneumo	218	47	100.0	187	7	ABM90236	Abm90236	Rice abio
146	47	100.0	137	7	ADCC45121	Adcc45121	S. pneumo	219	47	100.0	190	5	ABP60708	Abp60708	Spinacia
147	47	100.0	140	3	AAAG09942	Aag09942	Arabidops	220	47	100.0	191	5	ABP60706	Abp60706	Meembrya
148	47	100.0	140	3	AAAG37258	Aag37258	Arabidops	221	47	100.0	191	6	ABP81583	Abp81583	Streptoco
149	47	100.0	140	3	AAAG37257	Aag37257	Arabidops	222	47	100.0	194	8	ADP96469	Adp96469	Novel S.
150	47	100.0	140	3	AAAG38662	Aag38662	Arabidops	223	47	100.0	194	9	AEA60339	Aea60339	Streptoco
151	47	100.0	140	3	AAAG10594	Aag10594	Arabidops	224	47	100.0	196	8	ADH89354	Adh89354	Colias eu
152	47	100.0	140	5	ABP60814	Abp60814	Arabidops	225	47	100.0	206	8	ADH89864	Adh89864	Fusio pr
153	47	100.0	145	5	ABP60759	Abp60759	Corynebac	226	47	100.0	209	2	AAAR31931	Aar31931	Human TC-
154	47	100.0	145	6	ADAA34073	Adaa34073	Acinetoba	227	47	100.0	209	5	ABBT79754	Abb79754	Thioredox
155	47	100.0	147	3	AAAG30361	Aag30361	Arabidops	228	47	100.0	210	4	AAAB05136	Aab05136	Human T c
156	47	100.0	152	3	AAAG41898	Aag41898	Arabidops	229	47	100.0	222	8	ADY90428	Ady90428	Plant ful
157	47	100.0	154	7	ADP70797	Adp70797	PMFX-91 M	230	47	100.0	227	4	ABG29563	Abg29563	Novel hum
158	47	100.0	154	7	ADP70798	Adp70798	PMFX-96 M	231	47	100.0	232	8	ADP49017	Adp49017	HTLV-II g
159	47	100.0	154	7	ADP70795	Adp70795	PMFX-80 M	232	47	100.0	252	8	ADP49016	Adp49016	HTLV-I gp
160	47	100.0	154	7	ADP70796	Adp70796	PMFX-81 M	233	47	100.0	263	7	ADMO4124	Admo4124	Human pro
161	47	100.0	155	5	ABB97761	Abb97761	Human sec	234	47	100.0	265	2	AAW26620	Aaw26620	Thioredox
162	47	100.0	159	5	ABBT7952	Abb7952	Thioredox	235	47	100.0	271	8	AD119301	Ad119301	Ag2/PRA1-
163	47	100.0	161	8	AD033540	Ado33540	Thioredox	236	47	100.0	274	9	ADW47875	Adw47875	Respirato
164	47	100.0	161	9	ADZ66921	Adz66921	Tx-DP-TM	237	47	100.0	274	9	ADW47873	Adw47873	Respirato
165	47	100.0	161	9	ADZ66918	Adz66918	Tx-DP-TM	238	47	100.0	281	4	AAAB49947	Aab49947	A. cryzae
166	47	100.0	162	5	AAAG30360	Aag30360	Arabidops	239	47	100.0	283	3	ADW47881	Adw47881	Respirato
167	47	100.0	164	5	ADP41742	Adp41742	Human ova	240	47	100.0	283	9	ADW47877	Adw47877	Respirato
168	47	100.0	165	8	AD119317	Ad119317	Coccidiot	241	47	100.0	283	9	ADW47883	Adw47883	Respirato
169	47	100.0	165	8	ADW47601	Adw47601	Wild-type	242	47	100.0	283	9	ADW47879	Adw47879	Respirato
170	47	100.0	166	2	AAW59885	Aaw59885	Amino aci	243	47	100.0	284	5	ABP60840	Abp60840	Caenorhab

244	47	100.0	287	4	ABB61581	Abb61581 Drosophil	317	47	100.0	591	7	ADB67536	Adb67536 Human WT1
245	47	100.0	287	5	ABP60841	Abp60841 Drosophil	318	47	100.0	591	7	ADJ80769	Adj80769 Wilm's tu
246	47	100.0	290	5	ABP60837	Abp60837 Schistos	319	47	100.0	591	8	ADJ83689	Adj83689 Human WT1
247	47	100.0	296	2	AAR26213	Aar26213 Fusion pr	320	47	100.0	591	8	ADL57577	Adl57577 Human Ttx
248	47	100.0	296	2	AAR26051	Aar26051 Thioresox	321	47	100.0	591	8	ADO09132	Ado09132 Human Ttx
249	47	100.0	296	2	AAR45916	Aar45916 E.coli ch	322	47	100.0	602	8	ADM30972	Adm30972 Human Ttx
250	47	100.0	296	2	AAR50177	Aar50177 Thioresox	323	47	100.0	602	8	ADM30974	Adm30974 Human Ttx
251	47	100.0	296	2	AAR50177	Aar50177 Thioresox	324	47	100.0	602	8	ADM30970	Adm30970 Human Ttx
252	47	100.0	296	2	AAR76812	Aar76812 Thioresox	325	47	100.0	602	8	ADM30976	Adm30976 Human Ttx
253	47	100.0	323	6	AAO20588	Aao20588 Thioresox	326	47	100.0	602	8	AAM50661	Aam50661 Thioresox
254	47	100.0	323	6	AAO26516	Aao26516 Human thl	327	47	100.0	824	5	AAM48247	Aam48247 Thioresox
255	47	100.0	330	8	ADM30905	Adm30905 Human thl	328	47	100.0	824	7	ADC29712	Adc29712 A. thalia
256	47	100.0	330	8	ABP53264	Abp53264 Human MDD	329	47	100.0	858	7	ADG75020	Adg75020 Human Her
257	47	100.0	330	8	ADC13143	Adc13143 Human nov	330	47	100.0	1285	7	ADP70776	Adp70776 Male(1-37
258	47	100.0	333	8	ADR86213	Adr86213 Aspergill	331	47	100.0	1285	2	AAW47000	Aaw47000 HIS tagge
259	47	100.0	342	5	ABG33381	Abg33381 Human Ttx	332	44	93.6	19	5	AAE23038	Aae23038 Human thl
260	47	100.0	342	7	ADB67534	Adb67534 Human WT1	333	44	93.6	71	4	AAU23152	Aau23152 Novel hum
261	47	100.0	342	7	ADJ80767	Adj80767 Wilm's tu	334	44	93.6	71	4	AAW84127	Aaw84127 Human lmm
262	47	100.0	342	8	ADJ83687	Adj83687 Human WT1	335	44	93.6	71	4	AAU87497	Aau87497 Novel can
263	47	100.0	342	8	ADL57575	Adl57575 Human Ttx	336	44	93.6	88	5	ADL54812	Adl54812 Novel hum
264	47	100.0	342	8	ADO09130	Ado09130 Human Ttx	337	44	93.6	88	5	ABP60767	Abp60767 Dicyoste
265	47	100.0	355	6	ABRS4578	Abrs4578 Prostate	338	44	93.6	88	5	ABP60766	Abp60766 Dicyoste
266	47	100.0	355	7	ADB14461	Adb14461 Fusion co	339	44	93.6	89	3	AAQ44849	Aaq44849 Zea maye
267	47	100.0	355	7	ADG26984	Adg26984 Human pro	340	44	93.6	102	2	AAV35279	Aav35279 Chlamydia
268	47	100.0	366	9	ADY61037	Ady61037 Abiotic s	341	44	93.6	102	5	ABP60754	Abp60754 Chlamydia
269	47	100.0	374	6	ABP72770	Abp72770 Thioresox	342	44	93.6	102	5	ABP60723	Abp60723 Cyanidios
270	47	100.0	402	5	ABG67266	Abg67266 Polychoa	343	44	93.6	102	5	AAU09439	Aau09439 Chlamydo
271	47	100.0	407	5	ABG67270	Abg67270 Polychoa	344	44	93.6	103	5	ABP60775	Abp60775 Listeria
272	47	100.0	407	5	ABG67267	Abg67267 Polychoa	345	44	93.6	103	5	ABB48334	Abb48334 Listeria
273	47	100.0	408	2	AAW84315	Aaw84315 TrxA-rabb	346	44	93.6	103	8	ADM32932	Adm32932 Amino aci
274	47	100.0	410	5	ABG33382	Abg33382 Human Ttx	347	44	93.6	104	5	ABR30470	Abp30470 Streptoco
275	47	100.0	410	7	ADB67535	Adb67535 Human WT1	348	44	93.6	104	5	ABBS4990	Abbs4990 Lactococc
276	47	100.0	410	7	ADJ80768	Adj80768 Wilm's tu	349	44	93.6	104	5	ABP60785	Abp60785 Rhodospir
277	47	100.0	410	8	ADJ83688	Adj83688 Human WT1	350	44	93.6	104	6	ABU02257	Abu02257 S. pneumo
278	47	100.0	410	8	ADL57576	Adl57576 Human Ttx	351	44	93.6	104	6	ABP81634	Abp81634 Streptoco
279	47	100.0	421	8	ADO09131	Ado09131 Human Ttx	352	44	93.6	104	8	ADK46563	Adk46563 Streptoco
280	47	100.0	421	8	AAAS0663	Aaas0663 Thioresox	353	44	93.6	104	8	ADM32931	Adm32931 Amino aci
281	47	100.0	438	8	ADM30966	Adm30966 Human Ttx	354	44	93.6	104	8	ADV82057	Adv82057 Streptoco
282	47	100.0	438	8	ADM30964	Adm30964 Human Ttx	355	44	93.6	105	5	ABP60765	Abp60765 Dicyoste
283	47	100.0	438	8	ADM30968	Adm30968 Human Ttx	356	44	93.6	105	5	ABP60786	Abp60786 Rhodobact
284	47	100.0	438	8	ADM30962	Adm30962 Human Ttx	357	44	93.6	105	5	ABP60745	Abp60745 Alicyclob
285	47	100.0	447	8	ADU02345	Adu02345 Novel hum	358	44	93.6	105	8	ADO55473	Ado55473 D. discol
286	47	100.0	458	5	ABP60865	Abp60865 Mycobacte	359	44	93.6	106	5	ABP60791	Abp60791 Synechocy
287	47	100.0	458	5	ABP60778	Abp60778 Mycobacte	360	44	93.6	106	5	ABP60721	Abp60721 Anaerystis
288	47	100.0	458	5	ABP60694	Abp60694 Mycobacte	361	44	93.6	106	5	ABP60709	Abp60709 Anabaena
289	47	100.0	458	5	ABP60702	Abp60702 Mycobacte	362	44	93.6	106	5	ABP60764	Abp60764 Coprinus
290	47	100.0	458	6	AAO20628	Aao20628 Thioresox	363	44	93.6	107	5	ABP60725	Abp60725 Porphyra
291	47	100.0	458	6	AAO20619	Aao20619 Thioresox	364	44	93.6	107	5	ABP60790	Abp60790 Cyanidium
292	47	100.0	458	7	ADD26554	Add26554 M. leprae	365	44	93.6	107	5	ABP60722	Abp60722 Cyanidium
293	47	100.0	458	8	ADM30944	Adm30944 M. leprae	366	44	93.6	107	5	ABP60726	Abp60726 Porphyra
294	47	100.0	467	3	AAV79067	Aav79067 Murine se	367	44	93.6	108	9	ABR42151	Abr42151 L. pneumo
295	47	100.0	467	3	AAV85150	Aav85150 Mouse sec	368	44	93.6	109	2	AAK93015	Aak93015 Thioresox
296	47	100.0	467	9	ADM00726	Adm00726 Amino aci	369	44	93.6	109	5	ABP60792	Abp60792 Synechocy
297	47	100.0	485	7	ADP70799	Adp70799 Minicell	370	44	93.6	109	5	ABP60724	Abp60724 Griffliths
298	47	100.0	485	7	ADP70800	Adp70800 Minicell	371	44	93.6	109	5	ABP60836	Abp60836 Synechocy
299	47	100.0	485	7	ADP70802	Adp70802 Minicell	372	44	93.6	110	5	ABP60789	Abp60789 Streptococ
300	47	100.0	485	7	ADP70801	Adp70801 Minicell	373	44	93.6	110	8	ADV88658	Adv88658 Streptoco
301	47	100.0	499	9	AEA51601	Aea51601 RTV VP7 a	374	44	93.6	110	8	ADV79911	Adv79911 Streptoco
302	47	100.0	500	2	AAAR90303	Aaar90303 Thioresox	375	44	93.6	111	7	ADM80195	Adm80195 Human NOV
303	47	100.0	513	3	ABP60691	Abp60691 Phaseolin	376	44	93.6	111	9	ABE39008	Aeb39008 L. pneumo
304	47	100.0	516	6	ABG71115	Abg71115 Human Pet	377	44	93.6	112	5	ABG60236	Abg60236 Human Thl
305	47	100.0	518	6	ABG71114	Abg71114 Human Pet	378	44	93.6	112	5	AAU91276	Aau91276 Human NOV
306	47	100.0	522	5	AAAS0660	Aaas0660 Thioresox	379	44	93.6	112	5	AAU78664	Aau78664 Human NOV
307	47	100.0	530	5	AAAS0662	Aaas0662 Thioresox	380	44	93.6	112	7	ADC97112	Adc97112 E. faeciu
308	47	100.0	536	6	ADP70777	Adp70777 Male(1-38	381	44	93.6	114	3	AAQ54021	Aaq54021 Arabidops
309	47	100.0	546	7	ADP71271	Adp71271 P. falci	382	44	93.6	114	3	AAQ54021	Aaq54021 Arabidops
310	47	100.0	546	7	ADM6558	Adm6558 DRT-Trx42	383	44	93.6	114	5	ABP60696	Abp60696 Arabidops
311	47	100.0	551	4	AAAB5251	Aaab5251 Plant thl	384	44	93.6	114	5	ABP60680	Abp60680 Arabidops
312	47	100.0	551	4	AAAB5252	Aaab5252 Plant thl	385	44	93.6	114	5	ABP60727	Abp60727 Arabidops
313	47	100.0	572	9	AAEA5157	Aaea5157 VSV N ant	386	44	93.6	114	7	ADQ59276	Adq59276 Arabidops
314	47	100.0	580	7	ABO74197	Abot74197 Pseudomon	387	44	93.6	114	8	ADR94295	Adr94295 Novel S.
315	47	100.0	591	5	ABG33383	Abg33383 Human Ttx	388	44	93.6	114	8	ADR94295	Adr94295 Novel S.
316	47	100.0	591	5	ABG33383	Abg33383 Human Ttx	389	44	93.6	114	9	AEA58165	Aea58165 Streptoco

390	44	93.6	115	3	AAg12953	AAg12953	Arabidops	463	44	93.6	152	3	AAg26778	AAg26778	Zea mays
391	44	93.6	116	5	AAg45020	AAg45020	Zea mays	464	44	93.6	152	8	ADY06632	ADY06632	Plant ful
392	44	93.6	115	5	ABP60739	ABP60739	Pagopyrum	465	44	93.6	153	8	ADY87889	ADY87889	Plant ful
393	44	93.6	118	3	AAy70480	AAy70480	Catalpa b	466	44	93.6	159	3	AAg36125	AAg36125	Arabidops
394	44	93.6	118	5	AAy70483	AAy70483	Vernonia	467	44	93.6	160	5	ABP60832	ABP60832	Neisseria
395	44	93.6	118	5	ABP27942	ABP27942	Streptoco	468	44	93.6	160	7	ABO65111	ABO65111	Klebsiell
396	44	93.6	118	5	ABP27941	ABP27941	Streptoco	469	44	93.6	163	8	ADX89993	ADX89993	Plant ful
397	44	93.6	118	5	ABP60742	ABP60742	Ricinus c	470	44	93.6	163	8	ADX72134	ADX72134	Plant ful
398	44	93.6	119	5	ABP60826	ABP60826	Secale ce	471	44	93.6	167	5	ABP60716	ABP60716	Zea mays
399	44	93.6	120	3	AAy70481	AAy70481	Glycine m	472	44	93.6	167	8	ADM32940	ADM32940	Amino aci
400	44	93.6	122	2	AAy70481	AAy70481	Protein f	473	44	93.6	168	3	AAg20217	AAg20217	Arabidops
401	44	93.6	122	2	AAy70481	AAy70481	Protein f	474	44	93.6	169	4	AAg83359	AAg83359	Plant ful
402	44	93.6	122	3	AAy70479	AAy70479	Barley th	475	44	93.6	169	4	AAg80399	AAg80399	Co-fact
403	44	93.6	122	3	AAy70479	AAy70479	Barley th	476	44	93.6	169	5	ABP60682	ABP60682	Phaseolin
404	44	93.6	122	3	AAy70479	AAy70479	Barley th	477	44	93.6	172	5	ABP60718	ABP60718	Pisum sat
405	44	93.6	122	5	ABP60740	ABP60740	Rice thio	478	44	93.6	172	5	ABP60717	ABP60717	Oryza sat
406	44	93.6	122	7	AAE39220	AAE39220	Oryza sat	479	44	93.6	172	7	ABM87854	ABM87854	Rice abio
407	44	93.6	122	7	AAE39220	AAE39220	Barley th	480	44	93.6	172	8	ADM32941	ADM32941	Amino aci
408	44	93.6	122	7	AAE39223	AAE39223	Barley th	481	44	93.6	173	3	AAg45018	AAg45018	Zea mays
409	44	93.6	122	7	ADOS9274	ADOS9274	Rice thio	482	44	93.6	173	5	ABP60712	ABP60712	Arabidops
410	44	93.6	123	7	ADOS9272	ADOS9272	Barley th	483	44	93.6	175	5	ABP60720	ABP60720	Triticum
411	44	93.6	123	3	AAy70482	AAy70482	Glycine m	484	44	93.6	175	5	ABP60817	ABP60817	Arabidops
412	44	93.6	123	4	AAy70482	AAy70482	Zea mays	485	44	93.6	175	8	ADX88193	ADX88193	Plant ful
413	44	93.6	123	4	AAy70482	AAy70482	Wheat Tat	486	44	93.6	177	8	ADP90870	ADP90870	Brevibact
414	44	93.6	123	5	ABP65992	ABP65992	Blifidobac	487	44	93.6	179	8	ADY06451	ADY06451	Plant ful
415	44	93.6	124	4	AAy78905	AAy78905	C. glutam	488	44	93.6	179	8	ADY10996	ADY10996	Plant ful
416	44	93.6	125	5	AAy78905	AAy78905	C. glutam	489	44	93.6	180	8	ADY87804	ADY87804	Plant ful
417	44	93.6	125	5	AAy78905	AAy78905	C. glutam	490	44	93.6	180	8	ADY89807	ADY89807	Plant ful
418	44	93.6	125	5	AAy78905	AAy78905	C. glutam	491	44	93.6	180	8	ADY10998	ADY10998	Plant ful
419	44	93.6	126	5	ABP60743	ABP60743	M. xanthu	492	44	93.6	182	8	ADY11299	ADY11299	Plant ful
420	44	93.6	126	5	ABP60730	ABP60730	Triticum	493	44	93.6	183	4	ABM95783	ABM95783	W. xanthu
421	44	93.6	126	7	ADOS9275	ADOS9275	Nicotiana	494	44	93.6	185	4	AAg80918	AAg80918	Thioredox
422	44	93.6	127	2	AAy93016	AAy93016	Tobacco t	495	44	93.6	193	3	AAg37884	AAg37884	Arabidops
423	44	93.6	127	2	AAy93016	AAy93016	Soft whea	496	44	93.6	193	5	AAg60713	AAg60713	Arabidops
424	44	93.6	127	3	AAg28248	AAg28248	Wheat thi	497	44	93.6	194	3	AAg24095	AAg24095	Arabidops
425	44	93.6	127	3	AAg28248	AAg28248	Arabidops	498	44	93.6	194	3	AAg32511	AAg32511	Arabidops
426	44	93.6	130	2	AAy04690	AAy04690	Plant ful	499	44	93.6	194	3	AAg47218	AAg47218	Arabidops
427	44	93.6	130	2	AAy93017	AAy93017	Hard whea	500	44	93.6	197	8	ADP67695	ADP67695	Novel hum
428	44	93.6	131	4	AAg83360	AAg83360	P. patens	501	44	93.6	203	3	AAg39661	AAg39661	Arabidops
429	44	93.6	131	4	AAg80910	AAg80910	Co-factor	502	44	93.6	204	8	ADY77747	ADY77747	Plant ful
430	44	93.6	131	5	ABP60844	ABP60844	Phalaris	503	44	93.6	209	6	ABP80992	ABP80992	N. gonorr
431	44	93.6	131	5	ABP60821	ABP60821	Hordeum b	504	44	93.6	216	8	ADY110550	ADY110550	Plant ful
432	44	93.6	131	5	ABP60822	ABP60822	Lolium pe	505	44	93.6	217	3	AAg37883	AAg37883	Arabidops
433	44	93.6	131	5	ABP60823	ABP60823	Oryza sat	506	44	93.6	227	3	AAg34398	AAg34398	Arabidops
434	44	93.6	131	5	ABP60825	ABP60825	Secale ce	507	44	93.6	232	5	ABP60683	ABP60683	Phaseolin
435	44	93.6	131	7	ABM74315	ABM74315	DNA clone	508	44	93.6	248	3	AAg34397	AAg34397	Arabidops
436	44	93.6	133	5	AAg10853	AAg10853	Arabidops	509	44	93.6	268	8	ADP54556	ADP54556	Human PRO
437	44	93.6	133	5	ADY06180	ADY06180	Plant ful	510	44	93.6	268	9	ADY19732	ADY19732	PRO polyp
438	44	93.6	133	8	ADY09638	ADY09638	Plant ful	511	44	93.6	268	9	ADY15510	ADY15510	PRO polyp
439	44	93.6	134	3	AAg04653	AAg04653	Arabidops	512	44	93.6	268	9	ADY15512	ADY15512	PRO polyp
440	44	93.6	134	3	ADM32939	ADM32939	Amino aci	513	44	93.6	284	3	AAg25468	AAg25468	Arabidops
441	44	93.6	136	8	ADY06635	ADY06635	Plant ful	514	44	93.6	284	5	AAg49159	AAg49159	Arabidops
442	44	93.6	137	8	ADY09638	ADY09638	Plant ful	515	44	93.6	287	5	ABG32919	ABG32919	Thioredox
443	44	93.6	137	8	ADY09638	ADY09638	Plant ful	516	44	93.6	287	5	ABG32917	ABG32917	Oleosin-t
444	44	93.6	137	8	ADY08622	ADY08622	Plant ful	517	44	93.6	306	3	AAg25467	AAg25467	Arabidops
445	44	93.6	137	8	ADY78867	ADY78867	Plant ful	518	44	93.6	306	3	AAg49153	AAg49153	Arabidops
446	44	93.6	137	8	ADY04779	ADY04779	Plant ful	519	44	93.6	306	3	AAg49158	AAg49158	Arabidops
447	44	93.6	139	5	ABP60710	ABP60710	Escherich	520	44	93.6	306	3	AAg19243	AAg19243	Arabidops
448	44	93.6	139	5	ABP60710	ABP60710	Escherich	521	44	93.6	379	3	AAg25466	AAg25466	Arabidops
449	44	93.6	139	8	ADY10883	ADY10883	Plant ful	522	44	93.6	380	3	AAg19242	AAg19242	Arabidops
450	44	93.6	140	5	ABP60715	ABP60715	Chlamydom	523	44	93.6	380	3	AAg49157	AAg49157	Arabidops
451	44	93.6	140	8	ADY04782	ADY04782	Plant ful	524	44	93.6	380	3	AAg49152	AAg49152	Arabidops
452	44	93.6	141	8	ADY78767	ADY78767	Plant ful	525	44	93.6	399	3	AAg49151	AAg49151	Arabidops
453	44	93.6	141	8	ADY06170	ADY06170	Plant ful	526	44	93.6	399	8	ADM30997	ADM30997	Thale cre
454	44	93.6	141	8	ADY04783	ADY04783	Plant ful	527	44	93.6	445	8	ADM30997	ADM30997	Thale cre
455	44	93.6	141	8	ADY78677	ADY78677	Plant ful	528	44	93.6	446	8	ADM30956	ADM30956	Thale cre
456	44	93.6	144	3	AAg54790	AAg54790	Arabidops	529	44	93.6	447	8	ADM30954	ADM30954	Thale cre
457	44	93.6	144	3	AAg54790	AAg54790	Arabidops	530	44	93.6	447	8	ADM30960	ADM30960	Thale cre
458	44	93.6	144	8	ADY79859	ADY79859	Plant ful	531	44	93.6	479	7	ADP80719	ADP80719	Microsat
459	44	93.6	149	8	ADY93039	ADY93039	C. glutami	532	44	93.6	479	7	ADP80718	ADP80718	Microsat
460	44	93.6	150	8	ADY09570	ADY09570	Plant ful	533	44	93.6	483	7	ADP80718	ADP80718	Microsat
461	44	93.6	151	3	AAg44847	AAg44847	Zea mays	534	44	93.6	486	5	AAE23036	AAE23036	Human tci
462	44	93.6	151	8	ADP90872	ADP90872	Brevibacti	535	44	93.6	511	2	AAW76823	AAW76823	Human Tcf

682	43	91.5	747	7	ADc62491	Human	sec	755	43	91.5	747	7	ADG80616	Adg80616	Human	PRO
683	43	91.5	747	7	ADc42124	Human	sec	756	43	91.5	747	7	ADG53056	Adg53056	Human	sec
684	43	91.5	747	7	ADc50467	Novel	hum	757	43	91.5	747	7	ADG60376	Adg60376	Human	sec
685	43	91.5	747	7	ADc72014	Novel	hum	758	43	91.5	747	7	ADG80064	Adg80064	Human	PRO
686	43	91.5	747	7	ADc59993	Novel	hum	759	43	91.5	747	7	ADH55356	Adh55356	Novel	hum
687	43	91.5	747	7	ADc53000	Novel	hum	760	43	91.5	747	7	ADH55908	Adh55908	Novel	hum
688	43	91.5	747	7	ADc57354	Novel	hum	761	43	91.5	747	7	ADi61136	Adi61136	Human	sec
689	43	91.5	747	7	ADc65045	Novel	hum	762	43	91.5	747	7	ADi64127	Adi64127	Novel	hum
690	43	91.5	747	7	ADc51020	Novel	hum	763	43	91.5	747	7	ADi65076	Adi65076	Novel	hum
691	43	91.5	747	7	ADc65547	Human	PRO	764	43	91.5	747	7	ADi65575	Adi65575	Novel	hum
692	43	91.5	747	7	ADc54645	Novel	hum	765	43	91.5	747	7	ADH81989	Adh81989	Novel	hum
693	43	91.5	747	7	ADc53606	Novel	hum	766	43	91.5	747	7	ADH81437	Adh81437	Novel	hum
694	43	91.5	747	7	ADc59129	Novel	hum	767	43	91.5	747	7	ADH82606	Adh82606	Novel	hum
695	43	91.5	747	7	ADc56007	Novel	hum	768	43	91.5	747	7	ADN16005	Adn16005	Novel	hum
696	43	91.5	747	7	ADc58577	Novel	hum	769	43	91.5	747	7	ADN16634	Adn16634	Novel	hum
697	43	91.5	747	7	ADd03251	Novel	hum	770	43	91.5	747	7	ADN15453	Adn15453	Novel	hum
698	43	91.5	747	7	ADc90243	Novel	hum	771	43	91.5	747	7	ADN14901	Adn14901	Novel	hum
699	43	91.5	747	7	ADc69662	Human	PRO	772	43	91.5	747	8	ADc81163	Adc81163	Novel	hum
700	43	91.5	747	7	ADc48551	Human	PRO	773	43	91.5	747	8	ADd76611	Add76611	Human	PRO
701	43	91.5	747	7	ADd10080	Human	PRO	774	43	91.5	747	8	ADd87975	Add87975	Human	PRO
702	43	91.5	747	7	ADd04655	Novel	hum	775	43	91.5	747	8	ADd86379	Add86379	Human	PRO
703	43	91.5	747	7	ADc80611	Novel	hum	776	43	91.5	747	8	ADe75827	Ade75827	Human	PRO
704	43	91.5	747	7	ADd11118	Human	PRO	777	43	91.5	747	8	ADe48793	Ade48793	Human	sec
705	43	91.5	747	7	ADd10403	Human	sec	778	43	91.5	747	8	ADe41364	Ade41364	Human	sec
706	43	91.5	747	7	ADc47999	Human	PRO	779	43	91.5	747	8	ADe23403	Ade23403	Human	PRO
707	43	91.5	747	7	ADc80059	Novel	hum	780	43	91.5	747	8	ADe23955	Ade23955	Human	PRO
708	43	91.5	747	7	ADd11363	Human	sec	781	43	91.5	747	8	ADe24598	Ade24598	Human	PRO
709	43	91.5	747	7	ADd09528	Human	PRO	782	43	91.5	747	8	ADd87423	Add87423	Human	PRO
710	43	91.5	747	7	ADd41241	Novel	hum	783	43	91.5	747	8	ADd89289	Add89289	Human	PRO
711	43	91.5	747	7	ADd52380	Human	PRO	784	43	91.5	747	8	ADe18428	Ade18428	Human	PRO
712	43	91.5	747	7	ADd53120	Human	PRO	785	43	91.5	747	8	ADe88737	Ade88737	Human	PRO
713	43	91.5	747	7	ADd53672	Novel	hum	786	43	91.5	747	8	ADe80894	Ade80894	Human	sec
714	43	91.5	747	7	ADd37156	Human	sec	787	43	91.5	747	8	ADf61534	Adf61534	Human	sec
715	43	91.5	747	7	ADd51828	Human	PRO	788	43	91.5	747	8	ADf40226	Adf40226	Human	sec
716	43	91.5	747	7	ADd02627	Human	PRO	789	43	91.5	747	8	ADf46032	Adf46032	Human	sec
717	43	91.5	747	7	ADd02061	Human	PRO	790	43	91.5	747	8	ADe94757	Ade94757	Human	PRO
718	43	91.5	747	7	ADd54243	Novel	hum	791	43	91.5	747	8	ADe91168	Ade91168	Human	PRO
719	43	91.5	747	7	ADd54993	Human	sec	792	43	91.5	747	8	ADe93309	Ade93309	Human	PRO
720	43	91.5	747	7	ADd92560	Human	PRO	793	43	91.5	747	8	ADe93419	Ade93419	Human	PRO
721	43	91.5	747	7	ADd91456	Human	PRO	794	43	91.5	747	8	ADf24418	Adf24418	Human	sec
722	43	91.5	747	7	ADe04070	Human	PRO	795	43	91.5	747	8	ADf40850	Adf40850	Human	sec
723	43	91.5	747	7	ADe33367	Novel	hum	796	43	91.5	747	8	ADf23794	Adf23794	Human	sec
724	43	91.5	747	7	ADe22299	Human	PRO	797	43	91.5	747	8	ADf33777	Adf33777	Human	sec
725	43	91.5	747	7	ADd79523	Human	PRO	798	43	91.5	747	8	ADf35000	Adf35000	Human	PRO
726	43	91.5	747	7	ADe35547	Human	sec	799	43	91.5	747	8	ADf27244	Adf27244	Human	sec
727	43	91.5	747	7	ADe16661	Novel	hum	800	43	91.5	747	8	ADf27880	Adf27880	Human	sec
728	43	91.5	747	7	ADd73276	Human	sec	801	43	91.5	747	8	ADe92315	Ade92315	Novel	hum
729	43	91.5	747	7	ADe42059	Human	PRO	802	43	91.5	747	8	ADe90616	Ade90616	Human	PRO
730	43	91.5	747	7	ADe17876	Human	PRO	803	43	91.5	747	8	ADf41474	Adf41474	Human	sec
731	43	91.5	747	7	ADd92008	Human	PRO	804	43	91.5	747	8	ADf33153	Adf33153	Human	sec
732	43	91.5	747	7	ADe33471	Novel	hum	805	43	91.5	747	8	ADf25519	Adf25519	Human	sec
733	43	91.5	747	7	ADe34023	Novel	hum	806	43	91.5	747	8	ADf26620	Adf26620	Human	sec
734	43	91.5	747	7	ADd80075	Human	PRO	807	43	91.5	747	8	ADf34409	Adf34409	Human	sec
735	43	91.5	747	7	ADd93112	Human	PRO	808	43	91.5	747	8	ADf46646	Adf46646	Human	sec
736	43	91.5	747	7	ADd72634	Human	sec	809	43	91.5	747	8	ADe91763	Ade91763	Novel	hum
737	43	91.5	747	7	ADe19532	Human	PRO	810	43	91.5	747	8	ADG02342	Adg02342	Human	PRO
738	43	91.5	747	7	ADe18980	Human	PRO	811	43	91.5	747	8	ADG22128	Adg22128	Novel	hum
739	43	91.5	747	7	ADe43176	Human	PRO	812	43	91.5	747	8	ADG20198	Adg20198	Human	PRO
740	43	91.5	747	7	ADd95965	Human	PRO	813	43	91.5	747	8	ADf98104	Adf98104	Human	PRO
741	43	91.5	747	7	ADe22851	Human	PRO	814	43	91.5	747	8	ADG24321	Adg24321	Novel	hum
742	43	91.5	747	7	ADd78969	Human	PRO	815	43	91.5	747	8	ADf98675	Adf98675	Human	PRO
743	43	91.5	747	7	ADe32919	Novel	hum	816	43	91.5	747	8	ADG03506	Adg03506	Human	PRO
744	43	91.5	747	7	ADe42611	Human	PRO	817	43	91.5	747	8	ADf99227	Adf99227	Human	PRO
745	43	91.5	747	7	ADe17285	Human	sec	818	43	91.5	747	8	ADG16812	Adg16812	Human	PRO
746	43	91.5	747	7	ADd80627	Human	PRO	819	43	91.5	747	8	ADG05271	Adg05271	Human	PRO
747	43	91.5	747	7	ADd89655	Human	PRO	820	43	91.5	747	8	ADG19538	Adg19538	Human	PRO
748	43	91.5	747	7	ADe40939	Human	PRO	821	43	91.5	747	8	ADG13375	Adg13375	Human	PRO
749	43	91.5	747	7	ADe04738	Human	PRO	822	43	91.5	747	8	ADG08432	Adg08432	Novel	hum
750	43	91.5	747	7	ADe92867	Human	PRO	823	43	91.5	747	8	ADG15602	Adg15602	Human	PRO
751	43	91.5	747	7	ADf47299	Human	sec	824	43	91.5	747	8	ADf97000	Adf97000	Human	PRO
752	43	91.5	747	7	ADG21576	Novel	hum	825	43	91.5	747	8	ADG06185	Adg06185	Human	PRO
753	43	91.5	747	7	ADG23217	Novel	hum	826	43	91.5	747	7	ADG23769	Adg23769	Novel	hum
754	43	91.5	747	7	ADf97552	Human	PRO	827	43	91.5	747	8	ADG04058	Adg04058	Human	PRO

828	43	91.5	747	8	ADG24959	Adg24959	Novel	hum	901	42	89.4	62	4	AAU58028	AAU58028	Propionib
829	43	91.5	747	8	ADG07256	Adg07256	Novel	hum	902	42	89.4	62	6	ABM62346	ABM62346	Propionib
830	43	91.5	747	8	ADG07808	Adg07808	Novel	hum	903	42	89.4	62	6	ABM54547	ABM54547	Propionib
831	43	91.5	747	8	ADG55303	Adg55303	Novel	hum	904	42	89.4	71	3	AAg12496	AAg12496	Zea may
832	43	91.5	747	8	ADG60967	Adg60967	Novel	hum	905	42	89.4	71	3	AAg60135	AAg60135	Zea may
833	43	91.5	747	8	ADG62071	Adg62071	Novel	hum	906	42	89.4	81	3	AAg12495	AAg12495	Zea may
834	43	91.5	747	8	ADG82272	Adg82272	Novel	hum	907	42	89.4	84	9	ADY66554	ADY66554	Zea may
835	43	91.5	747	8	ADG57511	Adg57511	Novel	hum	908	42	89.4	93	3	AAg60134	AAg60134	Zea may
836	43	91.5	747	8	ADG56959	Adg56959	Novel	hum	909	42	89.4	94	4	ADG27717	ADG27717	Hum nov
837	43	91.5	747	8	ADG55855	Adg55855	Novel	hum	910	42	89.4	103	3	AAg60133	AAg60133	Zea may
838	43	91.5	747	8	ADG58615	Adg58615	Novel	hum	911	42	89.4	108	5	ABP60752	ABP60752	Chlorobiu
839	43	91.5	747	8	ADG70961	Adg70961	Novel	hum	912	42	89.4	110	6	AAU56505	AAU56505	Propionib
840	43	91.5	747	8	ADG58063	Adg58063	Novel	hum	913	42	89.4	110	6	ABM53024	ABM53024	Propionib
841	43	91.5	747	8	ADG53647	Adg53647	Novel	hum	914	42	89.4	111	3	AAg12494	AAg12494	Zea may
842	43	91.5	747	8	ADG71533	Adg71533	Novel	hum	915	42	89.4	139	4	ABP68209	ABP68209	Drosophil
843	43	91.5	747	8	ADG50632	Adg50632	Novel	hum	916	42	89.4	169	9	ABM91297	ABM91297	M. xanthu
844	43	91.5	747	8	ADG81720	Adg81720	Novel	hum	917	42	89.4	174	7	ADP74512	ADP74512	Mycodacce
845	43	91.5	747	8	ADH30682	Adh30682	Novel	hum	918	42	89.4	183	3	AAg11492	AAg11492	Arabidops
846	43	91.5	747	8	ADG50008	Adg50008	Novel	hum	919	42	89.4	183	5	ABP99365	ABP99365	Arabidops
847	43	91.5	747	8	ADG51880	Adg51880	Novel	hum	920	42	89.4	193	3	AAg11491	AAg11491	Arabidops
848	43	91.5	747	8	ADG52471	Adg52471	Novel	hum	921	42	89.4	201	8	ADX72965	ADX72965	Plant ful
849	43	91.5	747	8	ADG54139	Adg54139	Novel	hum	922	42	89.4	217	8	ADY07461	ADY07461	Plant ful
850	43	91.5	747	8	ADG54139	Adg54139	Novel	hum	923	42	89.4	372	8	ADX72752	ADX72752	Plant ful
851	43	91.5	747	8	ADG49384	Adg49384	Novel	hum	924	42	89.4	383	8	ADY10333	ADY10333	Plant ful
852	43	91.5	747	8	ADG81168	Adg81168	Novel	hum	925	42	89.4	432	1	AAp92149	AAp92149	Large env
853	43	91.5	747	8	ADG56407	Adg56407	Novel	hum	926	42	89.4	432	1	AAp92148	AAp92148	Large env
854	43	91.5	747	8	ADH12673	Adh12673	Novel	hum	927	42	89.4	459	2	AAp28990	AAp28990	Mouse Tcf
855	43	91.5	747	8	ADG48760	Adg48760	Novel	hum	928	42	89.4	459	5	AAU99985	AAU99985	Murine T-
856	43	91.5	747	8	ADG61519	Adg61519	Novel	hum	929	42	89.4	525	3	AAp25294	AAp25294	Eucalyptu
857	43	91.5	747	8	ADH28606	Adh28606	Novel	hum	930	42	89.4	553	3	AAp97403	AAp97403	Human apo
858	43	91.5	747	8	ADG54751	Adg54751	Novel	hum	931	42	89.4	606	4	ABM69121	ABM69121	Drosophil
859	43	91.5	747	8	ADG59791	Adg59791	Novel	hum	932	42	89.4	662	2	AAp68401	AAp68401	FelV-B en
860	43	91.5	747	8	ADG51256	Adg51256	Novel	hum	933	42	89.4	662	2	ABP66271	ABP66271	Drosophil
861	43	91.5	747	8	ADH43547	Adh43547	Novel	hum	934	41	87.2	45	5	ABP66088	ABP66088	Human ORF
862	43	91.5	747	8	ADG59200	Adg59200	Novel	hum	935	41	87.2	107	5	ABP60758	ABP60758	Corynebac
863	43	91.5	747	8	ADG62656	Adg62656	Novel	hum	936	41	87.2	108	5	ABP60751	ABP60751	Buchnera
864	43	91.5	747	8	ADH181215	Adh181215	Novel	hum	937	41	87.2	108	5	ABP60750	ABP60750	Buchnera
865	43	91.5	747	8	ADH25681	Adh25681	Novel	neu	938	41	87.2	120	9	AEBA0665	AEBA0665	L. pneumo
866	43	91.5	747	8	ADG09958	Adg09958	Novel	hum	939	41	87.2	120	9	AEBA7345	AEBA7345	L. pneumo
867	43	91.5	747	8	ADH15429	Adh15429	Novel	hum	940	41	87.2	126	6	ADA36599	ADA36599	Acinetoba
868	43	91.5	747	8	ADG09306	Adg09306	Novel	hum	941	41	87.2	142	4	ABM64146	ABM64146	Drosophil
869	43	91.5	747	8	ADH14761	Adh14761	Novel	hum	942	41	87.2	188	4	AAU39188	AAU39188	Propionib
870	43	91.5	747	8	ADH18356	Adh18356	Novel	hum	943	41	87.2	188	6	ABM35707	ABM35707	Propionib
871	43	91.5	747	8	ADJ63637	Adj63637	Novel	hum	944	41	87.2	353	7	ABO77648	ABO77648	Pseudomon
872	43	91.5	747	8	ADJ77532	Adj77532	Novel	hum	945	40	85.1	160	4	ABM60122	ABM60122	Drosophil
873	43	91.5	747	8	ADK82892	Adk82892	Novel	hum	946	39	83.0	103	5	ABM48767	ABM48767	Listeria
874	43	91.5	747	8	ADJ65654	Adj65654	Novel	hum	947	39	83.0	105	5	ABP60796	ABP60796	Treponema
875	43	91.5	747	8	ADM27790	Adm27790	Novel	hum	948	39	83.0	112	5	AAU83688	AAU83688	Human PRO
876	43	91.5	747	8	ADM17458	Adm17458	Novel	hum	949	39	83.0	161	9	ABM92721	ABM92721	M. xanthu
877	43	91.5	747	8	ADL07292	Adl07292	Novel	hum	950	39	83.0	165	7	ADG36909	ADG36909	B. subtili
878	43	91.5	747	8	ADM42514	Adm42514	Novel	hum	951	39	83.0	172	2	AAH80812	AAH80812	Amino aci
879	43	91.5	747	8	ADM28376	Adm28376	Novel	hum	952	39	83.0	172	2	AAH37845	AAH37845	Human XAG
880	43	91.5	747	8	ADJ95858	Adj95858	Novel	hum	953	39	83.0	172	2	AAH37845	AAH37845	Human XAG
881	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	954	39	83.0	172	2	AAH37845	AAH37845	Human XAG
882	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	955	39	83.0	172	2	AAH37845	AAH37845	Human XAG
883	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	956	39	83.0	172	2	AAH37845	AAH37845	Human XAG
884	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	957	39	83.0	172	2	AAH37845	AAH37845	Human XAG
885	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	958	39	83.0	172	2	AAH37845	AAH37845	Human XAG
886	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	959	39	83.0	172	2	AAH37845	AAH37845	Human XAG
887	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	960	39	83.0	172	2	AAH37845	AAH37845	Human XAG
888	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	961	39	83.0	172	2	AAH37845	AAH37845	Human XAG
889	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	962	39	83.0	172	2	AAH37845	AAH37845	Human XAG
890	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	963	39	83.0	172	2	AAH37845	AAH37845	Human XAG
891	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	964	39	83.0	172	2	AAH37845	AAH37845	Human XAG
892	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	965	39	83.0	172	2	AAH37845	AAH37845	Human XAG
893	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	966	39	83.0	172	2	AAH37845	AAH37845	Human XAG
894	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	967	39	83.0	172	2	AAH37845	AAH37845	Human XAG
895	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	968	39	83.0	172	2	AAH37845	AAH37845	Human XAG
896	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	969	39	83.0	172	2	AAH37845	AAH37845	Human XAG
897	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	970	39	83.0	172	2	AAH37845	AAH37845	Human XAG
898	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	971	39	83.0	172	2	AAH37845	AAH37845	Human XAG
899	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	972	39	83.0	172	2	AAH37845	AAH37845	Human XAG
900	43	91.5	747	8	ADJ96410	Adj96410	Novel	hum	973	39	83.0	172	2	AAH37845	AAH37845	Human XAG

974	39	83.0	172	7	ADB73331	Adb73331	Novel	hum
975	39	83.0	172	7	ADB78413	Adb78413	Novel	hum
976	39	83.0	172	7	ADB85061	Adb85061	Human	PRO
977	39	83.0	172	7	ADB78167	Adb78167	Novel	hum
978	39	83.0	172	7	ADB87233	Adb87233	Human	PRO
979	39	83.0	172	7	ADB84815	Adb84815	Human	PRO
980	39	83.0	172	7	ADB83930	Adb83930	Novel	hum
981	39	83.0	172	7	ADB73085	Adb73085	Novel	hum
982	39	83.0	172	7	ADC36923	Adc36923	Human	PRO
983	39	83.0	172	7	ADC21913	Adc21913	Human	PRO
984	39	83.0	172	7	ADC49944	Adc49944	Novel	hum
985	39	83.0	172	7	ADC49143	Adc49143	Novel	hum
986	39	83.0	172	7	ADC49660	Adc49660	Novel	hum
987	39	83.0	172	7	ADC47521	Adc47521	Novel	hum
988	39	83.0	172	7	ADC47266	Adc47266	Novel	hum
989	39	83.0	172	7	ADC78141	Adc78141	Novel	hum
990	39	83.0	172	7	ADD06376	Add06376	Novel	hum
991	39	83.0	172	7	ADD10517	Add10517	Human	sec
992	39	83.0	172	7	ADC7895	Adc7895	Novel	hum
993	39	83.0	172	7	ADD11477	Add11477	Human	sec
994	39	83.0	172	7	ADD50858	Add50858	Novel	hum
995	39	83.0	172	7	ADD51104	Add51104	Novel	hum
996	39	83.0	172	7	ADD37270	Add37270	Human	sec
997	39	83.0	172	7	ADD50585	Add50585	Human	PRO
998	39	83.0	172	7	ADD50339	Add50339	Human	PRO
999	39	83.0	172	7	ADD51350	Add51350	Novel	hum
1000	39	83.0	172	8	ADC48897	Adc48897	Novel	hum

ALIGNMENTS

RESULT 1
ID AAp71087 standard; peptide; 6 AA.

XX	AAp71087;
XX	25-MAR-2003 (revised)
DT	31-OCT-2002 (revised)
DT	06-JUN-1991 (first entry)
XX	Sequence of thioredoxin analogue.
XX	Redox active peptide; antioxidant; stress; ischaemia; lipid peroxidation;
KM	food industry; cosmetics; antibiotic.
XX	Unidentified.
XX	OS
XX	Key
FT	Location/Qualifiers
FT	/note= "optional, and may optionally be joined to a
FT	terminal blocking SP."
FT	Misc-difference 6
FT	/note= "see above"
XX	EP237189-A.
PN	16-SEP-1987.
XX	10-FEB-1987; 87EP-00301150.
XX	10-FEB-1986; 86US-00828112.
PR	14-MAR-1986; 86US-00839857.
PR	20-OCT-1986; 86US-00921287.
XX	(REPK) REPLIGEN CORP.
PA	Piglet VP, Mills CD;
XX	WPI; 1987-258442/37.
DR	New and known thioredoxin derivs. and analogues - useful for preventing
PT	

PT metal catalysed oxidative damage in biological reactions and disease states.
XX
PS Claim 7; Page 7; 7pp; English.

XX It is a redox active peptide which can be used in cpds. to treat stress and ischaemia, for inhibiting lipid peroxidn. due to drugs or toxic effects, as anti-inflammatory agents, to prevent DNA damage, and to maintain the biological activity of antibiotics or proteins. Thioredoxin can be used as a general antioxidant in the food and cosmetic industry. It may be used in prodn. processes for antibiotics, proteins or polypeptides. Therapeutic dose is 1 microgram/Kg - 10mg/Kg. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

CC Sequence 6 AA;

SQ

Query Match 100.0%; Score 47; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 1 WCGPCK 6

RESULT 2
ID ABP54936 standard; peptide; 6 AA.

XX	ABP54936;
XX	08-JAN-2003 (first entry)
DT	Active site peptide of thioredoxin.
XX	Thioredoxin; organoarsenical; arsenoxide; antiarthritic; antiout;
KM	osteopathic; antirheumatic; arthritis; therapy.
XX	Homo sapiens.
OS	WO200274305-A1.
PN	26-SEP-2002.
PD	19-MAR-2002; 2002WO-AU000310.
XX	19-MAR-2001; 2001AU-00003798.
PR	(UNIX) UNISEARCH LTD.
XX	Hogg PJ, Donoghue N;
PI	WPI; 2002-750519/81.
XX	Use of an impermeable cell membrane compound for the treatment of
PT	arthritis in vertebrates.
XX	Example 2 (b); Page 42; 91pp; English.
XX	The present sequence is that of a hexapeptide comprising the active site
CC	sequence of thioredoxin. The hexapeptide was used in an example from the
CC	invention that examined the binding of 4-(N-(S-
CC	glutathionylacetyl)amino)phenylarsenoxide (GSNO) to peptide and protein
CC	dithiols. The results indicated that GSNO selectively binds proteins
CC	containing closely spaced thiols. The invention provides a method for the
CC	treatment and/or prophylaxis of arthritis using a compound of formula A-
CC	(L-Y)P, where A is a cell-membrane impermeable pendant group, L is a
CC	linker and/or spacer, Y is an arsenoxide or arsenoxide equivalent, and P
CC	is an integer from 1 to 10. The compound, e.g. GSNO, is useful for the
CC	treatment of arthritic conditions such as calcific periarthritis,
CC	enteropathic, chronic, thumb, hip, peripheral, psoriatic, rheumatoid,
CC	septic or Jaccoud's arthritis, gout, hand or knee osteoarthritis,

CC juvenile osteoarthritis, oligoarthritis, and polyarthritis (all claimed).
 CC The compound blocks angiogenesis in the synovial tissue and leucocyte
 CC ingress that triggers inflammation, with no signs or symptoms of toxicity
 XX
 CC
 SQ Sequence 6 AA;

Query Match 100.0%; Score 47; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 1 WCGPCK 6

RESULT 3
 ADA08451
 ID ADA08451 standard; peptide; 6 AA.

AC ADA08451;

XX 06-NOV-2003 (first entry)

DE Mammalian peptide found in thioredoxin and protein disulphide isomerase.

XX Anti-angiogenesis plasmin fragment; plasminogen; plasminogen activator;
 KM plasmin reductase; reduced plasmin protein; anti-angiogenesis activator;
 KM urokinase-type plasminogen activator; A61; annexin II heterotetramer;
 KM annexin II p36 subunit; annexin II p11 subunit; thioredoxin;
 KM protein disulphide isomerase; modulating angiogenesis; mammalian;
 KM cleavage peptide.

XX Mammalia.

OS US2003083234-A1.

XX 01-MAY-2003.

PD 26-NOV-2002; 2002US-00304287.

XX 28-NOV-2001; 2001US-0333866P.

PA (WAIS/) WAISMAN D.

XX (KMON/) KMON M.

PI Waisman D, Kwon M;

XX WPI; 2003-596985/56.

DR Producing an anti-angiogenesis plasmin fragment, useful for modulating,
 PT e.g. promoting or inhibiting angiogenesis, comprises contacting a
 PT plasminogen polypeptide with a plasminogen activator and a plasmin
 PT reductase.

XX Example 2; Page 6; 29pp; English.

CC The present invention relates to a method for producing an anti-
 CC angiogenesis plasmin fragment. The method comprises contacting a
 CC plasminogen polypeptide with a plasminogen activator and a plasmin
 CC reductase, where a reduced plasmin protein is produced and the anti-
 CC angiogenesis plasmin fragment having anti-angiogenesis activity, is
 CC released from the reduced plasmin protein. The plasminogen activator is
 CC preferably a urokinase-type plasminogen activator. The angiogenesis
 CC plasmin fragment is A61. The plasmin reductase is selected from annexin
 CC II heterotetramer, annexin II p36 subunit, p11, thioredoxin, and protein
 CC disulphide isomerase. The annexin II heterotetramer is associated with a
 CC cell membrane. The method of the invention is useful for modulating (e.g.
 CC promoting or inhibiting) angiogenesis. The present sequence represents a
 CC mammalian cleavage peptide found in thioredoxin and protein disulphide
 CC isomerase.

XX Sequence 6 AA;

Query Match 100.0%; Score 47; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 1 WCGPCK 6

RESULT 4
 ADM32929
 ID ADM32929 standard; peptide; 6 AA.

AC ADM32929;

XX 17-JUN-2004 (first entry)

DE Amino acid sequence of the thioredoxin active site.

XX mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KM lung disease; cystic fibrosis.

XX Synthetic.

OS Key Location/Qualifiers

XX Active-site 1..6 "active site of thioredoxin"

FT Modified-site 2 /note= "this residue is in a reduced state"

FT Modified-site 5 /note= "this residue is in a reduced state"

XX WO2004024868-A2.

XX 25-MAR-2004.

PD 10-SEP-2003; 2003WO-US028526.

XX 10-SEP-2002; 2002US-0409960P.

XX 11-APR-2003; 2003US-0462082P.

PA (NAJB-) NAT JEWISH MEDICAL & RES CENT.

XX White CW;

XX WPI; 2004-270016/25.

DR Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.

XX Claim 13; Page 51; 69pp; English.

CC The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive
 CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC statistically significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
 CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for

CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. The present sequence represents an active site of a
CC thioredoxin which is used in the method of the invention.

XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 47; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
1 WCGPCK 6

DB

RESULT 5
ADP87509
ADP87509 standard; peptide; 6 AA.

XX ADP87509;

XX 23-SEP-2004 (first entry)

XX Thioredoxin family conserved catalytic site peptide.

XX 4-(1(Sulfonyl)-1H-indol-2-yl)-4(hydroxy)-cyclohexa-2; 5-dienone;
XX cytosolic; thioredoxin reductase inhibitor; proliferative condition;
XX colon cancer; renal cancer; thioredoxin; thioredoxin reductase;
XX cell cycle progression; cell proliferation; apoptosis;
XX catalytic site peptide.

XX Synthetic.

XX WO2004056361-A1.

XX 08-JUL-2004.

XX 20-DEC-2002; 2002WO-GB005842.

XX 20-DEC-2002; 2002WO-GB005842.

XX (CANC-) CANCER RES TECHNOLOGY LTD.

XX Stevens MFG, Westwell AD, Poole TD, Wells G, Berry JM;

XX WPI; 2004-517586/49.

XX New 4-(1(sulfonyl)-1H-indol-2-yl)-4(hydroxy)-cyclohexa-2,5-dienone
XX derivatives are thioredoxin reductase inhibitors useful for treating e.g.
XX colon or renal cancer.

XX Disclosure; Page 82; 141pp; English.

XX The present invention described 4-(1(Sulfonyl)-1H-indol-2-yl)-4(hydroxy)-
XX cyclohexa-2,5-dienone derivatives (I) and their salts, esters, amides,
XX solvates, hydrates or protected forms. (I) have cytosolic activities,
XX and can be used as thioredoxin reductase inhibitors. (I) can be used for
XX treating a proliferative condition (especially colon or renal cancer) or
XX a condition mediated by thioredoxin/thioredoxin reductase in the human or
XX animal body. (I) are also useful for inhibiting thioredoxin/thioredoxin
XX reductase and cell cycle progression, to regulate/inhibit cell
XX proliferation and/or to promote apoptosis in a cell in vitro or in vivo.
XX The present sequence represents a thioredoxin family conserved catalytic
XX site peptide, which is given in the exemplification of the present
XX invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 47; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
1 WCGPCK 6

DB

RESULT 6
ADP67423
ADP67423 standard; peptide; 6 AA.

XX ADP67423;

XX 23-SEP-2004 (first entry)

XX Thioredoxin and protein disulfide isomerase common sequence SEQ ID NO:4.

XX p11; p11 activity modulator; plasmidogen activation; cytosolic;
XX antisense therapy; cancer; tumour; tumour growth inhibition; thioredoxin;
XX protein disulfide isomerase.

XX Homo sapiens.

XX Synthetic.

XX WO2004054517-A2.

XX 01-JUL-2004.

XX 12-DEC-2003; 2003WO-US040029.

XX 13-DEC-2002; 2002US-0433140P.

XX (MED1-) MED1OMICS LLC.

XX (WAIS/) WAISMAN D.

XX WPI; 2004-487995/46.

XX Composition useful for inhibiting growth of tumor in patient, modulates
XX activity of p11 protein and effects change in level of plasmidogen
XX activation by a cell.

XX Example 2; SEQ ID NO 4; 140pp; English.

XX The present invention describes a composition (I) which modulates the
XX activity of a p11 protein and effects a change in the level of
XX plasmidogen activation by a cell. Also described: (I) making (M1) a
XX clonal cell line, which involves isolating a cell, then characterizing
XX the activity of a protein produced by the cell or clonal progeny of the
XX cell, where the protein is involved in plasmidogen activation; and (2) a
XX clonal cell line (II) useful in the identification of composition that
XX modulate p11 activity, where the clonal cell line is obtained by (M1).
XX (I) has cytosolic activity, and can be used in antisense therapy. (I) is
XX useful for modulating the activity of p11 which involves administering
XX (I) to a cell. The cell can be a human cancer cell, chosen from a HT1080
XX fibrosarcoma cell, a LNCaP prostate cancer cell and a CCR-22 colorectal
XX adenocarcinoma cell. (I) is also useful for reducing the development of
XX cancer in a patient e.g., mouse which involves administering (I) to a
XX cancer cell in the patient. (I) is useful for inhibiting the growth of
XX tumours or inhibiting tumour cell invasion in a patient, which involves
XX administering (I) to a cancer cell in the patient. (II) is useful for
XX administering a composition that modulates p11 activity which involves
XX administering the composition to (II) obtained by (M1), determining the
XX change in p11 activity of a cell of the clonal cell line relative to a
XX cell of a clonal cell line that had not received the composition, and
XX identifying the composition that produces a change in p11 activity. The
XX change in p11 activity is a change in the level of plasmidogen activation
XX activity. The present sequence represents a thioredoxin and protein
XX disulfide isomerase common sequence, which is used in the exemplification
XX of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 47; DB 8; Length 6;

PA (ASTR) ASTRA AB.
 XX
 PI Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX
 DR WPI; 1999-287953/24.
 XX
 PT Synthetic genes encoding immunoreactive peptides containing cysteine or
 XX methionine.
 PS Claim 32; Page 52; 104pp; English.
 XX
 CC The present invention describes nucleic acid molecules comprising a
 CC coding sequence encoding an immunoreactive peptide and further encoding a
 CC protein targeting sequence. The nucleic acid is administered to a patient
 CC so that its expression product, an immunoreactive peptide, modulates an
 CC immune response in a patient. The nucleic acid can also be used to treat
 CC cancer, either after surgery to remove a portion of the cancer or after
 CC ionizing radiation. A cytokine is also administered in conjunction with
 CC the nucleic acid. Cells containing the nucleic acid molecule can also be
 CC used for treatment. The immunoreactive peptide is immunosuppressive and can
 CC be used in patients with autoimmune disease. The present sequence
 CC represents a specifically claimed immunoreactive peptide from the present
 CC invention
 CC
 SQ Sequence 12 AA;
 XX

Query Match 100.0%; Score 47; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 1 WCGPCK 6

RESULT 10
 AAU08670
 ID AAU08670 standard; protein; 52 AA.
 XX
 AC AAU08670;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Thioresoxin domain markov model sequence #1.
 XX
 KM Thioresoxin; 22105; cytosratic; cardiant; haemostatic;
 KM cellular proliferative disorder; differentiative disorder; cancer;
 KM carcinoma; sarcoma; tumour; haemopoetic neoplastic disorder; leukemia;
 KM chronic myelogenous leukemia; cardiovascular disorder; atherosclerosis;
 KM ischaemia; thrombosis; hypertension.
 XX
 OS Synthetic.
 XX
 PN WO200166756-A2.
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US007139.
 XX
 PR 07-MAR-2000; 2000US-0187447P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Curtis RAJ;
 XX
 DR WPI; 2001-589945/66.
 XX
 PT Novel thioresoxin polypeptides and polynucleotides for treating a
 PT disorder associated with aberrant cellular proliferation or
 PT differentiation, e.g., cancer and to identify modulators for therapeutic
 PT use.
 XX
 PS Disclosure; Fig 3A; 126pp; English.

XX The invention relates to a novel human thioresoxin polypeptide, 22105,
 CC fragments of it and allelic variants. 22105 is useful for identifying a
 CC compound which modulates the activity or expression of the polypeptide
 CC and nucleic acid, where the binds to the polypeptide, and the binding is
 CC detected by direct detection of a test compound/polypeptide binding, by
 CC using a competition binding assay or an assay for 22105-mediated signal
 CC transduction, and the activity of the polypeptide is a redox activity or
 CC the ability to modulate protein processing, protein folding and protein
 CC secretion. Anti-22105 antibody is useful for detecting the presence of
 CC 22105 in a sample. A modulator of 22105 is useful for treating or
 CC preventing a disorder such as cellular proliferative or differentiative
 CC disorder (e.g. cancers, carcinomas, sarcomas and tumours), haemopoetic
 CC neoplastic disorder (e.g. leukemia and chronic myelogenous leukemia) or
 CC cardiovascular disorder (e.g. atherosclerosis, ischaemia, thrombosis,
 CC hypertension), characterised by aberrant activity or expression of a
 CC 22105 nucleic acid or polypeptide in a subject, where the agent is
 CC preferably a peptide, a phosphopeptide, a small molecule, an antibody or
 CC their combination, or an antisense, a ribozyme, a triple helix molecule,
 CC a 22105 nucleic acid or their combination (many examples of each disorder
 CC are given in the specification). The present sequence represents a
 CC thioresoxin domain sequence derived from a hidden markov model
 CC
 SQ Sequence 52 AA;
 XX

Query Match 100.0%; Score 47; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 7.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 20 WCGPCK 25

RESULT 11
 AAR42822
 ID AAR42822 standard; protein; 80 AA.
 XX
 AC AAR42822;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-MAY-1994 (first entry)
 XX
 DE zECEP 84.
 XX
 KM Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
 KM therapy; thioresoxin.
 XX
 OS Homo sapiens.
 XX
 PN WO9320107-A1.
 PD 14-OCT-1993.
 XX
 PF 06-APR-1993; 93WO-US003310.
 XX
 PR 06-APR-1992; 92US-00862832.
 PR 06-JUL-1992; 92US-00906842.
 XX
 PA (BIGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Silberstein DS, Balcewicz-Sablinska MK;
 XX
 DR WPI; 1993-336837/42.
 DR N-PSDB; AAQ49405.
 XX
 XX Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having
 PT Eosinophil-stimulating activity, for use in diagnosis and therapy.
 PS Example 3; Page 67; 96pp; English.
 XX
 CC A 14 kDa molecule designated various names (Eosinophil Cytotoxicity-
 CC Enhancing Factor (ECEF); thioresoxin and ADF) and encoding a polypeptide

CC of 104 amino acids has been found to support the growth of an EBV
 CC transformed B lymphocyte cell line in the manner of IL-1; to induce the
 CC expression of IL-2 receptors in a large granular lymphocyte cell line
 CC from an ATL patient in the manner of IL-1 and to mediate the growth
 CC inhibitory properties of interferon gamma. Recombinant ECEF (ECEP) 80 is
 CC a truncated version of the 104 amino acid polypeptide comprising the
 CC first 80 amino acids of the molecule. Some shortened ECEP's are useful
 CC because they retain eosinophil stimulating activity but lack
 CC proinflammatory diethyl reductase activity. In particular they can be
 CC used for killing tumour cells. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX SQ Sequence 80 AA;

Query Match 100.0%; Score 47; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 12

AA42821
 ID AA42821 standard; protein; 84 AA.

AC AA42821;

DT 25-MAR-2003 (revised)

DT 04-MAY-1994 (first entry)

XX DE RECF 84.

KW Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
 KW therapy; thioedoxin.

XX Homo sapiens.

XX WO320107-A1.

PD 14-OCT-1993.

PF 06-APR-1993; 93WO-US003310.

PR 06-APR-1992; 92US-00862832.

PR 06-JUL-1992; 92US-00906842.

XX (BGM) BRIGHAM & WOMENS HOSPITAL.

PI Silberstein DS, Balcewicz-Sablinska MK;

XX WPI; 1993-336837/42.

DR N-PSDB; AAQ49404.

PT Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having
 PT Eosinophil-stimulating activity, for use in diagnosis and therapy.

XX Example 3; Page 66; 96pp; English.

XX A 14 kDa molecule designated various names (Eosinophil Cytotoxicity-
 CC Enhancing Factor (ECF); thioedoxin and ADP) and encoding a polypeptide
 CC of 104 amino acids has been found to support the growth of an EBV
 CC transformed B lymphocyte cell line in the manner of IL-1; to induce the
 CC expression of IL-2 receptors in a large granular lymphocyte cell line
 CC from an ATL patient in the manner of IL-1 and to mediate the growth
 CC inhibitory properties of interferon gamma. Recombinant ECEF (ECEP) 84 is
 CC a truncated version of the 104 amino acid polypeptide comprising the
 CC first 84 amino acids of the molecule. Some shortened ECEP's are useful
 CC because they retain eosinophil stimulating activity but lack
 CC proinflammatory diethyl reductase activity. In particular they can be
 CC used for killing tumour cells. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX SQ Sequence 84 AA;

Query Match 100.0%; Score 47; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 13

ADJ68506
 ID ADJ68506 standard; protein; 84 AA.

AC ADJ68506;

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SegID312.

XX mitochondrial; human; screening assay; diabetes mellitus;

XX Huntington's disease; osteoarthritis;

XX Leber's hereditary optic neuropathy; LHON;

XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

XX neuroprotective; nootropic; antidiabetic; anticonvulsant; anticholinergic;
 XX osteopathic; ophthalmological; cyostatic.

XX Homo sapiens.

XX WO2003087768-A2.

PD 23-OCT-2003.

PF 04-APR-2003; 2003WO-US010870.

PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

DR WPI; 2003-845369/78.

PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function.
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.

XX Claim 1; SEQ ID NO 312; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, anticholinergic, osteopathic, ophthalmological and
 CC cyostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

SQ Sequence 84 AA;
 Query Match 100.0%; Score 47; DB 7; Length 84;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 |||||
 30 WCGPCK 35
 Db
 RESULT 14
 ABP60794
 ID ABP60794 standard; protein; 91 AA.
 XX
 AC ABP60794;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Thiocapsa roseopersicina thioerodoxin SEQ ID NO:143.
 XX
 KM Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 vasotropic; vulnerary; antibacterial; immunosuppressive; antitumor;
 food product; milk; wheat; oxidative stress; cataract; diabetes;
 chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 gastro intestinal bleeding; intestinal bowel disease; ulcer;
 gastro oesophageal reflux disease.
 KM
 OS Thiocapsa roseopersicina.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742900.
 XX
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 DR WPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 PT
 PS Claim 81; Page 243; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP6077 to

CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 CC
 SQ Sequence 91 AA;
 Query Match 100.0%; Score 47; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 |||||
 32 WCGPCK 37
 Db
 RESULT 15
 AAB49948
 ID AAB49948 standard; protein; 95 AA.
 XX
 AC AAB49948;
 XX
 DT 07-MAR-2001 (first entry)
 XX
 DE A. oryzae protein disulfide isomerase #3.
 XX
 KM Disulphide bond; allergy; protein disulfide isomerase variant; detergent;
 KM food additive; cosmetic.
 XX
 OS Aspergillus oryzae.
 XX
 PN WO200070064-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-DK000265.
 XX
 PR 17-MAY-1999; 99DK-00000683.
 PR 18-MAY-1999; 99DK-00000689.
 PR 02-JUN-1999; 99US-0137068P.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Hjort CM;
 PI
 DR WPI; 2001-070776/08.
 DR N-PSDB; AAC89030.
 XX
 PT Protein disulfide isomerase variant having increased reducing properties
 PT and decreased redox potential than native proteins, used to reduce
 PT allergenicity of allergic proteins in feed, food or cosmetic products.
 PT
 PS Claim 2; Page 76-77; 82pp; English.
 XX
 CC The present invention provides variants of the Aspergillus oryzae protein
 CC disulfide isomerase enzyme. These are capable of reducing disulphide
 CC bonds in proteins, which may be the cause of allergies in humans. The
 CC proteins can be used to reduce the allergenicity of foods, to treat
 CC scleroderms, in detergents, in food additives and in cosmetics
 CC
 SQ Sequence 95 AA;
 Query Match 100.0%; Score 47; DB 4; Length 95;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 |||||
 37 WCGPCK 42
 Db
 RESULT 16
 ABP60779
 ID ABP60779 standard; protein; 102 AA.
 XX

AC ABP60779;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Mycoplasma pneumoniae thioredoxin SEQ ID NO:128.
 XX
 KM Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cyostatic; antipsoriatic;
 KM vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KM bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 OS Mycoplasma pneumoniae.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742900.
 XX
 PR 05-JUL-2001; 2001US-0302885P.
 XX
 PR 04-DEC-2001; 2001US-0006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX
 DR WPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 238; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 102 AA;

Query Match 100.0%; Score 47; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 29 WCGPCK 34

RESULT 17

ABP60755
 ID ABP60755 standard; protein; 102 AA.
 XX
 AC ABP60755;
 XX
 DT 07-AUG-2003 (revised)
 DT 06-SEP-2002 (first entry)
 XX
 DE Peitact sp thioredoxin SEQ ID NO:104.
 XX
 KM Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cyostatic; antipsoriatic;
 KM vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KM bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 OS Unidentified.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742900.
 XX
 PR 05-JUL-2001; 2001US-0302885P.
 XX
 PR 04-DEC-2001; 2001US-0006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX
 DR WPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 230; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention. (Updated on 07-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 102 AA;

Query Match 100.0%; Score 47; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||

Db 27 WCGPCK 32

RESULT 18

ID ABP60756 standard; protein; 102 AA.

AC ABP60756;

DT 06-SEP-2002 (First entry)

DE Chlamydia trachomatis thioredoxin SEQ ID NO:105.

KM multimetric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; glyostatic; antiproticatic;
 KM vasotrophic; vitineary; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; evenomatoxin; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal; bowel disease; ulcer;
 KM gastro oesophageal reflux disease

OS Chlamydia trachomatis.

PN W0200250289-A1.

PD 27-JUN-2002.

PF 19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.

PR 04-DEC-2001; 2001US-00006038.

PA (SEMB-) SEMBIOSYS GENETICS IN

100

PI Del Val G, Zaplachinski S, Molone

DR WPI; 2002-508806/54.

PT Producing oil body a

PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.

PS Claim 81; Page 230; 362pp; English.

CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89553 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX
XX Sequence 102 AA;

Sequence 102 AA;

Query Match	100.0%;	Score 47;	DB 5;	Length 102;
Best Local Similarity	100.0%;	Pred. No. 13;		
Matches	6;	Conservative	0;	Mismatches 0; Indels

QY	1	WCGPCK	6
Db	27	WCGPCK	32

RESULT 19

ID ABP60753 standard; protein; 102 AA.

AC ABP60753;

DT 06-SEP-2002 (first entry)

DE Chlamydia muridarum thioredoxin SEQ ID NO:102.

KM Multienzyme protein; redox protein; thiorodoxin; thiorodoxin reductase;
KM oil body; ophthalmological; antidiabetic; cytostatic; antiporiatic;
KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
KM food product; milk; wheal; oxidative stress; cataract; diabetes;
KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing
KM gastric intestinal bleeding; intestinal bowel disease; ulcer;
KM gastro oesophageal reflux disease.

Chlamydia muridarum.

PN WO200250289-A1.

PD 27-JUN-2002.

PF 19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.

PR 04-DEC-2001; 2001US-00006038.

PA (SEMB-) SEMBIOSYS GENETICS IN

XX

PI Del Val G, Zaplachinski S, Molone

DR WPI; 2002-508806/54.

PT Producing oil body a

PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.

PS Claim 81; Page 229; 362pp; English

The present invention describes a method (M1) for producing an oil body associated with a recombinant multimeric protein complex (MPC). M1 comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting-protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface area of the human body or used to lighten the skin, or a pharmaceutical composition to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis, malignancies, reperfusion injury, wound healing, sepsis, gastric intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastric oesophageal reflux disease). ABN95963 and ABPE0677 for ABPE0964 represent sequence given in the exemplification of the present invention

invention

Sequenz

Query Match 100.0%; Score 47; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 27 WCGPCK 32

RESULT 20

ABP60777
 ID ABP60777 standard; protein; 102 AA.

AC ABP60777;
 XX

DT 06-SEP-2002 (first entry)

DE Mycoplasma genitalium thioedoxin SEQ ID NO:126.

XX Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
 XX oil body; ophthalmological; antidiabetic; cytoprotic; antiparasitic;
 KW vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro oesophageal reflux disease; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease.

XX Mycoplasma genitalium.

OS Mycoplasma genitalium.

PN WO200250289-A1.

XX 27-JUN-2002.

PF 19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.

PA 05-JUL-2001; 2001US-0302885P.

XX 04-DEC-2001; 2001US-0006038.

PA (SEMG) SEMBIOSYS GENETICS INC.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;

PI Del Val G, Zaplachinski S, Moloney M;

XX WPI; 2002-508806/54.

XX Producing oil body associated with recombinant multimeric protein complex

XX e.g. redox proteins and immunoglobulins comprises producing recombinant

XX polypeptides capable of forming the complex in cells comprising oil

XX bodies.

XX Claim 81; Page 237; 362pp; English.

XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention

XX SQ Sequence 102 AA;

Query Match 100.0%; Score 47; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 29 WCGPCK 34

RESULT 21

ADB09186
 ID ADB09186 standard; protein; 102 AA.

AC ADB09186;
 XX

DT 20-NOV-2003 (first entry)

DE Allotococcus oclis antigenic protein SEQ ID NO:3126.

XX Allotococcus oclidis; antigenic protein; immunogenic; immunisation;
 KW gene therapy; Gram-positive bacterium; infection.

XX Allotococcus oclis.

OS Allotococcus oclis.

PN WO2003048304-A2.

XX 12-JUN-2003.

PF 25-NOV-2002; 2002WO-US036123.

PR 29-NOV-2001; 2001US-0333777P.

XX 18-NOV-2002; 2002US-0426742P.

PA (AMHP) WYETH HOLDINGS CORP.

PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;

PI WPI; 2003-505284/47.

XX N-PSDB; ADB09185.

XX New Allotococcus oclidis polynucleotides and polypeptides, useful for

XX treating and diagnosing diseases, drug screening assays and monitoring of

XX effects during drug clinical trials.

XX Claim 33; SEQ ID NO 3126; 101pp; English.

XX The present invention describes an isolated polynucleotide (1) of
 CC Allotococcus oclidis genomic DNA, which encodes an antigenic protein.
 CC Allotococcus oclidis is a Gram-positive bacterium. Also described: (1)
 CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
 CC expression vector comprising the novel isolated polynucleotide (1), its
 CC complement, degenerate variant or fragment; (3) a genetically engineered
 CC host cell, transfected, transformed or infected with the vector of (2);
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
 CC composition comprising the polypeptide, its complement, biological
 CC equivalent or fragment, or the polynucleotide that is comprised in the
 CC expression vector; (6) a pharmaceutical composition comprising the
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)
 CC immunising against Allotococcus oclidis by administering to a host the
 CC immunogenic composition; (9) detecting and/or identifying Allotococcus
 CC oclidis in the biological sample; (10) a kit comprising a container
 CC containing the novel polynucleotide, its degenerate variant or fragment,
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the
 CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (I) can be used in gene therapy. The
 CC polynucleotides, polypeptides, antibodies and compositions of the present
 CC invention can be used for treating and diagnosing diseases, drug
 CC screening assays and monitoring of effects during drug clinical trials.
 CC The polynucleotides are useful for expressing and detecting Allotococcus

CC otitidis. The present sequence represents an *Allolococcus otitidis*
CC antigen protein from the present invention.
XX
SQ Sequence 102 AA;

Query Match 100.0%; Score 47; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 27 WCGPCK 32

RESULT 22

ABP60747
ID ABP60747 standard; protein; 103 AA.

AC ABP60747;
XX

DT 06-SEP-2002 (first entry)

DE *Bacillus subtilis* thioedoxin SEQ ID NO:96.

XX Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
XX oil body; ophthalmological; antidiabetic; cytosolic; antipsoptic;
XX vasotropic; vulnery; antibacterial; immunosuppressive; antilcer;
XX food product; milk; wheat; oxidative stress; cataract; diabetes;
XX chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
XX bronchiolmonary disease; malignancy; reperfusion injury; wound healing;
XX gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX gastro oesophageal reflux disease.

OS *Bacillus subtilis*.

XX WO200250289-A1.

XX 27-JUN-2002.

XX 19-DEC-2001; 2001WO-US050240.

XX 19-DEC-2000; 2000US-00742900.

XX 05-JUL-2001; 2001US-0302885P.

XX 04-DEC-2001; 2001US-0006038.

XX (SEMB-) SEMBIOSIS GENETICS INC.

XX (SYGN-) SYNGENTA PARTICIPATIONS AG.

XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
XX Del Val G, Zaplachinski S, Moloney M;

XX WPI; 2002-508806/54.

XX Producing oil body associated with recombinant multimeric protein complex
XX e.g. redox proteins and immunoglobulins comprises producing recombinant
XX polypeptides capable of forming the complex in cells comprising oil
XX bodies.

XX Claim 81; Page 227; 362pp; English.

XX The present invention describes a method (M1) for producing an oil body
XX associated with a recombinant multimeric protein complex (MPC). M1
XX comprises producing in a cell comprising oil bodies a first and second
XX recombinant polypeptide (P1, P2), where P1 is capable of associating with
XX P2 to form the MPC and associating the complex with an occlusion body
XX (OB) through an OB-targeting-protein capable of associating with OB and
XX P1. M1 is useful for producing an oil body associated with a recombinant
XX MPC. The oil bodies are further formulated for use in the preparation of
XX a food product such as milk or wheat based food product, personal care
XX product which reduces the oxidative stress on the surface area of the
XX human body or used to lighten the skin, or a pharmaceutical composition
XX used to treat chronic obstructive pulmonary disease (COPD), cataracts,
XX diabetes, envenomation, bronchiolmonary disease, psoriasis,

CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN69569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX

SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 27 WCGPCK 32

RESULT 23

ABG93246
ID ABG93246 standard; protein; 103 AA.

AC ABG93246;
XX

DT 21-NOV-2002 (first entry)

DE *C. albicans* BAX-associated protein fragment SEQ ID 450.

XX Bax; Bax-resistance; cytosolic; fungicide; immunosuppressive; virucide;
XX vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
XX apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
XX neurodegeneration; cell death.

OS *Candida albicans*.

XX WO200264766-A2.

XX 22-AUG-2002.

XX 21-DEC-2001; 2001WO-EP015398.

XX 22-DEC-2000; 2000EP-00870318.

XX 04-JAN-2001; 2001EP-00870002.

XX 09-JAN-2001; 2001EP-00870003.

XX (JANC-) JANSSEN PHARM NV.

XX Contreras RH, Eberhardt I, Luyten WMML, Reekmans RJ;

XX WPI; 2002-667002/71.

XX N-PADB; ABQ76512.

XX Claim 36; Fig 2; 344pp; English.

XX This invention describes a novel nucleic acid representing a synthetic
XX Bax gene. The Bax gene of the invention is useful for identifying Bax-
XX resistant yeast or fungi, identifying, or obtaining and identifying
XX Candida spp. sequences that are differentially expressed in a pathway
XX eventually leading to programmed cell death or identifying inhibitors or
XX inhibitor sequences of Bax-induced cell death. The products of the
XX invention have cytosolic, fungicide; immunosuppressive, virucide and
XX vasotropic activity and can be used in vaccines or for gene therapy. The
XX isolated nucleic acids, polypeptides, pharmaceutical compositions,
XX antisense molecules and antibodies are useful as medicaments or in
XX preparing a medicament for treating, preventing and/or alleviating
XX diseases associated with yeast or fungi or proliferative disorders, such
XX as cancer, or for preventing apoptosis in certain diseases. The compounds
XX or polypeptides, or the genetically modified organism are useful for
XX preparing a medicament for modifying the endogenic flora of humans and

CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention

XX
SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 24

ABG93156
ID ABG93156 standard; protein; 103 AA.

XX
AC ABG93156;

XX
DT 21-NOV-2002 (first entry)

XX
DE S. cerevisiae BAX-associated protein fragment SEQ ID 270.

KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death.

XX
OS Saccharomyces cerevisiae.

XX
PN WO200264766-A2.

XX
PD 22-AUG-2002.

XX
PF 21-DEC-2001; 2001WO-EP015398.

XX
PR 22-DEC-2000; 2000EP-00870318.

XX
PR 04-JAN-2001; 2001EP-00870002.

XX
PR 09-JAN-2001; 2001EP-00870003.

XX
PA (JANC) JANSSEN PHARM NV.

XX
PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

XX
DR WPI; 2002-667002/71.

XX
DR N-PSDB; ABQ76422.

PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.

XX
PS Claim 36; Fig 1; 34pp; English.

CC This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and

CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention

XX
SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 25

ABG93328
ID ABG93328 standard; protein; 103 AA.

XX
AC ABG93328;

XX
DT 21-NOV-2002 (first entry)

XX
DE C. albicans BAX-associated protein fragment SEQ ID 614.

KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death.

XX
OS Candida albicans.

XX
PN WO200264766-A2.

XX
PD 22-AUG-2002.

XX
PF 21-DEC-2001; 2001WO-EP015398.

XX
PR 22-DEC-2000; 2000EP-00870318.

XX
PR 04-JAN-2001; 2001EP-00870002.

XX
PR 09-JAN-2001; 2001EP-00870003.

XX
PA (JANC) JANSSEN PHARM NV.

XX
PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

XX
DR WPI; 2002-667002/71.

XX
DR N-PSDB; ABQ76594.

PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.

XX
PS Claim 36; Fig 2; 34pp; English.

CC This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and

CC other mammals. The vaccine is useful for immunizing against yeast or
 CC fungal infections. Apoptosis-related diseases include autoimmune disease,
 CC ischaemia, diseases related with viral infections or neurodegenerations.
 CC This sequence represents a polypeptide associated with the Bax gene
 CC described in the disclosure of the invention

XX SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
 |||||
 Db 29 WCGSPCK 34

RESULT 26

ABP73948
 ID ABP73948 standard; protein; 103 AA.

XX ABP73948;

XX 30-JAN-2003 (first entry)

XX Candida albicans essential protein SEQ ID NO 7785.

XX Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;

XX signal transduction; DNA replication; cell division; growth;

XX proliferation; Candida albicans; fungicide; antifungal.

XX Candida albicans.

XX WO200253728-A2.

XX 11-JUL-2002.

XX 26-DEC-2001; 2001WO-US049486.

XX 29-DEC-2000; 2000US-0259128P.

XX 20-FEB-2001; 2001US-00792024.

XX 22-AUG-2001; 2001US-0314050P.

XX (ELITRA) ELITRA PHARM INC.

XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX WPI; 2002-566694/60.

XX N-PSDB; AB232498.

XX Constructing strains for identifying gene products as effective targets
 PT for therapeutic intervention, by inactivating in the strain one allele of
 PT a gene and placing other allele of the gene under conditional expression.

XX Claim 44; SEQ ID NO 7785; 167bp + Sequence Listing; English.

XX The invention relates to constructing (M1) a strain of diploid fungal
 CC cells in which both alleles of a gene are modified, comprising modifying
 CC one allele by insertion or replacement by a cassette having an

CC expressible selectable marker and modifying other allele by
 CC recombination, of a promoter replacement fragment with a heterologous

CC promoter, so that expression of the second allele is regulated by the
 CC promoter. (M1) is useful for constructing a strain of diploid fungal

CC cells in which both alleles of a gene are modified. The diploid fungal
 CC cells having both alleles modified are useful for identifying a gene that

CC is essential to the survival or growth of a fungus, a gene that
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene

CC agent, an antifungal agent that inhibits the growth of a diploid fungus
 CC and for identifying a therapeutic agent for treatment of a mammalian

CC disease. (M1) is useful for identifying a compound which modulates the
 CC activity of a gene product, preferably enzymatic activity, carbon

CC compound catabolism, biosynthetic, transporter, transcriptional,

CC translational, signal transduction, DNA replication and cell division
 CC activity. The method is useful for identifying a compound having the
 CC ability to inhibit growth or proliferation of C. albicans cells and for
 CC treating infection by C. albicans. The present sequence is that of an
 CC essential Candida albicans protein used in the method of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office

XX SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
 |||||
 Db 29 WCGSPCK 34

RESULT 27

ABR41607
 ID ABR41607 standard; protein; 103 AA.

XX ABR41607;

XX 02-JUN-2003 (first entry)

XX Human DITHP electron transfer-associated protein.

XX Human; ditp; diagnostic and therapeutic polynucleotide; diagnosis;

XX cancer; cell proliferative disorder; autoimmune disorder;

XX inflammatory disorder; infection; hormonal disorder; metabolic disorder;

XX neurological disorder; gastrointestinal disorder; transport disorder;

XX connective tissue disorder; drug screening; proteome analysis;

XX gene therapy; antisense therapy; genotyping; transgenic animal; knock in;

XX disease model; toxicological testing; transcript imaging;

XX electron transfer-associated protein.

XX Homo sapiens.

XX WO200297031-A2.

XX 05-DEC-2002.

XX 27-MAR-2002; 2002WO-US010056.

XX 28-MAR-2001; 2001US-0279619P.

XX 29-MAR-2001; 2001US-0280067P.

XX 16-MAR-2001; 2001US-0280068P.

XX 17-MAY-2001; 2001US-0291829P.

XX 17-MAY-2001; 2001US-0291849P.

XX 19-JUN-2001; 2001US-0299428P.

XX 20-JUN-2001; 2001US-0299776P.

XX 20-JUN-2001; 2001US-0300001P.

XX (INCY-) INCYTE GENOMICS INC.

XX Dafo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

XX DuFour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;

XX Peralta CH, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstlin EH;

XX Flores V, Marwaha R, Lo A, Lan XY, Urashka ME;

XX WPI; 2003-129518/12.

XX N-PSDB; ACC46545.

XX Novel human diagnostic and therapeutic polypeptide useful for identifying
 PT test compound which specifically binds to a polypeptide encoded by human
 PT diagnostic and therapeutic polynucleotide, and to induce antibodies.

XX Claim 27; SEQ ID NO 1142; 591bp; English.

XX The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC6080-ACC6749) and to their encoded
 CC proteins (DITHP, ABR41156-ABR41812). The invention also relates to
 CC polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
 CC detecting dithp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridisation
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dithp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a DITHP protein which is associated with
 CC electron transfer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 103 AA;
 SQ

Query Match 100.0%; Score 47; DB 6; Length 103;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 26 WCGPCK 31

RESULT 28
 ADK90669
 ID ADK90669 standard; protein; 103 AA.
 XX
 AC ADK90669;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Baker's yeast thioredoxin 2 (THX2) protein SegID 14.
 XX
 KW baker's yeast; THX2; transgenic; abiotic stress response; crop plant;
 KW oxidoreductase stress-related protein; ORSRP; environmental stress;
 KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
 KW thioredoxin; THX; Quantitative Trait Locus; QTL.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO2004018687-A2.
 XX
 PD 04-MAR-2004.
 XX
 PF 01-JUL-2003; 2003WO-EP006994.
 XX
 PR 07-AUG-2002; 2002EP-00017671.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Chardonnens A, Puzio P;
 XX
 PI WPI; 2004-226856/21.
 XX
 DR N-PSDB; ADK90668.

XX New transgenic plant cell transformed by oxidoreductase stress-related
 PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
 PT plant with increased environmental stress tolerance.
 XX

Example 2; SEQ ID NO 14; 140pp; English.

XX This invention relates to novel transgenic plant cells transformed by
 CC genes encoding proteins associated with the abiotic stress response.
 CC Specifically, it refers to transgenic crop plants expressing the
 CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
 CC increased tolerance and/or resistance to environmental stresses such as
 CC salinity, drought, temperature, chemicals or pathogens. The present
 CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/or
 CC thioredoxin (THX) proteins, where expression is under the control of an
 CC inducible tissue-specific or developmentally-specific promoter and
 CC furthermore it provides antisense oligos and RNA interference molecules
 CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
 CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
 CC associated with environmental stress tolerance. This polypeptide sequence
 CC is a baker's yeast THX protein of the invention.
 XX

Sequence 103 AA;
 SQ

Query Match 100.0%; Score 47; DB 8; Length 103;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 29
 ADM32933
 ID ADM32933 standard; protein; 103 AA.
 XX
 AC ADM32933;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Amino acid sequence of a thioredoxin polypeptide.
 XX
 KW mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KW lung disease; cystic fibrosis; enzyme.
 XX
 OS Saccharomyces cerevisiae.
 OS Synthetic.
 XX
 PN WO2004024868-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 10-SEP-2003; 2003WO-US028526.
 XX
 PR 10-SEP-2002; 2002US-0409960P.
 XX
 PR 11-APR-2003; 2003US-0462082P.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI White CM;
 XX
 PD WPI; 2004-270016/25.
 XX
 DR Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.
 XX
 PS Disclosure; Page 64; 69pp; English.
 XX
 CC The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive

CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thiorodoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thiorodoxin selected from prokaryotic
CC thiorodoxin, yeast thiorodoxin, plant thiorodoxin and mammalian
CC thiorodoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thiorodoxin active site of the protein, and thiorodoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of, excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thiorodoxin polypeptides
CC which may be used in the method of the invention.

CC Sequence 103 AA;

Query Match 100.0%; Score 47; DB 8; Length 103;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
DB 29 WCGPCK 34

RESULT 30

ID AAR42820 standard; protein; 104 AA.

XX AAR42820;

XX 25-MAR-2003 (revised)

DT 04-MAY-1994 (first entry)

XX RECEF 104.

XX Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
KM therapy; thiorodoxin.

XX Homo sapiens.

XX WO9320107-A1.

PD 14-OCT-1993.

PF 06-APR-1993; 93WO-US003310.

PR 06-APR-1992; 92US-00862832.

PR 06-JUL-1992; 92US-00906642.

XX (BGM) BRIGHAM & WOMENS HOSPITAL.

XX Silberstein DS, Balcewicz-Sablinska MK;

XX WPI; 1993-336837/42.

DR N-PSDB; AAO49403.

XX Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having

XX Eosinophil-stimulating activity, for use in diagnosis and therapy.

XX Example 3; Page 65; 96pp; English.

CC A 14 kDa molecule designated various names (Eosinophil Cytotoxicity-
CC Enhancing Factor (ECEF); thiorodoxin and ADF) has been found to support
CC the growth of an BBV transformed B lymphocyte cell line in the manner of

CC IL-1; to induce the expression of IL-2 receptors in a large granular
CC lymphocyte cell line from an ATL patient in the manner of IL-1 and to
CC mediate the growth inhibitory properties of interferon gamma. Recombinant
CC ECEF (RECEF) 104 is the full length 104 amino acid polypeptide encoded by
CC this molecule and was produced for comparison studies against shortened
CC versions of the polypeptide. Some shortened ECEF's are useful because
CC they retain eosinophil stimulating activity but lack proinflammatory
CC dihol reductase activity. In particular they can be used for killing
CC tumour cells. (Updated on 25-MAR-2003 to correct PN field.)

CC Sequence 104 AA;

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
DB 30 WCGPCK 35

RESULT 31

ID AAR47855 standard; protein; 104 AA.

XX AAR47855;

XX 25-MAR-2003 (revised)

DT 18-JUL-1994 (first entry)

XX Human ADF-polypeptide.

XX ADF; thiorodoxin; pancreatitis; amylase; lipase; free radicals;

KM protein folding; denaturing; renaturing.

XX Homo sapiens.

XX EP579958-A1.

PD 26-JAN-1994.

PF 18-JUN-1993; 93EP-00109794.

PR 19-JUN-1992; 92JP-00161454.

XX (AJIN) AJINOMOTO KK.

XX Asano T, Kennochi T, Isono K, Hirakawa T, Hamuro J;

XX WPI; 1994-027626/04.

DR N-PSDB; AAO5511.

XX Use of a polypeptide having human ADF (thiorodoxin) activity - for the

XX prophylaxis or therapeutic treatment of pancreatitis or diseases which

XX accompany pancreatic disorders.

XX Claim 2; Page 9; 15pp; English.

XX The ADF polypeptide suppresses the release of the pancreatic enzymes

XX amylase and lipase into the blood thereby suppressing pancreatitis. The

XX ADF is also capable of eliminating free radicals which can cause organ

XX damage, as well as refolding denatured proteins which have been denatured

XX by free radicals. The ADF may be isolated from cultured human derived

XX cells and prepared by chemical synthesis or recombinant techniques

XX (Updated on 25-MAR-2003 to correct PN field.)

QY 1 WCGPCK 6

Query Match 100.0%; Score 47; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 30 WCGPCK 35

RESULT 32

AAR72389

ID AAR72389 standard; protein; 104 AA.

AAR72389;

10-NOV-1995 (first entry)

Recombinant human ADF.

ADP; inflammation; radiation sickness; fermentation; recombinant.

Homo sapiens.

Key Location/Qualifiers

FT Active-site 31..34

JP07079780-A.

28-MAR-1995.

20-SEP-1993; 93JP-00233361.

20-SEP-1993; 93JP-00233361.

(AJIN) AJINOMOTO KK.

WPI: 1995-157850/21.

N-PSDB; AAO87817.

Prepn. of recombinant human ADF by direct expression in E. coli - for treating inflammation and radiation sickness caused by commercially produced free radical(s).

Claim 2; Page 7-8; 11pp; Japanese.

The DNA sequence encoding human ADF was inserted into a plasmid which was then used to transform E.coli. The E.coli was then cultured and the CC recombinantly produced ADF harvested. Human ADF can be used as a treating agent for inflammation and radiation sickness

Sequence 104 AA;

Query Match 100.0%; Score 47; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WCGPCK 6

30 WCGPCK 35

RESULT 33

AAG80708

ID AAG80708 standard; protein; 104 AA.

AAG80708;

18-MAR-2002 (first entry)

S. cerevisiae TRX2 protein.

TRX2; yeast; thioredoxin; lesion; intracellular redox.

Saccharomyces cerevisiae.

JP2001288103-A.

16-OCT-2001.

02-MAR-2000; 2000JP-00057204.

02-FEB-2000; 2000JP-00025258.

(ORIY) ORIENTAL YEAST CO LTD.

WPI: 2002-117628/16.

N-PSDB; ABA97065.

A thioredoxin composition stable in solution used for treating and/or preventing lesions and diseases related to intracellular redox condition.

Claim 4; Page 14-15; 19pp; Japanese.

This invention describes a novel thioredoxin (TRX) composition, stable in solution which contains a yeast TRX derived from Saccharomyces cerevisiae X2180-1A. The TRX composition of the invention can be used for treating and/or preventing lesions and diseases related to intracellular redox conditions. This sequence represents the S. cerevisiae TRX2 protein described in the method of the invention

Sequence 104 AA;

Query Match 100.0%; Score 47; DB 5; Length 104;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WCGPCK 6

30 WCGPCK 35

RESULT 34

ABP60927

ID ABP60927 standard; protein; 104 AA.

ABP60927;

06-SEP-2002 (first entry)

Staphylococcus aureus thioredoxin reductase SEQ ID NO:276.

Multimeric protein; redox protein; thioredoxin; thioredoxin reductase; oil body; ophthalmological; antidiabetic; cytostatic; antipruritic; vasotropic; vulnery; antibacterial; immunosuppressive; antitumor; food product; milk; wheat; oxidative stress; cataract; diabetes; chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis; bronchiopulmonary disease; malignancy; reperfusion injury; wound healing; gastro intestinal bleeding; intestinal bowel disease; ulcer; gastro oesophageal reflux disease.

Staphylococcus aureus.

WO200250289-A1.

27-JUN-2002.

19-DEC-2001; 2001WO-US050240.

19-DEC-2000; 2000US-00742900.

05-JUL-2001; 2001US-0302885P.

04-DEC-2001; 2001US-0006038.

(SEMB-) SEMBIOSYS GENETICS INC.

(SYGN) SYNGENTA PARTICIPATIONS AG.

Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;

Del Val G, Zaplachinski S, Moloney M;

WPI: 2002-508806/54.

Producing oil body associated with recombinant multimeric protein complex

PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.

PS Claim 82; Page 323; 362pp; English.

The present invention describes a method (M1) for producing an oil body associated with a recombinant multimeric protein complex (MPC). M1 comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface area of the human body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, emphysema, bronchiolopulmonary disease, psoriasis, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastro oesophageal reflux disease). ABN859569 to ABN895953 and ABPe0677 to ABPe0964 represent sequence given in the exemplification of the present invention

SQ Sequence 104 AA;

Query Match Similarity	100.0%	Score 47	DB 5	Length 104
Beet Local Similarity	100.0%	Pred. No. 14		
Matches	6	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	1 WCGPCK	6		
DB	28 WCGPCK	33		

RESULT 35
ABP60803
ID ABP60803 standard; protein; 104 AA.

DT 06-SEP-2002 (first entry)

DE Homo sapiens thioredoxin SEQ ID NO:152.

KM Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KM oil body; ophthalmological; antidiabetic; cytoskeletal; antipariatic;
KM vasostropic; vulnairiology; antibacterial; immunosuppressive; antitumor;
KM food product; milk; wheat; oxidative stress; catarract; diabetes;
KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KM gastro intestinal bleeding; intestinal; bowel disease; ulcer;
KM gastro oesophageal reflux disease

OS Homo sapiens.

PN W0200250289-A1.

PD 27-JUN-2002.

19-DEC-2001; 2001WO-US050240.

19-DEC-2000; 2000US-00742900.

04-DEC-2001; 2001US-00006038.

PA (SEMB-) SEMBIOSYS GENETICS IN

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Van Rooijen G, Deckers H, Heifetz

XX

[illegible]

DR WPI; 2002-508806/54.

PT producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.

PS Claim 81; Page 246; 362pp; English.

The present invention describes a method (M1) for producing an oil body associated with a recombinant multimeric protein complex (MPC). M1 comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting-protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface area of the human body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, emphysema, bronchiolopulmonary disease, psoriasis, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastro oesophageal reflux disease). ABRN95565 to ABRN85993 and ABB60677 to ABB60964 represent sequence given in the exemplification of the present invention.

SQ Sequence 104 AA;

Query Match	Similarity	Score	DB	Length
Best Local	100.0%	100.0%	Pred. No. 14	
Matches	6	Conservative	0	Mismatches
			0	Indels
			0	Gaps
QY	1 WCGPCK	6		
DB	30 WCGPCK	35		

RESULT 36
ABP60797
ID ABP60797 standard; protein; 104 AA.

DT 06-SEP-2002 (first entry)

DE Bos taurus thioredoxin SEQ ID NO:146.

KM Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KM oil body; ophthalmological; antidiabetic; cytosolic; antiproteolytic;
KM vasostolic; pulmonary; antibacterial; immunosuppressive; antilucer;
KM food product; milk; wheat; oxidative stress; cataract; diabetes;
KM chronic obstructive pulmonary disease; emphysema; pleuritis; sepsis;
KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
KM gastro oesophageal reflux disease

Bos taurus.

PN W0200250289-A1.

27-JUN-2002
PD

19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.

04-DEC-2001; 2001US-00006038.

04-DEC-2001; 2001US-00006038.

PA (SEMB-) SEMBIOSYS GENETICS INC.

[illegible]

PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M,
 XX
 DR MPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 244; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 104 AA;
 XX
 QY Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 1 WCGPCK 6
 30 WCGPCK 35
 XX
 RESULT 37
 ABP60812
 ID ABP60812 standard; protein; 104 AA.
 AC ABP60812;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Ovis aries thiredoxin SEQ ID NO:161.
 XX
 XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytosolic; antipsoptic;
 KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 OS Ovis aries.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00060638.
 XX

PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M,
 XX
 DR MPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 249; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 104 AA;
 XX
 QY Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 1 WCGPCK 6
 30 WCGPCK 35
 XX
 RESULT 38
 ABP60805
 ID ABP60805 standard; protein; 104 AA.
 AC ABP60805;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Macaca mulatta thiredoxin SEQ ID NO:154.
 XX
 XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytosolic; antipsoptic;
 KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 OS Macaca mulatta.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742900.
 XX

PR 05-JUL-2001; 2001US-0302885P.
PR 04-DEC-2001; 2001US-00006038.
XX
XX (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
PI Del Val G, Zaplachinski S, Moloney M;
XX MPI; 2002-508806/54.
XX
XX
XX Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX
XX Claim 81; Page 247; 362pp; English.
XX
XX The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP69964 represent sequence given in the exemplification of the present
CC invention
XX
XX Sequence 104 AA;
SQ

Query Match 100.0%; Score 47; DB 5; Length 104;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 30 WCGPCK 35

RESULT 39
ID ABP60806 standard; protein; 104 AA.
XX
AC ABP60806;
XX
DT 06-SEP-2002 (first entry)
XX
DE Mus musculus thioedoxin SEQ ID NO:155.
XX
KM Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
KM oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
KM vasotrophic; vulnery; antibacterial; immunosuppressive; antitumor;
KM food product; milk; wheat; oxidative stress; cataract; diabetes;
KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KM bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
KM gastro oesophageal reflux disease.
XX
XX Mus musculus.
OS
PN WO200250289-A1.
XX
PD 27-JUN-2002.
XX

PF 19-DEC-2001; 2001WO-US050240.
XX
XX 19-DEC-2000; 2000US-00742900.
PR 05-JUL-2001; 2001US-0302885P.
PR 04-DEC-2001; 2001US-00006038.
XX
XX (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
PI Del Val G, Zaplachinski S, Moloney M;
XX MPI; 2002-508806/54.
XX
XX
XX Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX
XX Claim 81; Page 247; 362pp; English.
XX
XX The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN85565 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX
XX Sequence 104 AA;
SQ

Query Match 100.0%; Score 47; DB 5; Length 104;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 30 WCGPCK 35

RESULT 40
ID ABP60809 standard; protein; 104 AA.
XX
AC ABP60809;
XX
DT 06-SEP-2002 (first entry)
XX
DE Oryctolagus cuniculus thioedoxin SEQ ID NO:158.
XX
KM Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
KM oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
KM vasotrophic; vulnery; antibacterial; immunosuppressive; antitumor;
KM food product; milk; wheat; oxidative stress; cataract; diabetes;
KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KM bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
KM gastro oesophageal reflux disease.
XX
XX Oryctolagus cuniculus.
OS
PN WO200250289-A1.
XX
XX

XX 27-JUN-2002.
 PD 19-DEC-2001; 2001WO-US050240.
 XX 19-DEC-2001; 2001WO-US050240.
 XX 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX WPI; 2002-508806/54.
 DR
 XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 PS Claim 81; Page 248; 362pp; English.
 XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX Sequence 104 AA;
 SQ
 Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 DB 30 WCGPCK 35
 RESULT 41
 ABP60810
 ID ABP60810 standard; protein; 104 AA.
 AC ABP60810;
 XX 06-SEP-2002 (first entry)
 DT Rattus norvegicus thiodoxin SEQ ID NO:159.
 XX
 DE Multimeric protein; redox protein; thiodoxin; thiodoxin reductase;
 XX oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
 XX vasoregic; vulnary; antibacterial; immunosuppressive; antitumor;
 XX food product; milk; wheat; oxidative stress; cataract; diabetes;
 XX chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 XX bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 XX gastro intestinal bleeding; intestinal bowel disease; ulcer;
 XX gastro oesophageal reflux disease.

OS Rattus norvegicus.
 XX
 XX WO200250289-A1.
 PN
 XX 27-JUN-2002.
 PD 19-DEC-2001; 2001WO-US050240.
 XX 19-DEC-2001; 2001WO-US050240.
 XX 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX WPI; 2002-508806/54.
 DR
 XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 PS Claim 81; Page 248-249; 362pp; English.
 XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX Sequence 104 AA;
 SQ
 Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 DB 30 WCGPCK 35
 RESULT 42
 ABP60801
 ID ABP60801 standard; protein; 104 AA.
 AC ABP60801;
 XX 06-SEP-2002 (first entry)
 DT Gallus gallus thiodoxin SEQ ID NO:150.
 XX
 DE Multimeric protein; redox protein; thiodoxin; thiodoxin reductase;
 XX oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
 XX vasoregic; vulnary; antibacterial; immunosuppressive; antitumor;
 XX food product; milk; wheat; oxidative stress; cataract; diabetes;
 XX chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 XX bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;

KW chlorodexin; THX; Quantitative Trait Locus; QTL.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO2004018687-A2.
 XX
 PD 04-MAR-2004.
 XX
 PF 01-JUL-2003; 2003WO-EP006994.
 XX
 PR 07-AUG-2002; 2002EP-00017671.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Chardonnais A, Puzio P;
 XX
 DR WPI; 2004-226856/21.
 DR N-PSDB; ADR90666.
 XX
 PT New transgenic plant cell transformed by oxidoreductase stress-related
 PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
 XX plant with increased environmental stress tolerance.
 XX
 PS Example 2; SEQ ID NO 12; 140bp; English.
 XX
 CC The invention relates to novel transgenic plant cells transformed by
 CC genes encoding proteins associated with the abiotic stress response.
 CC Specifically, it refers to transgenic crop plants expressing the
 CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
 CC increased tolerance and/or resistance to environmental stresses such as
 CC salinity, drought, temperature, chemicals or pathogens. The present
 CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/or
 CC thioredoxin (THX) proteins, where expression is under the control of an
 CC inducible tissue-specific or developmentally-specific promoter and
 CC furthermore it provides antisense oligos and RNA interference molecules
 CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
 CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
 CC associated with environmental stress tolerance. This polypeptide sequence
 CC is a baker's yeast THX protein of the invention.
 XX
 SQ Sequence 104 AA;
 XX

Query Match 100.0%; Score 47; DB 8; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 45
 ADO59801
 ID ADO59801 standard; protein; 104 AA.
 XX
 AC ADO59801;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE B. subtilis metabolic pathway gene, trxA, protein.
 XX
 KW chip; metabolic pathway; acoA; ahpc; ahpf; citB; clpC; clpP; codY; csprA;
 KW csprB; des; dnaK; eno; glrA; groEL; groL; lbpA; lbpB; katA; katB; lcpP;
 KW lch; opuAB; phoA; phoD; pds; purC; purN; pyrB; pyrE; sigB; trnA; trxA;
 KW ydjF; fermentation monitoring; process control; increased efficiency.
 XX
 OS Bacillus subtilis.
 XX
 PN DE10242433-A1.
 PN
 PD 25-MAR-2004.
 PD
 PF 11-SEP-2002; 2002DE-01042433.
 PF

XX
 PR 11-SEP-2002; 2002DE-01042433.
 XX
 PA (HENK) HENKEL KGAA.
 PA (UYGR) UNIV GREIFSWALD.
 XX
 PI Feesche J, Maurer K, Breves R, Schweder T, Hecker M, Juergen B,
 PI Voigt B;
 XX
 DR WPI; 2004-271050/26.
 DR N-PSDB; ADO59800.
 XX
 PT Chip carrying probes for specific genes, useful for rapid monitoring of
 PT organism status, particularly during fermentation.
 XX
 PS Disclosure; SEQ ID NO 78; 138bp; German.
 XX
 CC The invention relates to a chip that carries probes for at least one
 CC regulated genes involved in the corresponding metabolic pathways in other
 CC organisms. The specified genes are acoA, ahpc, citB, clpC, clpP,
 CC codY, csprA, csprB, des, dnaK, eno, glrA, groEL, groL, lbpA, lbpB, katA,
 CC katB, lcpP, lch, opuAB, phoA, phoD, pds, purC, purN, pyrB, pyrE, sigB,
 CC trnA, trxA and ydjF. The specification includes a table identifying the
 CC products of these genes. The chips are used to determine the
 CC physiological condition of organisms being used in a biological process,
 CC especially for monitoring fermentations for production of a protein or
 CC low molecular weight compound, but also for laboratory-scale cloning and
 CC expression analysis. The method is quicker than gel electrophoretic
 CC methods currently used, so allows a more rapid intervention for process
 CC control and thus increased efficiency. The present sequence represents
 CC the amino acid sequence of a B. subtilis metabolic pathway gene protein.
 XX

Query Match 100.0%; Score 47; DB 8; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 28 WCGPCK 33

RESULT 46
 ADS88157
 ID ADS88157 standard; protein; 104 AA.
 XX
 AC ADS88157;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human protein of a TNF-alpha signalling pathway protein complex Seqid 12.
 XX
 KW protein complex; tumour necrosis factor-alpha signalling pathway;
 KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
 KW inflammatory bowel disease; infectious disease; septic shock;
 KW bacterial infection; neurological disease; stroke-induced inflammation;
 KW neurodegenerative disease; cancer; antiinflammatory; antiautistic;
 KW antirheumatic; cytoskeletal; antibacterial; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035783-A2.
 PN
 PD 29-APR-2004.
 PD
 PF 24-SEP-2003; 2003WO-EP050655.
 PF
 PR 26-SEP-2002; 2002EP-00021809.
 PR 10-FEB-2003; 2003EP-00100274.
 XX
 PA (CELL-) CELLZOME AG.
 XX

PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
 XX Supertl-Furga G, Kruse U;
 XX WPI; 2004-348460/32.
 DR
 PT New protein complex comprising at least one first and second protein of
 PT the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for
 PT diagnosing or treating inflammation, neurological diseases, infectious
 PT diseases or cancer.
 XX
 PS Example; SEQ ID NO 12; 1980pp; English.
 XX
 CC This invention relates to novel protein complexes of the tumour necrosis
 CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
 CC methods for preparing these complexes comprising at least two component
 CC proteins, as well as screening methods to identify modulators of the
 CC pathway, which include antibodies, agonists and antagonists thereof. The
 CC present invention describes a protein complex and kit that are useful for
 CC diagnosing, prognosing or treating chronic inflammatory diseases such as
 CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
 CC such as septic shock and bacterial infections; neurological diseases such
 CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
 CC cancer. Accordingly, these complexes can be used for the development of
 CC pharmaceutical compositions that exhibit anti-inflammatory, antiarthritic,
 CC antiheumatic, cytostatic and antibacterial activities and can be used
 CC for gene therapy purposes. In particular, the invention further provides
 CC siRNA-oligonucleotides useful for inhibiting protein expression for in
 CC vitro or cell culture assays. This polypeptide is a human protein that
 CC can be used in combination with other proteins provided in the
 CC specification to form novel complexes of the TNF-alpha signalling pathway
 CC of the invention.
 CC
 SQ Sequence 104 AA;
 XX
 XX
 Query Match 100.0%; Score 47; DB 8; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGSPCK 6
 DB 30 WCGSPCK 35
 XX
 RESULT 47
 AAP92141
 ID AAP92141 standard; protein; 105 AA.
 XX
 AC AAP92141;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JUN-1990 (first entry)
 XX
 DE Recombinant human adult T cell leukaemia derived factor.
 XX
 KM Human adult T cell leukaemia derived factor; hADF; cancer;
 KM immunodeficiency disease.
 XX
 OS Homo sapiens.
 XX
 PI Key Location/Qualifiers
 FH Region 2..105
 FT /note= "Claim 1"
 FT
 XX
 PN EP299206-A.
 XX
 PD 18-JAN-1989.
 XX
 PF 10-JUN-1988; 88BP-00109311.
 XX
 PR 12-JUN-1987; 87JP-00146348.
 PR 31-MAY-1988; 88BP-00134218.
 XX
 PA (AJIN) AJINOMOTO KK.

XX
 PI Yodoi J, Tagaya Y, Maeda M, Matsui H, Kondo N, Hamuro J;
 XX
 DR WPI; 1989-016762/03.
 DR N-PSDB; AAN93083.
 XX
 PT Recombinant human adult T cell leukaemia derived factor polypeptide -
 PT used for treating cancer, immuno-deficiency disease etc.
 XX
 PS Disclosure; Page; 24pp; English.
 XX
 CC DNA encoding the polypeptide was sequenced from a gene bank prep. from
 CC mRNA isolated from ATL-2 cells from patient with adult T leukaemia virus.
 CC Vectors contg. the DNA can be used to transform host cells for prodn. of
 CC hADF polypeptide. The polypeptide causes differentiation and induces
 CC growth of lymphocytes and fibroblasts. The N-terminal Met is optional.
 CC Similar peptides with deletions, substs. and allelic derivs. may also be
 CC used. See also AAP94809. (Updated on 25-MAR-2003 to correct PR field.)
 CC
 SQ Sequence 105 AA;
 XX
 XX
 Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGSPCK 6
 DB 31 WCGSPCK 36
 XX
 RESULT 48
 AAR42819
 ID AAR42819 standard; protein; 105 AA.
 XX
 AC AAR42819;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-MAY-1994 (first entry)
 XX
 DE ECEF/thioredoxin/hADF.
 XX
 KM Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
 KM therapy; thioredoxin.
 XX
 OS Homo sapiens.
 XX
 PN WO9320107-A1.
 XX
 PD 14-OCT-1993.
 XX
 PF 06-APR-1993; 93WO-US003310.
 XX
 PR 06-APR-1992; 92US-00862832.
 PR 06-JUL-1992; 92US-00906842.
 XX
 PA (BGMH) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Silberstein DS, Balcewicz-Sablinska MK;
 XX
 DR WPI; 1993-336837/42.
 DR N-PSDB; AAQ49402.
 XX
 PT Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having
 PT Eosinophil-stimulating activity, for use in diagnosis and therapy.
 XX
 PS Disclosure; Fig 6; 96pp; English.
 XX
 CC A 14 kDa molecule was isolated by three separate groups and found to
 CC support the growth of an EBV transformed B lymphocyte cell line in the
 CC manner of IL-1. It was also found to induce the expression of IL-2
 CC receptors in a large granular lymphocyte cell line from an ATL patient in
 CC the manner of IL-1. The molecule has been designated various names, these
 CC being Eosinophil Cytotoxicity-Enhancing Factor; (ECEF) thioredoxin and

CC ADF. The molecule has also been found to mediate the growth inhibitory
 CC properties of interferon gamma. Some shortened ECEP's are useful because
 CC they retain eosinophil stimulating activity but lack proinflammatory
 CC diethylol reductase activity. In particular they can be used for killing
 CC tumour cells. (Updated on 25-Mar-2003 to correct PN field.)

SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 31 WCGPCK 36

RESULT 49

AAK37700
 ID AAK37700 standard; protein; 105 AA.

XX AAK37700;

DT 09-NOV-1993 (first entry)

XX ADF.

KM Human; ADF; transgenic; mouse; beta-actin; promoter; terminator;
 KW resistant; stress; anti-inflammatory drugs.

OS Homo sapiens.

XX JP05130819-A.

XX 28-MAY-1993.

XX 12-NOV-1991; 91JP-00295618.

XX 12-NOV-1991; 91JP-00295618.

XX (AJIN) AJINOMOTO KK.

XX WPI; 1993-208254/26.

DR N-PSDB; AAQ43433.

PT New human ADF transgenic mouse - is resistant to stress and is useful for
 PT prepn. of antiinflammatory drugs.

PS Claim 3; Page 5; 10pp; Japanese.

CC This sequence represents human ADF. The DNA encoding this sequence may be
 CC used in the production of a transgenic mouse. The transgenic mouse
 CC contains, in the 5' to 3' direction, a human beta-actin promoter, the
 CC human ADF coding gene, a termination codon, a human beta-actin poly(A)
 CC signal and a human beta-actin terminator. The transgenic mouse is
 CC resistant to stress. It is useful in the research of the mechanism of
 CC stress and for the development of anti-inflammatory drugs

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 31 WCGPCK 36

RESULT 50

AAK47856
 ID AAK47856 standard; protein; 105 AA.

XX

AC AAK47856;

XX 25-MAR-2003 (revised)

DT 18-JUL-1994 (first entry)

XX Human ADF-polypeptide.

KM ADF; thioredoxin; pancreatitis; amylase; lipase; free radicals;
 KW protein folding; denaturing; renaturing.

OS Homo sapiens.

XX EP579958-A1.

XX 26-JAN-1994.

XX 18-JUN-1993; 93EP-00109794.

XX 19-JUN-1992; 92JP-00161454.

XX (AJIN) AJINOMOTO KK.

XX Asano T, Kermochi T, Isono K, Hirakawa T, Hamuro J;

XX WPI; 1994-027626/04.

DR N-PSDB; AAQ55112.

PT Use of a polypeptide having human ADF (thioredoxin) activity - for the
 PT prophylaxis or therapeutic treatment of pancreatitis or diseases which
 PT accompany pancreatic disorders.

XX Claim 2; Page 12; 15pp; English.

CC The ADF polypeptide suppresses the release of the pancreatic enzymes
 CC amylase and lipase into the blood thereby suppressing pancreatitis. The
 CC ADF is also capable of eliminating free radicals which can cause organ
 CC damage, as well as refolding denatured proteins which have been denatured
 CC by free radicals. The ADF may be isolated from cultured human derived
 CC cells and prepared by chemical synthesis or recombinant techniques
 CC (Updated on 25-Mar-2003 to correct PN field.)

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 31 WCGPCK 36

RESULT 51

AAK72390
 ID AAK72390 standard; protein; 105 AA.

XX AAK72390;

XX 10-NOV-1995 (first entry)

XX Recombinant human ADF.

XX ADF; inflammation; radiation sickness; fermentation; recombinant.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Active-site 32..35

XX JP07079780-A.

XX 28-MAR-1995.

XX

```

PF 20-SEP-1993; 93JP-00233361.
XX
PR 20-SEP-1993; 93JP-00233361.
XX
PA (AJIN ) AJINOMOTO KK.
XX
DR WPI; 1995-157850/21.
XX
DR N-PSDB; AA087818.
XX
PT Prepn. of recombinant human ADF by direct expression in E. coli - for
PT treating inflammation and radiation sickness caused by commercially
PT produced free radical(s).
XX
PS Claim 3; Page 8; 11pp; Japanese.
XX
CC The DNA sequence encoding human ADF was inserted into a plasmid which was
CC then used to transform E.coli. The E.coli was then cultured and the
CC recombinantly produced ADF harvested. Human ADF can be used as a treating
CC agent for inflammation and radiation sickness
XX
SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGSPCK 6
DB 31 MCGSPCK 36

RESULT 52
AAW69567
ID AAW69567 standard; protein; 105 AA.
XX
AC AAW69567;
XX
DT 15-OCT-1998 (first entry)
XX
DB Human thioredoxin mutant C62S/C69S/C73S.
XX
KW Human; thioredoxin; mutant; variant; TRX; AP-1; transcriptional activity;
KW Ref-1.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 62 /note= "Cys in wild type"
FT Misc-difference 69 /note= "Cys in wild type"
FT Misc-difference 73 /note= "Cys in wild type"
XX
EP853088-A2.
XX
PD 15-JUL-1998.
XX
PE 14-JAN-1998; 98EP-00100535.
XX
PR 14-JAN-1997; 97JP-00004489.
XX
PA (ORIV ) ORIENTAL YEAST CO LTD.
PA (YODO/) YODOI J.
XX
PI Yodoi J;
XX
DR WPI; 1998-364621/32.
XX
PT New thioredoxin variants with amino acid substitutions for cysteine
PT except at active centre for increasing stability in non-reducing
PT conditions - used with Ref-1 to enhance AP-1 transcriptional activity.

```

```

XX
PS Example 3; Page; 14pp; English.
XX
CC The present sequence represents a human thioredoxin (TRX) variant derived
CC from the wild-type sequence (obtained from Genbank), as stated in the
CC specification. TRX variants can be made stable under non-reducing
CC conditions by substituting at least one or all Cys residues by other
CC amino acid residues, except that Cys residues in the active centre of TRX
CC remain unmodified. Also described in the present invention is a factor
CC for enhancing the transcriptional activity of AP-1 which comprises the
CC TRX variant and Ref-1 associated with each other via an S-S bond. TRX
CC variants can be used with Ref-1 to enhance AP-1 transcriptional activity.
CC TRX variants do not form multimers and are stable under non-reducing
XX conditions
XX
SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGSPCK 6
DB 31 MCGSPCK 36

RESULT 53
AAV25908
ID AAV25908 standard; protein; 105 AA.
XX
AC AAV25908;
XX
DT 06-OCT-1999 (first entry)
XX
DE Human thioredoxin protein.
XX
KW Thioredoxin; thioredoxin reductase; human; antisense; primer; metastasis;
KW cytosolic; tumour growth inhibitor; detection; nuclease resistant;
KW phosphorothioate linkage.
XX
OS Homo sapiens.
XX
PN WO938963-A1.
XX
PD 05-AUG-1999.
XX
PE 29-JAN-1999; 99WO-CA000077.
XX
PR 30-JAN-1998; 98US-0073196P.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH, Lee YS;
XX
DR WPI; 1999-469328/39.
XX
DR N-PSDB; AA200544.
XX
PT Antisense oligonucleotides against thioredoxin and thioredoxin reductase
PT genes, useful for inhibiting tumor growth and metastasis.
XX
PS Disclosure; Fig 2; 88pp; English.
XX
CC This invention describes novel antisense oligonucleotides against
CC thioredoxin and thioredoxin reductase gene which have cytostatic activity
CC and are useful for inhibiting tumour growth and metastasis in mammals.
CC They may also be used as hybridization probes to detect the presence of
CC the thioredoxin and thioredoxin reductase mRNAs in mammalian cells. They
CC may also be used as molecular weight markers. The antisense
CC oligonucleotides are nuclease resistant due to the presence of
CC phosphorothioate internucleotide linkages. This sequence represents the
CC human thioredoxin protein
XX
SQ Sequence 105 AA;

```

Query Match 100.0%; Score 47; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 54
 AAG03956
 ID AAG03956 standard; protein; 105 AA.

AC AAG03956;
 DT 06-OCT-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 8037.
 XX
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GBST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 DR N-PSDB; AAC03962.
 XX
 DR N-PSDB; AAC03962.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 8037; 71bp + Sequence listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 CC
 SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 3; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 55
 ABP60700

ID ABP60700 standard; protein; 105 AA.

XX ABP60700;

AC 06-SEP-2002 (first entry)

DE Human thioredoxin protein SEQ ID NO:47.

XX
 XX
 KW Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytostatic; antipneumatic;
 KW vasotropic; vulnary; antibacterial; immunosuppressive; antileuk;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease.

XX Homo sapiens.

XX WO200250289-A1.

XX 27-JUN-2002.

XX 19-DEC-2001; 2001WO-US050240.

XX 19-DEC-2000; 2000US-00742900.

XX 05-JUL-2001; 2001US-0302885P.

XX 04-DEC-2001; 2001US-00006038.

XX (SEMB-) SEMBIOSYS GENETICS INC.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmata BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX N-PSDB; ABR89591.

XX WPI; 2002-508806/54.

XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.

XX Disclosure; Page 203; 362pp; English.

XX The present invention describes a method (M1) for producing an oil body

XX associated with a recombinant multimeric protein complex (MPC). M1

XX comprises producing in a cell comprising oil bodies a first and second

XX recombinant polypeptide (P1, P2), where P1 is capable of associating with

XX P2 to form the MPC and associating the complex with an occlusion body

XX (OB) through an OB-targeting protein capable of associating with OB and

XX P1. M1 is useful for producing an oil body associated with a recombinant

XX MPC. The oil bodies are further formulated for use in the preparation of

XX a food product such as milk or wheat based food product, personal care

XX product which reduces the oxidative stress on the surface area of the

XX human body or used to lighten the skin, or a pharmaceutical composition

XX used to treat chronic obstructive pulmonary disease (COPD), cataracts,

XX diabetes, envenomation, bronchiopulmonary disease, psoriasis,

XX malignancies, reperfusion injury, wound healing, sepsis, gastro

XX intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD

XX (gastro oesophageal reflux disease). ABR89569 to ABR89593 and ABP60677 to

XX ABP6064 represent sequence given in the exemplification of the present

XX invention

SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 56
ABP60757
ID ABP60757 standard; protein; 105 AA.
XX
AC ABP60757;
XX
DT 06-SEP-2002 (first entry)
XX
DE Corynebacterium nephridii thioresoxin SEQ ID NO:106.
XX
XX Multimeric protein; redox protein; thioresoxin; thioresoxin reductase;
XX oil body; ophthalmological; antidiabetic; cytostatic; antiproliferative;
XX vasoregulatory; antibacterial; immunosuppressive; antitumor;
XX food product; milk; wheat; oxidative stress; cataract; diabetes;
XX chronic obstructive pulmonary disease; emphysema; peritonitis; sepsis;
XX bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
XX gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX gastro oesophageal reflux disease.
XX
XX Corynebacterium nephridii.
XX
XX WO200250289-A1.
XX
PD 27-JUN-2002.
XX
XX 19-DEC-2001; 2001WO-US050240.
XX
PR 19-DEC-2000; 2000US-00742800.
XX
PR 05-JUL-2001; 2001US-0302885P.
XX
PR 04-DEC-2001; 2001US-0000603P.
XX
XX (SEMB-) SEMBIOSYS GENETICS INC.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK,
PI Del Val G, Zaplachinski S, Moloney M;
XX
XX MPI; 2002-508806/54.
XX
DR Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX
XX
PS Claim 81, Page 230; 362pp; English.
XX
XX The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, emphysema, bronchiolopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX
SQ Sequence 105 AA;
XX

Query Match 100.0%; Score 47; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 57
ABG93363
ID ABG93363 standard; protein; 105 AA.
XX
AC ABG93363;
XX
DT 21-NOV-2002 (first entry)
XX
DE Human BAX-associated protein fragment SEQ ID 684.
XX
XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
XX vasoregulatory; vaccine; gene therapy; proliferative disorder; cancer;
XX apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
XX neurodegeneration; cell death.
XX
XX Homo sapiens.
XX
XX WO200264766-A2.
XX
PD 22-AUG-2002.
XX
XX 21-DEC-2001; 2001WO-EP015398.
XX
PR 22-DEC-2000; 2000EP-00870318.
XX
PR 04-JAN-2001; 2001EP-00870002.
XX
PR 09-JAN-2001; 2001EP-00870003.
XX
XX (JANC) JANSSEN PHARM NV.
XX
PI Contreras RH, Eberhardt I, Luyten WML, Reekmans RJ;
XX
XX MPI; 2002-667002/71.
XX
DR N-PSDB; ABQ76629.
XX
XX
PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX
XX
PS Claim 36; Fig 2; 344pp; English.
XX
XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide, immunosuppressive, virucide and
CC vasoregulatory activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antitumor molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenous flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention
XX
XX
SQ Sequence 105 AA;
XX

Query Match 100.0%; Score 47; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 31 WCGPCK 36

RESULT 58

ABO07225
 ID ABO07225 standard; protein; 105 AA.

AC ABO07225;

DT 13-AUG-2003 (first entry)

DE Human p53 modifying protein, SEQ ID 185.

KM Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 KM antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KM lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KM apoptotic disorder; cell proliferation disorder.

OS Homo sapiens.

PN WO200299122-A1.

PD 12-DEC-2002.

PF 03-JUN-2002; 2002WO-US017382.

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

PA (EXEL-) EXELIXIS INC.

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP,

DR WPI; 2003-156859/15.

DR N-PSDB; ACD13398.

PT Identifying modulators of the p53 pathway for use in treating apoptotic

PT or cell proliferation disorders, comprises screening for agents that

PT modulate activity of a human ortholog of genes that modify the p53

PT pathway in Drosophila.

PS Example 2; Page 536; 678pp; English.

CC The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human orthologue of genes that modify the p53 pathway in
 CC Drosophila) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood of disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer.
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,

CC apoptotic or cell proliferation disorders. The present sequence
 CC represents a human p53 pathway modifying protein

CC Sequence 105 AA;

Query Match

Best Local Similarity 100.0%; Score 47; DB 6; Length 105;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 31 WCGPCK 36

RESULT 59

ABR92158
 ID ABR92158 standard; protein; 105 AA.

AC ABR92158;

DT 10-SEP-2003 (first entry)

DE Human cervical cancer cell marker protein SEQ ID NO:226.

KM Human; cervical cancer; cervical cancer marker; cancer therapy;
 KM detection; gene therapy; vaccine.

OS Homo sapiens.

PN WO2002101075-A2.

PD 19-DEC-2002.

PF 12-JUN-2002; 2002WO-US018638.

PR 13-JUN-2001; 2001US-0298155P.

PR 13-JUN-2001; 2001US-0298159P.

PR 14-NOV-2001; 2001US-0335936P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;

PI Ganavarapu M, Glatt K, Hoersch S;

DR WPI; 2003-156867/15.

DR N-PSDB; ACF12941.

PS Claim 4; Page 377-378; 386pp; English.

CC ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
 CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
 CC normal indicates the presence of cervical cancer. Also described: (1) a
 CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
 CC assessing (M1) whether a patient is afflicted with cervical cancer,
 CC comprising comparing the level of expression of a marker in a patient's
 CC sample, and the normal level of expression of the marker in a control non
 CC -cervical cancer sample, where a significant increase in the level of
 CC expression of the marker in the patient's sample relative to that in the
 CC control sample is an indication that the patient is afflicted with
 CC cervical cancer. (I) has cytostatic activity, and can be used in gene
 CC therapy and in vaccines. (I) is useful in detecting, characterizing,
 CC preventing and treating human cervical cancers. (I) may also be used in
 CC various prognostic and diagnostic assays, pharmacogenomics and in
 CC monitoring clinical trials

CC Sequence 105 AA;

Query Match

Best Local Similarity 100.0%; Score 47; DB 6; Length 105;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 31 WCGPCK 36

RESULT 60
ADD67269
ID ADD67269 standard; protein; 105 AA.
AC ADD67269;
XX
XX
DT 15-JAN-2004 (first entry)
XX
XX Thiorodoxin protein SEQ ID NO:127.
DE
XX apparatus combination; binding site collection; pattern recognition;
KM profiling; screening.
XX
XX Mus musculus.
OS
PN WO2003062402-A2.
XX
PD 31-JUL-2003.
XX
XX 24-JAN-2003; 2003WO-US002397.
PF
XX 24-JAN-2002; 2002US-0352011P.
PR
XX (POIN-) POINTILLISTE INC.
PA
XX Ault-Riche D, Kasaner PD;
PI
XX WPI; 2003-636736/60.
DR
XX
XX New combination comprising an addressable collection of binding sites,
PT software comprising instructions for pattern recognition and an imager
PT for detecting patterns, useful for profiling a sample.
XX
XX
PS Example 7; SEQ ID NO 127; 309pp; English.
XX
XX The present invention describes a combination of apparatus (I)
CC comprising: (a) an addressable collection of binding sites; and (b)
CC software comprising instructions for pattern recognition and/or an imager
CC for detecting patterns. The addressable collection of binding sites
CC comprises: (a) capture agents, where each capture agent is preselected to
CC specifically bind to a pre-selected tag; and (b) tagged reagents, each
CC comprising one of the pre-selected tags, where each locus in the
CC collection comprises the same capture agent, where the tagged reagent
CC comprises a molecule and a tag, each tag is pre-selected to specifically
CC bind to a capture agent, where each tag is bound to a capture agent,
CC forming a complex of the tagged reagent with the capture agent, where
CC each locus comprises tagged reagents and where each of the different
CC molecules at each locus comprises the same pre-selected tag. Also
CC described: (1) a system for profiling samples; (2) a method for profiling
CC a sample; (3) a computer system or computer readable medium comprising
CC the database produced by the method of profiling a sample; (4) a method
CC for preparing a capture system that displays a collection of binding
CC sites; (5) a positionally addressable collection of binding sites
CC comprising capture agents bound to a solid support and tagged reagents;
CC and (6) a method for screening samples. The combination (I) is useful for
CC profiling a sample. The present sequence is used in the exemplification
CC of the present invention.
XX
XX
SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |

Db 31 WCGPCK 36

RESULT 61
ADF30728.
ID ADF30728 standard; protein; 105 AA.
XX
XX ADF30728;
AC
XX
XX
DT 12-FEB-2004 (first entry)
XX
XX Rat angiogenesis modulating protein #146.
DE
XX rat; angiogenesis; angiogenesis modulating protein;
KM retinal neovascularisation; choroidal neovascularisation;
KM chronic inflammation; myocardial ischaemia; stroke;
KM coronary artery disease; peripheral vascular disease.
XX
XX Rattus norvegicus.
OS
XX
XX US2003162706-A1.
PN
XX
XX 28-AUG-2003.
PD
XX
XX 10-DEC-2002; 2002US-00316253.
PF
XX
XX 08-FEB-2002; 2002US-0355295P.
PR
XX 26-JUN-2002; 2002US-0391758P.
XX
XX (PROC) PROCTER & GAMBLE CO.
PA
XX
XX Peters KG, Thompson LJ, Wang F, Greis KD;
PI
XX
XX WPI; 2003-711557/67.
DR
XX N-PSDB; ADF30727.
DR
XX
XX Treating angiogenesis-mediated disorder, e.g., retinal or choroidal
PT neovascularization or diseases associated with chronic inflammation,
PT myocardial ischemia, stroke, coronary artery disease or peripheral
PT vascular disease.
XX
XX
PS Claim 2; SEQ ID NO 291; 26pp; English.
XX
XX The invention relates to a method of treating an angiogenesis-mediated
CC disorder in a subject. The method is useful for treating angiogenesis-
CC mediated disorder, e.g., retinal or choroidal neovascularisation or
CC diseases associated with chronic inflammation, myocardial ischaemia,
CC stroke, coronary artery disease or peripheral vascular disease. The
CC present sequence is used in the exemplification of the invention.
XX
XX
SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 31 WCGPCK 36

RESULT 62
ADJ70213
ID ADJ70213 standard; protein; 105 AA.
XX
XX ADJ70213;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human heat mitochondrial protein as a therapeutic target SeqID2019.
DE
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
KM Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cyostatic.
 XX
 OS Homo sapiens.
 XX
 PN MO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 DR WPI; 2003-845369/78.
 XX
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function.
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 2019; 180bp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cyostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 105 AA;
 XX
 QY Query Match 100.0%; Score 47; DB 7; Length 105;
 QY Best Local Similarity 100.0%; Pred. No. 14;
 QY Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 QY |||||
 QY 31 WCGPCK 36
 Db
 XX
 RESULT 63
 ADJ47593
 ID ADJ47593 standard; protein; 105 AA.
 XX
 AC ADJ47593;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Wild-type Trx coding sequence, SEQ ID 1.
 XX
 KW Antidiabetic; Antiarteriosclerotic; Neuroprotective; Nootropic;
 KW Antiparinsonian; Anticonvulsant; Cardiant; Cardiovascular;
 KW Antirheumatic; Antiarthritic; Cyostatic; Antiporiatic; Gene Therapy;
 XX

KW thiorodoxin; Trx; atherosclerosis; diabetes; apoptotic disease;
 KW mitochondrial disease; cardiac dysfunction;
 KW anglogenesis dependent disease; neurodegenerative disease;
 KW rheumatoid arthritis; cancer; psoriasis.
 XX
 OS unidentified.
 XX
 PN MO2004013283-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 22-JUL-2003; 2003WO-US022847.
 XX
 PR 02-AUG-2002; 2002US-0401073P.
 XX
 PA (UYRP) UNIV ROCHESTER.
 XX
 PI Min W, Yingmei L;
 PI N-PSDB; ADJ47596.
 DR WPI; 2004-157111/15.
 DR N-PSDB; ADJ47596.
 XX
 PT New mutant thiorodoxin molecule which is resistant to oxidizing effects
 PT of cytokines or reactive oxygen species, useful for treating or
 PT diagnosing atherosclerosis, diabetes, Alzheimer's disease, myocardial
 PT infarction or cancer.
 XX
 PS Disclosure; SEQ ID NO 1; 145bp; English.
 XX
 CC The present invention relates to mutant thiorodoxin (Trx) proteins and
 CC their coding sequences, where the thiorodoxin molecule is resistant to
 CC the oxidizing effects of cytokines or reactive oxygen species or
 CC resistant to S-nitrosylation of a SH-group by nitrous oxide. The mutant
 CC Trx proteins are useful for treating or diagnosing atherosclerosis,
 CC diabetes, apoptotic disease, mitochondrial dysfunction disease or cardiac
 CC dysfunction. Mitochondrial dysfunction diseases include Kearns-Sayre
 CC syndrome or encephalomyopathy lactic acidosis and stroke-like episodes.
 CC Apoptotic diseases include neurodegenerative diseases, e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral
 CC sclerosis, multiple sclerosis or peripheral neuropathy. Cardiac
 CC dysfunction includes myocardial infarction, cardiomyopathy, arterial
 CC hypertension or heart failure. The mutant Trx proteins are also useful
 CC for treating or diagnosing anglogenesis dependent diseases, e.g.
 CC rheumatoid arthritis, cancer or psoriasis. The present sequence is the
 CC wild-type Trx protein, from which the mutants of the invention were
 CC generated.
 XX
 SQ Sequence 105 AA;
 XX
 QY Query Match 100.0%; Score 47; DB 8; Length 105;
 QY Best Local Similarity 100.0%; Pred. No. 14;
 QY Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 QY |||||
 QY 31 WCGPCK 36
 Db
 XX
 RESULT 64
 ADL82895
 ID ADL82895 standard; protein; 105 AA.
 XX
 AC ADL82895;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human PRO38337, SEQ ID 97.
 XX
 KW Immunosuppressive; Cyostatic; Antiarthritic; Antirheumatic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 KW Gene Therapy; Pro; B cell related disorder; cancer;
 KW Immune-mediated inflammatory disease; human.
 XX

OS Homo sapiens.
XX
PN WO2004024097-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029097.
XX
PR 16-SEP-2002; 2002US-0411392P.
XX
PA (GENTH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX
DR MPI: 2004-329389/30.
DR N-PSDB; ADL82894.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
PS Claim 10; Fig 97; 695pp; English.
XX
CC The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IgM deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated hemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
DB 31 WCGPCK 36
XX
RESULT 65
ADM32938
ID ADM32938 standard; protein; 105 AA.
XX
AC ADM32938;
XX
DT 17-UTN-2004 (first entry)
XX
DE Amino acid sequence of a thioresdoxin polypeptide.
XX
KM mucus; sputum; thioresdoxin; active site; cohesive mucus; cohesive sputum;
XX lung disease; cystic fibrosis; enzyme.
XX
OS Homo sapiens.
XX Synthetic.
XX
PN WO2004024868-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028526.

XX
PR 10-SEP-2002; 2002US-0409960P.
XX
PR 11-APR-2003; 2003US-0462082P.
XX
PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
PI White CW;
XX
DR MPI: 2004-270016/25.
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioresdoxin active-site in
PT reduced state.
XX
PS Disclosure; Page 66-67; 69pp; English.
XX
CC The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioresdoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC volume of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioresdoxin selected from prokaryotic
CC thioresdoxin, yeast thioresdoxin, plant thioresdoxin and mammalian
CC thioresdoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioresdoxin active site of the protein, and thioresdoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32938ADM32941 represent thioresdoxin polypeptides
CC which may be used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
DB 31 WCGPCK 36
XX
RESULT 66
ADM32935
ID ADM32935 standard; protein; 105 AA.
XX
AC ADM32935;
XX
DT 17-UTN-2004 (first entry)
XX
DE Amino acid sequence of a thioresdoxin polypeptide.
XX
KM mucus; sputum; thioresdoxin; active site; cohesive mucus; cohesive sputum;
XX lung disease; cystic fibrosis; enzyme.
XX
OS Mus musculus.
XX Synthetic.
XX
PN WO2004024868-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028526.

XX 10-SEP-2002; 2002US-040960P.
PR 11-APR-2003; 2003US-0462082P.
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
PA
XX
PI White CW;
XX
DR WPI; 2004-270016/25.
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioredoxin active-site in
PT reduced state.
XX
PS Disclosure; Page 65; 69pp; English.
XX
CC The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioredoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioredoxin selected from prokaryotic
CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
CC thioredoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioredoxin active site of the protein, and thioredoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
CC which may used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
RESULT 67
ADM32936
ID ADM32936 standard; protein; 105 AA.
XX
AC ADM32936;
XX
DT 17-JUN-2004 (first entry)
XX
DE Amino acid sequence of a thioredoxin polypeptide.
XX
KW mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
KW lung disease; cystic fibrosis; enzyme.
XX
XX Rattus norvegicus.
OS Synthetic.
XX
PN WO2004024868-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028526.

XX 10-SEP-2002; 2002US-040960P.
PR 11-APR-2003; 2003US-0462082P.
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
PA
XX
PI White CW;
XX
DR WPI; 2004-270016/25.
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioredoxin active-site in
PT reduced state.
XX
PS Disclosure; Page 65-66; 69pp; English.
XX
CC The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioredoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioredoxin selected from prokaryotic
CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
CC thioredoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioredoxin active site of the protein, and thioredoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
CC which may used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
RESULT 68
ADM32937
ID ADM32937 standard; protein; 105 AA.
XX
AC ADM32937;
XX
DT 17-JUN-2004 (first entry)
XX
DE Amino acid sequence of a thioredoxin polypeptide.
XX
KW mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
KW lung disease; cystic fibrosis; enzyme.
XX
XX Bos taurus.
OS Synthetic.
XX
PN WO2004024868-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028526.

XX 10-SEP-2002; 2002US-0409960P.
PR 11-APR-2003; 2003US-0462082P.
XX
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
PA
XX
XX White CW;
PI
XX
XX WPI; 2004-270016/25.
DR
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioredoxin active-site in
PT reduced state.
XX
XX
PS Disclosure; Page 66; 69pp; English.
XX
XX The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioredoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioredoxin selected from prokaryotic
CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
CC thioredoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioredoxin active site of the protein, and thioredoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
XX which may be used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
XX
RESULT 69
ADM32934
ID ADM32934 standard; protein; 105 AA.
XX
AC ADM32934;
XX
DT 17-JUN-2004 (first entry)
XX
DE Amino acid sequence of a thioredoxin polypeptide.
XX
KM mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
KM lung disease; cystic fibrosis; enzyme.
XX
XX Gallus gallus.
OS Synthetic.
XX
XX MO2004024868-A2.
PN
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028526.

XX 10-SEP-2002; 2002US-0409960P.
PR 11-APR-2003; 2003US-0462082P.
XX
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
PA
XX
XX White CW;
PI
XX
XX WPI; 2004-270016/25.
DR
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioredoxin active-site in
PT reduced state.
XX
XX
PS Disclosure; Page 64-65; 69pp; English.
XX
XX The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioredoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioredoxin selected from prokaryotic
CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
CC thioredoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioredoxin active site of the protein, and thioredoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
XX which may be used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
XX
RESULT 70
ADO19655
ID ADO19655 standard; protein; 105 AA.
XX
AC ADO19655;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #292.
XX
XX Human; PRO; immune related disorder; systemic lupus erythematosus;
KM rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KM systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KM autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KM diabetes mellitus; renal disease; demyelinating disease;
KM central nervous system; peripheral nervous system;
KM demyelinating polyneuropathy; Guillain-Barre syndrome;
KM chronic inflammatory demyelinating polyneuropathy.
XX
XX Homo sapiens.
OS
XX

PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR MPI: 2004-420067/39.
 DR N-PSDB; ADO19654.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86398 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7; SEQ ID NO 584; 1731bp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polynuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polynuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 CC
 SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

Search completed: February 23, 2006, 00:37:12
 Job time : 163 secs

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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:38:49 / Search time 23.5 Seconds
(without alignments)
24.566 Million cell updates/sec

Title: US-10-660-118A-3

Perfect score: 47

Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	89	E84409	thioredoxin [import
2	47	100.0	102	G64213	thioredoxin - Myco
3	47	100.0	102	S73896	thioredoxin - Myco
4	47	100.0	102	B71503	probable thioredox
5	47	100.0	102	C81600	thioredoxin TC0826
6	47	100.0	103	TXBY2	thioredoxin II - Y
7	47	100.0	103	T39085	thioredoxin II - f
8	47	100.0	104	A28086	thioredoxin - rabd
9	47	100.0	104	B37192	thioredoxin - Bac1
10	47	100.0	104	TXBY1	thioredoxin I - ye
11	47	100.0	104	S77780	thioredoxin - Myco
12	47	100.0	104	A59394	thioredoxin - Clos
13	47	100.0	104	B84037	thioredoxin trxa l
14	47	100.0	104	E89885	thioredoxin [import
15	47	100.0	105	A30006	thioredoxin - chic
16	47	100.0	105	JH0568	thioredoxin [valid
17	47	100.0	105	JH0568	thioredoxin - rhes
18	47	100.0	105	S04107	thioredoxin - mous
19	47	100.0	105	S04352	thioredoxin - rat
20	47	100.0	105	TXRX	thioredoxin - cory
21	47	100.0	105	B97700	thioredoxin [import
22	47	100.0	105	D97279	thioredoxin [import
23	47	100.0	106	S33357	thioredoxin - Stre
24	47	100.0	106	H64622	thioredoxin - He11
25	47	100.0	106	A49888	thioredoxin - Pent
26	47	100.0	106	AG2579	thioredoxin C-1 tr
27	47	100.0	107	A26622	thioredoxin - Chro
28	47	100.0	107	S47867	thioredoxin-like p
29	47	100.0	107	T02814	thioredoxin TRXRp1
30	47	100.0	107	AH3504	thioredoxin C-1 (l
31	47	100.0	107	E64047	thioredoxin - Haem
32	47	100.0	108	G82991	thioredoxin PA5240
33	47	100.0	108	AD0471	thioredoxin 1 [imp
34	47	100.0	108	D82338	thioredoxin VC0306
35	47	100.0	109	S35497	thioredoxin - Salm
36	47	100.0	109	TXEC	thioredoxin [valid
37	47	100.0	109	S27053	thioredoxin - Emer
38	47	100.0	109	AF0922	thioredoxin [import
39	47	100.0	110	A87688	thioredoxin [import
40	47	100.0	110	C81090	thioredoxin NMB136
41	47	100.0	110	B81850	thioredoxin 1 NMA1
42	47	100.0	113	S57775	thioredoxin h, cyt
43	47	100.0	115	T29044	hypothetical prote
44	47	100.0	115	B70851	probable trxc prot
45	47	100.0	117	E70107	thioredoxin (trxa)
46	47	100.0	118	S34812	thioredoxin h2 - c
47	47	100.0	121	T39387	thioredoxin h1 - f
48	47	100.0	127	S19498	thioredoxin homolo
49	47	100.0	127	B91218	thioredoxin 1 [imp
50	47	100.0	127	C66064	thioredoxin 1 [imp
51	47	100.0	129	B96621	probable thioredox
52	47	100.0	129	T08084	dynein light chain
53	47	100.0	130	D71707	thioredoxin (trxa)
54	47	100.0	133	F97361	thioredoxin C-1 (l
55	47	100.0	145	S70356	thioredoxin C3 - c
56	47	100.0	148	B66721	probable thioredox
57	47	100.0	156	T08086	dynein light chain
58	47	100.0	177	T09495	thioredoxin m - ra
59	47	100.0	179	T00893	thioredoxin m - ra
60	47	100.0	181	TXSPM	thioredoxin m prec
61	47	100.0	182	T07837	thioredoxin f prec
62	47	100.0	182	S20929	thioredoxin f prec
63	47	100.0	182	E95539	hypothetical prote
64	47	100.0	185	D95115	thioredoxin family
65	47	100.0	186	S85044	probable M-type th
66	47	100.0	190	S04661	thioredoxin f prec
67	47	100.0	191	T12261	thioredoxin f prec
68	47	100.0	191	H97984	conserved hypotet
69	47	100.0	290	T40552	thioredoxin-like p
70	47	100.0	322	AH3011	thioredoxin trxa l
71	47	100.0	329	AH3559	thioredoxin [import
72	47	100.0	331	G98272	probable thioredox
73	47	100.0	458	S77662	thioredoxin-disulf
74	47	100.0	88	B46264	thioredoxin 2 - al
75	47	93.6	102	H66572	thioredoxin [import
76	47	93.6	102	D72052	thioredoxin CP0088
77	47	93.6	103	A11228	thioredoxin [import
78	47	93.6	103	AC1582	thioredoxin [import
79	47	93.6	104	A28215	thioredoxin - Rhod
80	47	93.6	104	H95206	thioredoxin [import
81	47	93.6	104	H98071	thioredoxin-disulf
82	47	93.6	104	C46264	thioredoxin 3 - al
83	47	93.6	104	D86830	thioredoxin [import
84	47	93.6	104	C81432	thioredoxin Cj0147
85	47	93.6	105	A46264	thioredoxin 1 - al
86	47	93.6	106	A35135	thioredoxin - Rhod
87	47	93.6	107	A32956	thioredoxin m - Sy
88	47	93.6	107	TXAI	thioredoxin 1 - An
89	47	93.6	107	S31915	thioredoxin - red
90	47	93.6	107	S73146	thioredoxin A - re
91	47	93.6	107	S46521	thioredoxin - Porp
92	47	93.6	107	S46958	thioredoxin A - Sy
93	47	93.6	107	B53307	thioredoxin - Stre
94	47	93.6	107	AD1813	thioredoxin [import
95	47	93.6	108	AH2101	thioredoxin [import
96	47	93.6	109	A55124	thioredoxin - Chlo
97	47	93.6	109	S77444	hypothetical prote
98	47	93.6	109	S46522	thioredoxin A - Gr
99	47	93.6	110	T36576	thioredoxin - Stre
100	47	93.6	110	T42061	thioredoxin - Stre
101	47	93.6	110	AD2039	thioredoxin [import
102	47	93.6	114	JQ2242	thioredoxin h - Ar

103	44	93.6	116	2	T10739	176	39	83.0	181	2	S45556	chloredoxin relate
104	44	93.6	119	2	T10170	177	39	83.0	197	2	T29930	hypothetical prote
105	44	93.6	118	2	T50867	178	39	83.0	351	2	T18066	hypothetical prote
106	44	93.6	122	2	T04090	179	39	83.0	358	2	T17619	hypothetical prote
107	44	93.6	123	2	B70873	180	39	83.0	2567	2	A49551	filamin, Muller ce
108	44	93.6	125	2	T50866	181	39	83.0	5825	2	T12117	polyprotein - lava
109	44	93.6	126	1	S16590	182	38	80.9	40	2	B41440	protein disulfide-
110	44	93.6	131	2	T50862	183	38	80.9	63	2	PK0084	chloredoxin h2 - c
111	44	93.6	131	2	T50863	184	38	80.9	72	2	S15137	chloredoxin h2 - s
112	44	93.6	131	2	T50864	185	38	80.9	100	2	T49043	hypothetical prote
113	44	93.6	131	2	T50865	186	38	80.9	106	2	AD1802	chloredoxin homolo
114	44	93.6	133	2	S58123	187	38	80.9	106	2	AD1802	chloredoxin (clone
115	44	93.6	139	2	G70464	188	38	80.9	134	2	C69410	chloredoxin (trx-3
116	44	93.6	139	2	H91059	189	38	80.9	151	2	AB3263	chloredoxin h2 - s
117	44	93.6	139	2	G85904	190	38	80.9	154	2	H83526	probable thioredox
118	44	93.6	139	2	AB0831	191	38	80.9	176	1	A47384	probable thioredox
119	44	93.6	139	2	B65036	192	38	80.9	318	2	S67190	thioredoxin 2 [imp
120	44	93.6	140	1	S57774	193	38	80.9	338	2	C82590	robable thioredoxi
121	44	93.6	141	2	G75455	194	38	80.9	359	2	T03644	chloredoxin m prec
122	44	93.6	142	2	G75612	195	38	80.9	359	2	T37880	chloredoxin - Dein
123	44	93.6	145	2	AD0397	196	38	80.9	361	2	T00437	chloredoxin 1 - De
124	44	93.6	160	2	D81247	197	38	80.9	364	2	T09614	thioredoxin 2 [imp
125	44	93.6	167	2	T03957	198	38	80.9	369	2	T47259	thioredoxin-relate
126	44	93.6	172	1	S38909	199	38	80.9	378	2	A47300	thioredoxin M - ma
127	44	93.6	173	2	F84530	200	38	80.9	431	2	S45038	chloredoxin m prec
128	44	93.6	174	2	T29491	201	38	80.9	439	2	S19656	probable thioredox
129	44	93.6	185	2	F75549	202	38	80.9	440	2	JC4369	cytochrome c bioge
130	44	93.6	194	2	T00482	203	38	80.9	440	2	T15352	probable thioredox
131	44	93.6	216	2	S72901	204	38	80.9	440	2	T01115	hypothetical prote
132	44	93.6	216	2	A70545	205	38	80.9	443	2	D86183	hypothetical prote
133	44	93.6	222	2	H87210	206	38	80.9	481	2	UC5378	protein disulfide-
134	44	93.6	220	2	B87921	207	38	80.9	482	2	S34275	protein disulfide-
135	44	93.6	258	2	C38095	208	38	80.9	485	2	S71863	protein disulfide-
136	44	93.6	281	2	S49353	209	38	80.9	488	1	JC3385	protein disulfide-
137	44	93.6	282	2	S49352	210	38	80.9	488	2	T23055	hypothetical prote
138	44	93.6	299	2	B87262	211	38	80.9	489	2	S68280	protein disulfide-
139	44	93.6	340	2	T33313	212	38	80.9	491	2	S71862	protein disulfide-
140	44	93.6	366	2	S61796	213	38	80.9	492	2	T38093	probable protein d
141	44	93.6	606	2	T31557	214	38	80.9	493	2	T34092	hypothetical prote
142	43	91.5	105	2	S76386	215	38	80.9	496	2	A54757	protein disulfide-
143	43	91.5	105	2	AG2042	216	38	80.9	497	1	A32820	protein disulfide-
144	43	91.5	107	2	T33843	217	38	80.9	498	2	S62626	protein disulfide-
145	43	91.5	111	1	A32233	218	38	80.9	501	2	B86351	protein disulfide-
146	43	91.5	115	2	AF2098	219	38	80.9	504	1	A28807	protein disulfide-
147	43	91.5	119	2	T18644	220	38	80.9	504	2	S41661	protein disulfide-
148	43	91.5	119	2	T08871	221	38	80.9	505	1	S55507	protein disulfide-
149	43	91.5	151	2	B96796	222	38	80.9	505	2	S63994	protein disulfide-
150	43	91.5	160	2	A82020	223	38	80.9	505	2	S68363	protein disulfide-
151	43	91.5	242	2	A96499	224	38	80.9	505	2	JC5704	protein disulfide-
152	43	91.5	464	2	T46333	225	38	80.9	505	2	JC2291	protein disulfide-
153	43	91.5	578	2	T02392	226	38	80.9	508	1	A30007	protein disulfide-
154	43	91.5	788	2	T26967	227	38	80.9	508	1	ISRUSS	protein disulfide-
155	42	89.4	108	2	B55124	228	38	80.9	508	1	ISRUSS	protein disulfide-
156	42	89.4	140	2	G87183	229	38	80.9	509	1	A38362	protein disulfide-
157	42	89.4	273	2	B31479	230	38	80.9	509	1	ISRUSS	protein disulfide-
158	42	89.4	534	1	VCWVSF	231	38	80.9	510	1	ISRUSS	protein disulfide-
159	42	89.4	662	1	VCWVJB	232	38	80.9	512	1	ISAASS	protein disulfide-
160	42	89.4	662	1	VCWVGF	233	38	80.9	512	2	A41440	protein disulfide-
161	42	89.4	662	2	A25982	234	38	80.9	513	2	T05974	protein disulfide-
162	42	89.4	668	1	VCWVFP	235	38	80.9	513	1	S69181	protein disulfide-
163	42	89.4	837	1	T02761	236	38	80.9	515	1	ISCHSS	protein disulfide-
164	41	87.2	108	2	S02802	237	38	80.9	515	2	T06262	probable protein d
165	41	87.2	108	2	B84999	238	38	80.9	515	2	S57942	protein disulfide-
166	41	87.2	113	2	F82526	239	38	80.9	517	2	JC7623	protein disulfide-
167	41	87.2	210	2	A87523	240	38	80.9	519	2	S66673	disulfide isomeras
168	41	87.2	289	2	E83138	241	38	80.9	522	1	ISBYS8	protein disulfide-
169	39	83.0	103	2	A11275	242	38	80.9	532	2	T07927	protein disulfide-
170	39	83.0	103	2	A11638	243	38	80.9	584	2	S06318	endoplasmic reticu
171	39	83.0	105	2	G97090	244	38	80.9	638	1	ISMSEF	protein disulfide-
172	39	83.0	105	2	D71265	245	38	80.9	643	1	S12476	protein disulfide-
173	39	83.0	146	2	C70314	246	38	80.9	645	1	A23723	protein disulfide-
174	39	83.0	165	2	E69869	247	38	80.9	664	2	S44756	probable protein d
175	39	83.0	178	2	T19587	248	38	80.9	1152	2	F86363	hypothetical prote

249	37	78.7	170	2	H87704	thiol-disulfide in
250	37	78.7	176	1	I64161	cytochrome c bioge
251	37	78.7	363	2	T37630	protein disulfide-
252	36	76.6	105	2	E98087	conserved hypotnet
253	36	76.6	106	2	A82870	thioredoxin U0589
254	36	76.6	116	2	D84285	hypothetical prote
255	36	76.6	118	2	S58118	thioredoxin (clone
256	36	76.6	118	2	S58120	thioredoxin (clone
257	36	76.6	119	2	T08142	thioredoxin h homo
258	36	76.6	119	2	D86330	Fe9.21 protein -
259	36	76.6	123	2	T08141	thioredoxin h homo
260	36	76.6	123	2	T14379	thioredoxin PBC-2
261	36	76.6	125	2	S58119	thioredoxin (clone
262	36	76.6	133	2	C90180	thioredoxin (trxA-
263	36	76.6	135	2	C90393	hypothetical prote
264	36	76.6	140	2	T15738	thioredoxin 2 VC40
265	36	76.6	149	2	B82423	hypothetical prote
266	36	76.6	149	2	T23939	hypothetical prote
267	36	76.6	151	2	T32957	hypothetical prote
268	36	76.6	155	2	T29947	hypothetical prote
269	36	76.6	170	2	E69891	cytochrome c bioge
270	36	76.6	177	2	B83840	thioredoxin (thiol
271	36	76.6	200	2	H71366	probable thioredox
272	36	76.6	221	2	T04271	probable thioredox
273	36	76.6	227	2	B70790	hypothetical prote
274	36	76.6	229	1	B43685	nonstructural prot
275	36	76.6	229	1	D43685	nonstructural prot
276	36	76.6	278	2	E83336	cytochrome c bioge
277	36	76.6	357	2	S23526	cinamyl-alcohol d
278	36	76.6	357	2	S23525	cinamyl-alcohol d
279	36	76.6	380	2	G01639	transmethylase prot
280	36	76.6	445	1	B65000	NAOH2 dehydrogenas
281	36	76.6	445	1	AB0797	NAOH2 dehydrogenas
282	36	76.6	445	2	AB5869	NAOH dehydrogenase
283	36	76.6	445	2	H91024	NAOH dehydrogenase
284	36	76.6	448	2	F83316	NAOH dehydrogenase
285	36	76.6	461	2	AE0311	NAOH2 dehydrogenase
286	36	76.6	562	2	A55588	mannosyl-glycoprot
287	36	76.6	603	2	UC7900	beta-N-acetylgluco
288	36	76.6	654	2	B56011	transcription fact
289	36	76.6	961	1	TSHP4	chromospondin 4 p
290	36	76.6	1021	2	I39207	leukocyte surface
291	36	76.6	1023	2	G96509	pro-pol-dutrase po
292	36	76.6	1182	2	T29097	transcription fact
293	36	76.6	2109	2	I38414	transcription fact
294	36	76.6	2148	2	A56011	thioredoxin (trx-4
295	35	74.5	105	2	H69517	secreted protein,
296	35	74.5	168	2	AF0632	secreted periplasm
297	35	74.5	169	2	H81980	probable periplasm
298	35	74.5	169	2	B81036	thioredoxin NMB184
299	35	74.5	188	2	A75532	cytochrome c bioge
300	35	74.5	203	2	AC3483	thiol-disulfide in
301	35	74.5	221	2	S40401	thioredoxin-1like p
302	35	74.5	222	2	AD2999	thiol-disulfide in
303	35	74.5	222	2	E98284	thiol-disulfide in
304	35	74.5	395	2	B72381	alcohol dehydrogen
305	35	74.5	401	2	A13312	ATP synthase beta
306	35	74.5	552	2	F75311	ABC transporter, A
307	35	74.5	566	2	T06724	protein disulfide-
308	35	74.5	574	2	T25887	hypothetical prote
309	35	74.5	601	2	T21814	hypothetical prote
310	34	72.3	105	2	E86673	thioredoxin H-type
311	34	72.3	108	2	F83309	probable thioredox
312	34	72.3	122	2	T28977	hypothetical prote
313	34	72.3	128	2	AD2300	thioredoxin (impor
314	34	72.3	158	2	S62213	calcium channel be
315	34	72.3	167	2	G64183	hypothetical prote
316	34	72.3	185	2	A81327	probable lipoprote
317	34	72.3	199	2	A97682	thiol disulfide in
318	34	72.3	199	2	A12906	thiol-disulfide in
319	34	72.3	211	2	A82614	thioredoxin XF1990
320	34	72.3	251	2	S23821	hypothetical prote
321	34	72.3	251	2	C45557	regulatory protein
322	32	72.3	263	1	ASLJFP	vif protein - fe1i
323	34	72.3	271	2	G82838	formamidyrimidin
324	34	72.3	292	2	H84285	succinate dehydrog
325	34	72.3	337	2	E95288	probable zinc-bind
326	34	72.3	367	1	A46355	site-specific DNA-
327	34	72.3	367	2	T18185	probable site-spec
328	34	72.3	407	2	T24951	hypothetical prote
329	34	72.3	436	2	T27039	hypothetical prote
330	34	72.3	483	2	B82722	hypothetical prote
331	34	72.3	485	2	T19557	ribulose-bisphosph
332	34	72.3	486	2	T19559	ribulose-bisphosph
333	34	72.3	508	1	SYHMT	histidine-tRNA lig
334	34	72.3	508	2	E96804	probable thioredox
335	34	72.3	623	2	T16384	hypothetical prote
336	34	72.3	625	2	T10661	serine/threonine-s
337	34	72.3	687	2	T19988	hypothetical prote
338	34	72.3	961	2	H86181	hypothetical prote
339	34	72.3	1007	2	T01437	hypothetical prote
340	34	72.3	1041	2	T29010	hypothetical prote
341	34	72.3	2970	2	T08839	polypeptide - marm
342	33	70.2	54	2	S42768	ary protein - Eura
343	33	70.2	62	2	S15676	chorionic gonadotr
344	33	70.2	67	2	A55210	hem 5'-region hyp
345	33	70.2	74	2	S25773	testis-specific pr
346	33	70.2	80	2	I65235	testicular luteini
347	33	70.2	118	2	PN0141	luteolin beta chai
348	33	70.2	118	2	PN0139	luteolin beta chai
349	33	70.2	119	2	AC1465	luteolin beta chai
350	33	70.2	123	2	D75363	luteolin beta chai
351	33	70.2	130	2	C87136	luteolin beta chai
352	33	70.2	132	2	D39741	luteolin beta chai
353	33	70.2	138	2	S00512	testicular luteini
354	33	70.2	139	2	I52320	luteolin beta chai
355	33	70.2	141	1	UTR0B	luteolin beta chai
356	33	70.2	141	1	UTR0B	luteolin beta chai
357	33	70.2	141	1	UTR0B	luteolin beta chai
358	33	70.2	141	1	UTR0B	luteolin beta chai
359	33	70.2	141	1	UTR0B	luteolin beta chai
360	33	70.2	141	1	UTR0B	luteolin beta chai
361	33	70.2	141	2	A33675	beta-crystallin BC
362	33	70.2	157	2	S16728	polymerase 2x2
363	33	70.2	163	2	E72473	probable thioredox
364	33	70.2	170	2	S01449	hypothetical prote
365	33	70.2	195	2	S24228	BH-1 protein homo
366	33	70.2	216	2	PR0375	natural killer cel
367	33	70.2	277	2	AE2947	hypothetical prote
368	33	70.2	277	2	D98335	ABC transporter, A
369	33	70.2	283	2	C86535	hypothetical prote
370	33	70.2	283	2	H72087	hypothetical prote
371	33	70.2	291	2	S77611	killer toxin KPI p
372	33	70.2	293	2	JN0651	rRNA methyltransfe
373	33	70.2	299	2	G96902	transcription regu
374	33	70.2	302	2	W2BE9	gene y protein - h
375	33	70.2	309	2	AB0838	virulence protein
376	33	70.2	310	2	D63386	unknown protein [1
377	33	70.2	332	1	WGSMMH	hmgromycin B phosp
378	33	70.2	345	2	E87061	biotin synthase (i
379	33	70.2	345	2	E87061	biotin synthase (E
380	33	70.2	347	2	T17645	hypothetical prote
381	33	70.2	349	2	G70542	site-specific DNA
382	33	70.2	359	1	JT0391	site-specific DNA
383	33	70.2	359	2	A27159	pocassium channel
384	33	70.2	363	2	B97199	uncharacterized co
385	33	70.2	367	2	H86764	protein RING zinc
386	33	70.2	398	1	S24802	polymerase 6x2
387	33	70.2	415	2	S51977	FUN50 protein - yea
388	33	70.2	417	2	S51961	FUN50 protein - yea
389	33	70.2	426	2	B36467	hypothetical prote
390	33	70.2	433	2	B84566	hypothetical prote
391	33	70.2	442	2	AD2475	hypothetical prote
392	33	70.2	458	2	D70325	hypothetical prote
393	33	70.2	483	2	H87492	Yef family protei
394	33	70.2	489	2	JC4324	lignostilbene alph

395	33	70.2	527	2	T37055	probable oxidoredu
396	33	70.2	535	2	S58224	oestrogen receptor
397	33	70.2	535	2	T00824	probable thioderox
398	33	70.2	537	2	T48599	hypothetical prote
399	33	70.2	539	2	H97279	phosphoenolpyruvat
400	33	70.2	551	2	S77442	cytochrome-c oxida
401	33	70.2	561	2	AD2011	hypothetical prote
402	33	70.2	572	2	S14200	GRESAG protein - T
403	33	70.2	582	2	S10099	transcription fact
404	33	70.2	608	2	E84750	hypothetical prote
405	33	70.2	608	2	T03278	gene ERTIN protein
406	33	70.2	613	2	UC7762	SOX-3 protein - gu
407	33	70.2	678	1	I77530	proprotein convert
408	33	70.2	692	2	A97013	hypothetical prote
409	33	70.2	695	2	E70923	hypothetical prote
410	33	70.2	773	2	J02187	P87 protein - Card
411	33	70.2	956	1	A46016	thrombospondin 3 -
412	33	70.2	956	2	A57121	jagged protein pre
413	33	70.2	1220	2	A56136	hypothetical prote
414	33	70.2	1257	2	T01020	variant-specific s
415	33	70.2	2228	2	T14029	polypotein - dour
416	33	70.2	3005	2	T08841	hypothetical prote
417	32	68.1	75	2	T21519	chitredoxin M-2 -
418	32	68.1	126	2	S74493	chitredoxin M-2 -
419	32	68.1	169	1	KTH0B	chitogonadotropin
420	32	68.1	171	2	AC2081	hypothetical prote
421	32	68.1	174	2	AD2081	hypothetical prote
422	32	68.1	187	2	T36816	hypothetical prote
423	32	68.1	202	2	T50635	hypothetical prote
424	32	68.1	220	2	T30688	hypothetical prote
425	32	68.1	244	2	T40018	glutaredoxin-like
426	32	68.1	274	2	I52825	gene MAC25 protein
427	32	68.1	280	2	F96608	probable chitinase
428	32	68.1	282	2	S50031	proteasyclin-stimu
429	32	68.1	309	2	I41075	site-specific DNA-
430	32	68.1	312	2	E85073	hypothetical prote
431	32	68.1	314	1	T50537	succinate dehydrog
432	32	68.1	316	1	G90406	succinate dehydrog
433	32	68.1	317	1	T45163	succinate dehydrog
434	32	68.1	317	2	D90446	alcohol dehydrogen
435	32	68.1	325	2	B70000	cytochrome-c oxida
436	32	68.1	344	2	UC7920	35k hemin binding
437	32	68.1	346	1	H69789	probable alcohol d
438	32	68.1	348	2	E84143	L-1-tiltol 2-dehydro
439	32	68.1	354	2	E81178	probable alcohol d
440	32	68.1	354	2	H81925	probable alcohol d
441	32	68.1	370	2	C83128	2,3-butanediol deh
442	32	68.1	370	2	A86737	(R,R)-butanediol d
443	32	68.1	382	2	S51962	FUN49 protein - ye
444	32	68.1	411	2	A55610	corticosteroid-rele
445	32	68.1	430	2	A56726	corticosteroid-rec
446	32	68.1	431	2	I49149	CRF receptor - mou
447	32	68.1	431	2	I49149	saunagine/corticoc
448	32	68.1	448	2	T48966	hypothetical prote
449	32	68.1	453	2	T15374	hypothetical prote
450	32	68.1	454	2	T21358	hypothetical prote
451	32	68.1	459	2	JC6520	interferon regulat
452	32	68.1	486	2	T39456	zinc finger protei
453	32	68.1	488	1	I39769	aldenide dehydroge
454	32	68.1	504	2	G02474	interferon regulat
455	32	68.1	525	2	T21357	hypothetical prote
456	32	68.1	669	2	T08827	hypothetical prote
457	32	68.1	744	2	A45622	surface antigen gp
458	32	68.1	755	2	A44315	carilage oligomer
459	32	68.1	761	2	C64813	ybbu protein - Bac
460	32	68.1	761	2	G90728	probable enzyme [l
461	32	68.1	761	2	H85579	probable enzyme yb
462	32	68.1	774	1	P31V50	RNA-directed RNA p
463	32	68.1	774	2	S13670	basic polymerase 2
464	32	68.1	975	2	I48974	receptor-protein t
465	32	68.1	976	2	A36355	protein-tyrosine k
466	32	68.1	977	2	S49004	tyrosine kinase Mp
467	32	68.1	1073	2	T01955	hypothetical prote
468	32	68.1	1103	2	T13590	distal tail fiber
469	32	68.1	1321	2	T29308	hypothetical prote
470	32	68.1	1372	2	T29309	hypothetical prote
471	32	68.1	2703	1	A24420	notch protein - fr
472	32	68.1	4302	2	A38971	polycyclic kidney
473	32	68.1	4302	2	A38804	thrombospondin pre
474	31.5	67.0	1178	1	NTSRPM	neurotoxin P2 - sc
475	31	66.0	35	1	A59356	neurotoxin P2 - sc
476	31	66.0	55	2	S25774	testis-specific pr
477	31	66.0	55	1	WTFP	testis-specific pr
478	31	66.0	56	2	H81133	rubredoxin NMB093
479	31	66.0	63	2	S25772	testis-specific pr
480	31	66.0	65	2	A72324	terredoxin - Therm
481	31	66.0	68	2	S25775	testis-specific pr
482	31	66.0	73	2	A60136	keratin, scale (cl
483	31	66.0	98	1	KRGLBS	keratin, feather -
484	31	66.0	114	1	E64423	ychn protein homol
485	31	66.0	114	2	D75422	hypothetical prote
486	31	66.0	116	2	S09845	hypothetical prote
487	31	66.0	124	2	T13559	hypothetical prote
488	31	66.0	124	2	A83707	hypothetical prote
489	31	66.0	128	2	J01002	keratin, claw - ch
490	31	66.0	131	2	A87461	hypothetical prote
491	31	66.0	141	2	D82843	DNA polymerase III
492	31	66.0	150	2	H86488	protein T32E20.29
493	31	66.0	155	1	KRCHS	keratin, scale - c
494	31	66.0	158	1	ZBBE11	17k zinc-binding p
495	31	66.0	161	2	T48767	hypothetical prote
496	31	66.0	162	2	T49420	hypothetical prote
497	31	66.0	179	2	A87654	hypothetical prote
498	31	66.0	186	2	T31643	hypothetical prote
499	31	66.0	186	2	T03808	alanine-tRNA ligas
500	31	66.0	190	2	S52130	vasculat endotheli
501	31	66.0	190	2	B40080	vasculat endotheli
502	31	66.0	192	2	A72646	hypothetical prote
503	31	66.0	195	2	S39677	hypothetical prote
504	31	66.0	201	2	S16897	alanine-tRNA ligas
505	31	66.0	201	2	S16899	alanine-tRNA ligas
506	31	66.0	205	2	F71491	probable UDP-gluc
507	31	66.0	218	2	F81650	UDP-N-acetylglucos
508	31	66.0	220	2	G86164	protein F15K9.8 [l
509	31	66.0	222	2	A59263	tetraspan TSPAN-2
510	31	66.0	232	2	A41551	vasculat endotheli
511	31	66.0	232	2	D96663	unknown protein, 5
512	31	66.0	233	2	D84797	hypothetical prote
513	31	66.0	241	2	C82852	competence protein
514	31	66.0	243	2	C75608	hypothetical prote
515	31	66.0	244	2	S30860	hypothetical prote
516	31	66.0	245	2	A43905	sperm outer dense
517	31	66.0	246	2	T33965	hypothetical prote
518	31	66.0	247	2	I48699	outer dense fiber
519	31	66.0	265	2	B48151	sperm tail protein
520	31	66.0	289	2	JC5938	thioredoxin-like p
521	31	66.0	296	2	T07367	thioredoxin-like p
522	31	66.0	302	2	A96789	protein T32E18.2 (
523	31	66.0	303	2	T47356	hypothetical prote
524	31	66.0	321	2	AD0580	lipidic acid synthe
525	31	66.0	323	2	I48667	MHA3 (keratin acid
526	31	66.0	332	2	I48691	regulatory protein
527	31	66.0	334	2	A48151	sperm tail protein
528	31	66.0	338	2	E82432	hypothetical prote
529	31	66.0	340	1	C70538	probable 6-phospho
530	31	66.0	345	2	T25561	hypothetical prote
531	31	66.0	356	1	A35253	2-dehydro-3-deoxy-
532	31	66.0	356	1	ADRCYH	2-dehydro-3-deoxy-
533	31	66.0	356	2	AB0833	2-dehydro-3-deoxy-
534	31	66.0	356	2	H91061	hypothetical prote
535	31	66.0	356	2	D85906	hypothetical prote
536	31	66.0	356	2	AC0399	2-dehydro-3-deoxy-
537	31	66.0	357	2	D83292	phospho-2-dehydro-
538	31	66.0	362	2	I37459	keratin Ha3-II, ty
539	31	66.0	373	2	T33145	hypothetical prote
540	31	66.0	380	2	A71181	probable isomerase

541	31	66.0	380	2	H75159	3-isopropylmalate	614	31	66.0	842	2	C81396	alanine-tRNA ligas
542	31	66.0	381	2	A33477	protein-glutamine	615	31	66.0	847	2	A64675	alanine-tRNA ligas
543	31	66.0	386	2	T51171	homoaconitate hydr	616	31	66.0	847	2	P71842	alanine-tRNA ligas
544	31	66.0	392	2	A60777	keratin 2, type I, n	617	31	66.0	860	2	G82310	alanyl-tRNA synth
545	31	66.0	395	1	U00396	nodulation protein	618	31	66.0	874	2	H96503	alanyl-tRNA synth
546	31	66.0	396	2	C84797	hypothetical prote	619	31	66.0	873	2	H63533	protein PgC16.17 (
547	31	66.0	397	2	G97335	subtilisin-like se	620	31	66.0	874	2	P81063	alanyl-tRNA synth
548	31	66.0	399	2	F82657	beta-ketoacyl-[ACP	621	31	66.0	874	2	P81804	alanine-tRNA ligas
549	31	66.0	404	2	T50073	keratin, 47.6K typ	622	31	66.0	874	2	I64095	alanine-tRNA ligas
550	31	66.0	409	2	T47298	probable replicati	623	31	66.0	875	2	A60401	alanine-tRNA ligas
551	31	66.0	412	1	KRSHL1	keratin, 48K type	624	31	66.0	876	1	SYECAT	alanine-tRNA ligas
552	31	66.0	413	1	S34305	nodulation protein	625	31	66.0	876	2	AP0843	alanine-tRNA ligas
553	31	66.0	413	2	T08297	conserved hypothe	626	31	66.0	876	2	B91073	alanyl-tRNA synth
554	31	66.0	416	2	A61404	keratin A, type I	627	31	66.0	877	2	S76394	hypothetical prote
555	31	66.0	416	2	S60034	keratin, type I, n	628	31	66.0	877	2	H71647	alanine-tRNA ligas
556	31	66.0	416	2	A46559	hypothetical prote	629	31	66.0	878	2	C71305	leucine-tRNA ligas
557	31	66.0	416	2	A99419	3-isopropylmalate	630	31	66.0	878	2	B84977	alanine-tRNA ligas
558	31	66.0	416	2	G69524	3-isopropylmalate	631	31	66.0	878	2	B85917	alanyl-tRNA synth
559	31	66.0	417	2	H72362	3-isopropylmalate	632	31	66.0	878	2	G97865	alanine-tRNA ligas
560	31	66.0	418	2	C72394	hypothetical prote	633	31	66.0	880	2	AC2108	alanyl-tRNA synth
561	31	66.0	419	2	D69051	3-isopropylmalate	634	31	66.0	880	2	H87562	alanyl-tRNA synth
562	31	66.0	419	2	B49418	spermatogenesis fa	635	31	66.0	881	2	A97107	alanyl-tRNA synth
563	31	66.0	420	2	B64425	homoaconitate hydr	636	31	66.0	885	2	AG3350	alanyl-tRNA synth
564	31	66.0	422	2	C97290	3-isopropylmalate	637	31	66.0	887	2	AG2806	alanyl-tRNA synth
565	31	66.0	423	2	B75045	probable 3-isoprop	638	31	66.0	889	2	AD2215	two-component hydr
566	31	66.0	424	1	S12793	nodulation protein	639	31	66.0	890	2	F75289	alanyl-tRNA synth
567	31	66.0	424	1	ZZZRCL	nodulation protein	640	31	66.0	900	2	P97585	alanyl-tRNA synth
568	31	66.0	426	1	ZZZRCA	nodulation protein	641	31	66.0	900	2	C64232	alanyl-tRNA synth
569	31	66.0	426	2	A95321	NodN-ACETYLGLUCO	642	31	66.0	900	2	S73748	alanyl-tRNA synth
570	31	66.0	428	2	A69085	3-isopropylmalate	643	31	66.0	906	2	D82899	alanyl-tRNA synth
571	31	66.0	432	2	C70381	large subunit of i	644	31	66.0	916	2	C82844	alanyl-tRNA synth
572	31	66.0	433	2	B69495	acnitrace (acn) ho	645	31	66.0	955	2	D96538	cytosolic tRNA-Ala
573	31	66.0	434	2	D75373	3-isopropylmalate	646	31	66.0	955	2	A45441	thrombospondin 4 -
574	31	66.0	452	2	T36042	probable plasmid r	647	31	66.0	958	2	S62065	alanine-tRNA ligas
575	31	66.0	455	2	A55050	enigma - human	648	31	66.0	959	2	T38247	probable alanyl-tr
576	31	66.0	463	2	T49460	transcription regu	649	31	66.0	965	2	S62935	hypothetical prote
577	31	66.0	464	2	H90140	chlorodoxin reduct	650	31	66.0	967	1	SYMTAT	alanine-tRNA ligas
578	31	66.0	483	2	AG1898	keratin type II, m	651	31	66.0	968	2	I60107	alanine-tRNA ligas
579	31	66.0	508	1	KRSHL2	probable replicati	652	31	66.0	968	2	T29466	hypothetical prote
580	31	66.0	527	2	D84517	hydrogenase (BC 1,	653	31	66.0	982	2	T15967	hypothetical prote
581	31	66.0	574	1	HQCLIP	N-acetyl-beta-D-g1	654	31	66.0	989	2	S32671	alanine-tRNA ligas
582	31	66.0	580	2	S72211	complement C8 alph	655	31	66.0	1075	2	T00341	hypothetical prote
583	31	66.0	584	1	C8HUA	probable transcrip	656	31	66.0	1149	2	S67039	DNA-directed RNA p
584	31	66.0	585	2	I46686	hypothetical prote	657	31	66.0	1172	2	P96503	protein PgC16.13 (
585	31	66.0	597	2	S72468	probable transcrip	658	31	66.0	1196	1	DNBEHR	DNA-binding protei
586	31	66.0	604	2	T36966	hypothetical prote	659	31	66.0	1196	1	DNBEKS	DNA-binding protei
587	31	66.0	616	2	B84500	probable retroelem	660	31	66.0	1196	1	DNBEV1	major DNA-binding
588	31	66.0	633	2	A75069	dipeptide transpor	661	31	66.0	1197	1	A48350	DNA-binding protei
589	31	66.0	642	2	H97019	acnitrace A (impor	662	31	66.0	1364	2	T00250	MGFP2 protein - hu
590	31	66.0	659	2	F70453	acnitrace - Aquife	663	31	66.0	1465	2	S31262	TyB protein - years
591	31	66.0	667	1	VCLUGL	env polypeptide pr	664	31	66.0	1467	2	PC1253	TyB protein - years
592	31	66.0	670	2	T33304	hypothetical prote	665	31	66.0	1743	2	T15893	hypothetical prote
593	31	66.0	680	2	UC5133	protein-glutamine	666	31	66.0	1786	1	NMMSB1	laminin beta-1 cha
594	31	66.0	693	1	S61067	homoaconitate hydr	667	31	66.0	1802	2	S52611	TyB protein - years
595	31	66.0	695	2	S66662	protein-glutamine	668	31	66.0	1803	2	S56894	TyB protein - years
596	31	66.0	708	2	A53185	G-box-binding fact	669	31	66.0	1983	2	AC1922	two-component hydr
597	31	66.0	712	2	A45638	immunodominant nic	670	31	66.0	2282	2	T42717	DNA-binding protei
598	31	66.0	721	2	T38665	antigenic homoacon	671	31	66.0	2630	2	T08868	polypeptide PI - A
599	31	66.0	724	2	A48569	antigenic Em100 - E1	672	31	66.0	3034	2	T14119	seven-pass transme
600	31	66.0	728	2	S50387	acnitrace hydrat	673	31	66.0	4957	2	T03455	ALR protein - huma
601	31	66.0	778	2	T38347	acnitrace hydrat	674	31	66.0	5262	2	T03454	ALR protein - huma
602	31	66.0	779	2	S57805	acnitrace hydrat	675	31	66.0	80	2	T12928	thioredoxin - Bac
603	31	66.0	780	2	T52543	acnitrace hydrat	676	31	66.0	96	2	A10535	hypothetical prote
604	31	66.0	781	2	A35544	acnitrace hydrat	677	31	66.0	105	2	C95223	thioredoxin, proba
605	31	66.0	781	2	S57528	acnitrace hydrat	678	31	66.0	119	2	T17930	thioredoxin-like p
606	31	66.0	788	2	S44831	acnitrace hydrat	679	31	66.0	130	2	T51879	hypothetical prote
607	31	66.0	789	2	S46631	acnitrace hydrat	680	31	66.0	133	2	T37311	hypothetical prote
608	31	66.0	817	1	TGHUM1	protein-glutamine	681	31	66.0	150	2	S15914	hypothetical prote
609	31	66.0	824	2	B38423	protein-glutamine	682	31	66.0	235	2	T09930	thioredoxin homolo
610	31	66.0	824	2	P72408	leucine-tRNA ligas	683	31	66.0	247	1	D64740	proline-phosphos
611	31	66.0	832	2	A40205	Na+/H+-exchangin	684	31	66.0	255	2	S31096	proline-rich prote
612	31	66.0	835	2	T26086	hypothetical prote	685	31	66.0	277	2	S57381	protein disulfide
613	31	66.0	836	2	A54269	protein-glutamine	686	31	66.0	285	2	S51247	thioredoxin homolo

687	30	63.8	310	2	T17980	hypothetical prote
688	30	63.8	326	1	GOVZML	T2 protein - myxom
689	30	63.8	328	2	D70574	hypothetical prote
690	30	63.8	343	2	T06273	benzothiadiazole-i
691	30	63.8	348	2	C86607	disulfide bond iso
692	30	63.8	348	2	G72016	probable disulfide
693	30	63.8	349	2	E71847	lipopolysaccharide
694	30	63.8	349	2	G64668	lipopolysaccharide
695	30	63.8	357	2	T23460	hypothetical prote
696	30	63.8	367	2	T02767	hypothetical prote
697	30	63.8	367	2	T02990	cinamyl-alcohol d
698	30	63.8	368	2	T38901	probable dimeric d
699	30	63.8	409	2	T03718	suppressor 2 prote
700	30	63.8	432	2	T28931	hypothetical prote
701	30	63.8	437	2	T03161	hypothetical prote
702	30	63.8	470	2	C70672	hypothetical prote
703	30	63.8	483	2	T47974	hypothetical prote
704	30	63.8	496	2	S55665	hypothetical prote
705	30	63.8	510	2	T10494	pectinesterase (EC
706	30	63.8	513	2	T34546	hypothetical prote
707	30	63.8	514	2	S48730	Cry j II protein -
708	30	63.8	514	2	JC2498	second major aller
709	30	63.8	514	2	UC7100	polygalacturonase
710	30	63.8	515	2	T03717	GFP-binding protei
711	30	63.8	527	2	P96552	hypothetical prote
712	30	63.8	527	2	P96552	probable spermidin
713	30	63.8	554	2	T36545	chitol disulfide in
714	30	63.8	565	2	E91268	chitol disulfide in
715	30	63.8	565	2	C86109	inner membrane cop
716	30	63.8	565	2	S55364	inner membrane cop
717	30	63.8	567	2	AE1044	chitol,disulfide in
718	30	63.8	567	2	B81408	probable chitol-dis
719	30	63.8	579	2	A64100	inner membrane cop
720	30	63.8	580	2	H86189	hypothetical prote
721	30	63.8	582	2	S69720	hypothetical prote
722	30	63.8	585	2	A10042	chitol,disulfide in
723	30	63.8	600	2	A82043	inner membrane cop
724	30	63.8	751	2	T15403	hypothetical prote
725	30	63.8	758	2	C82784	c-type cytochrome
726	30	63.8	815	2	T15402	hypothetical prote
727	30	63.8	861	2	A48825	Notch homolog Mrc
728	30	63.8	865	2	D72206	valine-tRNA ligase
729	30	63.8	889	2	C72565	probable valyl-tRN
730	30	63.8	1223	2	T10365	helicase - Oxygia
731	30	63.8	1251	2	B86194	hypothetical prote
732	30	63.8	1307	2	S53412	probable membrane
733	30	63.8	1664	2	P84485	probable retroelam
734	30	63.8	2276	2	T00076	hypothetical prote
735	30	63.8	2437	2	S42612	transmembrane prot
736	30	63.8	2534	2	A35844	Xotch protein - Af
737	30	63.8	2531	2	S18188	notch protein homo
738	30	63.8	2531	2	A46019	notch-1 protein -
739	30	63.8	2555	2	A40043	notch protein homo
740	29.5	62.8	570	2	G85046	hypothetical prote
741	29	61.7	132	1	AH2029	hypothetical prote
742	29	61.7	132	1	MFIV2J	matrix protein M2
743	29	61.7	200	2	E81314	probable periplasm
744	29	61.7	227	2	T06634	hypothetical prote
745	29	61.7	230	2	G97215	nifH-related domi
746	29	61.7	250	2	E82821	NADH-ubiquinone ox
747	29	61.7	253	2	D69964	conserved hypochet
748	29	61.7	265	2	E82716	ATP synthase, A ch
749	29	61.7	269	2	S48978	hypothetical prote
750	29	61.7	272	2	B72208	hypothetical prote
751	29	61.7	309	2	T51900	carbonic anhydrase
752	29	61.7	309	2	G70882	probable oxidoredu
753	29	61.7	321	1	F87102	probable phosphos
754	29	61.7	324	1	B70885	probable phosphos
755	29	61.7	354	2	F71721	hypothetical prote
756	29	61.7	374	2	S69627	hypothetical prote
757	29	61.7	385	2	P81341	3-deoxy-manno-occu
758	29	61.7	385	2	T22822	hypothetical prote
759	29	61.7	392	2	A75593	alcohol dehydrogen
760	29	61.7	426	2	F75394	hypothetical prote
761	29	61.7	488	2	T10675	hypothetical prote
762	29	61.7	519	2	T45847	acetylcholine rece
763	29	61.7	591	2	E83039	probable chitol-dis
764	29	61.7	598	2	T45827	pectinesterase-lik
765	29	61.7	600	2	H95379	probable adenine d
766	29	61.7	601	2	F81074	chitol-disulfide in
767	29	61.7	608	2	A53195	afamin precursor
768	29	61.7	613	2	B81868	chitol-disulfide in
769	29	61.7	628	2	AD0632	membrane protein.
770	29	61.7	662	1	A31349	arachidonate 15-11
771	29	61.7	663	1	A35087	arachidonate 12-11
772	29	61.7	663	1	S32825	arachidonate 12-11
773	29	61.7	666	2	T31461	probable magnesium
774	29	61.7	686	2	T15795	hypothetical prote
775	29	61.7	700	2	A32392	protein kinase C (
776	29	61.7	1018	2	S44758	C14B9.6 protein -
777	29	61.7	1165	2	T38867	probable DNA-dirc
778	29	61.7	1422	2	T18404	chromatin remodel
779	29	61.7	1955	1	ACGH	agrin precursor -
780	29	61.7	2052	2	T18290	FYVE finger-contai
781	29	61.7	2137	2	T05244	hypothetical prote
782	29	61.7	2207	2	T24629	glutamate synthase
783	29	61.7	2361	2	T24864	hypothetical prote
784	28.5	60.6	256	2	D97086	formate/nitrite fa
785	28.5	60.6	507	2	S73199	protochlorophyllid
786	28.5	60.6	1171	2	A42916	metabotropic gluta
787	28.5	60.6	1180	2	JC2132	metabotropic gluta
788	28.5	60.6	1212	2	JC2131	metabotropic gluta
789	28	59.6	30	2	S07484	proteinase inhibi
790	28	59.6	39	2	C37264	E2 glycoprotein -
791	28	59.6	55	1	FEPE	ferredoxin 214Fe-4
792	28	59.6	58	2	S10063	isoprenolign G1 -
793	28	59.6	59	2	S00371	serum basic protei
794	28	59.6	60	1	TI80R	metallothionein pr
795	28	59.6	61	2	S14049	ORF MSV185 hypot
796	28	59.6	62	2	T28346	ferredoxin 214Fe-4
797	28	59.6	65	2	B25103	restriction inhibi
798	28	59.6	66	1	QABPL	restriction inhibi
799	28	59.6	73	2	S30512	cytochrome c-type
800	28	59.6	76	2	S10068	restriction inhibi
801	28	59.6	80	2	T02063	metallothionein-11
802	28	59.6	82	2	T06986	hypothetical prote
803	28	59.6	88	2	JQ2360	wheat aluminum ind
804	28	59.6	98	2	D89856	hypothetical prote
805	28	59.6	100	1	TI80R	basic proteinase i
806	28	59.6	100	1	TI80SP	spleen basic prote
807	28	59.6	103	2	D89959	hypothetical prote
808	28	59.6	103	2	A86584	CT631 hypothetical
809	28	59.6	104	2	A71817	probable thioredox
810	28	59.6	104	2	B64702	thioredoxin - Heli
811	28	59.6	104	2	S18821	cytochrome c552 pr
812	28	59.6	105	2	D95341	probable CycB2 cyt
813	28	59.6	106	2	H89854	hypothetical prote
814	28	59.6	107	2	E84056	thioredoxin H1 BH3
815	28	59.6	107	2	G68998	thioredoxin H1 hom
816	28	59.6	108	2	A60627	glycoprotein hormo
817	28	59.6	109	2	G65201	hypothetical 11.8
818	28	59.6	112	2	C83864	thioredoxin BH175
819	28	59.6	113	2	T38499	hypothetical prote
820	28	59.6	114	2	E70759	probable fdxa prot
821	28	59.6	116	2	B53701	cryptidin-related p
822	28	59.6	117	2	AC1831	hypothetical prote
823	28	59.6	119	2	T51229	gonadotropin alpha
824	28	59.6	124	1	QGVZEL	Fli protein - vacc
825	28	59.6	130	2	S47637	ribosomal protein
826	28	59.6	130	2	S57137	probable membrane
827	28	59.6	133	2	H42513	J5L 15.2K protein
828	28	59.6	133	2	T28520	hypothetical prote
829	28	59.6	133	2	H72160	M5L protein - vari
830	28	59.6	133	2	S33096	USL protein - vari
831	28	59.6	134	2	T30680	hypothetical prote
832	28	59.6	134	2	A54002	pollen allergen Lo

833	28	59.6	137	2	A63424	906	28	59.6	290	2	T21185	hypothetical prote
834	28	59.6	138	2	C64491	907	28	59.6	293	2	S63845	transcription elon
835	28	59.6	144	2	G86293	908	28	59.6	294	2	T39774	hypothetical prote
836	28	59.6	144	2	B84728	909	28	59.6	296	2	B71305	hypothetical prote
837	28	59.6	145	2	T34303	910	28	59.6	297	1	S49348	cytochrome-c oxida
838	28	59.6	147	2	AD0421	911	28	59.6	298	2	S39539	osteonectin precur
839	28	59.6	152	2	T04811	912	28	59.6	300	2	S18992	osteonectin precur
840	28	59.6	152	2	S46272	913	28	59.6	301	2	S17361	transcription elon
841	28	59.6	154	2	A96544	914	28	59.6	301	2	S34159	transcription elon
842	28	59.6	154	2	P82633	915	28	59.6	301	2	A29950	transcription elon
843	28	59.6	154	2	A86086	916	28	59.6	301	2	G71206	tryptophan-tRNA li
844	28	59.6	162	2	T42001	917	28	59.6	302	1	GEHNS	osteonectin precur
845	28	59.6	163	2	E91238	918	28	59.6	303	1	GEHNS	osteonectin precur
846	28	59.6	166	1	B64019	919	28	59.6	303	2	S72364	transcription elon
847	28	59.6	166	2	T09593	920	28	59.6	303	2	S72365	transcription elon
848	28	59.6	168	2	A31196	921	28	59.6	303	2	T21125	hypothetical prote
849	28	59.6	168	2	D75144	922	28	59.6	304	1	GERON	osteonectin precur
850	28	59.6	168	2	A71184	923	28	59.6	309	2	A42921	transcription elon
851	28	59.6	170	2	A35944	924	28	59.6	313	2	A67282	MutT/nudix family
852	28	59.6	180	2	B83460	925	28	59.6	314	2	S31868	glucocorticoid rec
853	28	59.6	180	2	S47662	926	28	59.6	316	2	AC0329	conserved hypotet
854	28	59.6	180	2	S47663	927	28	59.6	317	2	B69185	conserved hypotet
855	28	59.6	180	2	T17614	928	28	59.6	318	2	H86342	hypothetical prote
856	28	59.6	185	2	AF0787	929	28	59.6	320	2	T42062	thioredoxin-disulf
857	28	59.6	185	2	A10960	930	28	59.6	321	2	A44230	putahate dioxygen
858	28	59.6	185	2	A64989	931	28	59.6	322	1	A53307	thioredoxin-disulf
859	28	59.6	185	2	P85858	932	28	59.6	322	2	T36577	thioredoxin reduct
860	28	59.6	185	2	D91014	933	28	59.6	324	2	T42656	hypothetical prote
861	28	59.6	188	2	AD0334	934	28	59.6	326	1	A47016	toluene-4-monooxyg
862	28	59.6	191	2	B84890	935	28	59.6	326	1	A59241	DNA-directed DNA p
863	28	59.6	193	2	AG1279	936	28	59.6	326	2	UC7094	nine-heme cytochro
864	28	59.6	193	2	AG1642	937	28	59.6	328	2	A99416	alcohol dehydrogen
865	28	59.6	195	2	JH0719	938	28	59.6	328	2	DB3275	DNA polymerase III
866	28	59.6	197	2	A82556	939	28	59.6	329	1	A36952	CDP-6'-deoxy-delta
867	28	59.6	198	2	S70515	940	28	59.6	329	2	AE0378	cdp-6'-deoxy-delta-
868	28	59.6	198	2	I52655	941	28	59.6	330	1	GZMSA	Ig gamma-2a chain
869	28	59.6	199	2	H86154	942	28	59.6	332	2	A69224	polyferredoxin 4x2
870	28	59.6	207	2	A69446	943	28	59.6	332	2	T25779	hypothetical prote
871	28	59.6	207	2	T49552	944	28	59.6	332	2	T26145	hypothetical prote
872	28	59.6	213	2	D70592	945	28	59.6	335	2	H87243	hypothetical prote
873	28	59.6	215	2	T01349	946	28	59.6	336	1	C41659	mosA/NirX family F
874	28	59.6	215	2	H87196	947	28	59.6	336	2	F81849	benzoate 1,2-dioxy
875	28	59.6	216	2	JX0265	948	28	59.6	336	2	H81091	probable CDP-6-deo
876	28	59.6	218	2	S51381	949	28	59.6	337	2	C83332	toluate 1,2-dioxyg
877	28	59.6	218	2	T45979	950	28	59.6	337	2	A12723	naphthalene 1,2-di
878	28	59.6	220	1	A33872	951	28	59.6	337	2	B37505	phenol hydroxylase
879	28	59.6	228	2	P72685	952	28	59.6	340	2	T32931	hypothetical prote
880	28	59.6	228	2	JX01350	953	28	59.6	340	2	C87732	protein W03D8.4 [I
881	28	59.6	235	2	JX0167	954	28	59.6	340	2	A10165	probable oxidoredu
882	28	59.6	236	2	E97101	955	28	59.6	340	2	G96985	galactose mutarota
883	28	59.6	238	1	A46508	956	28	59.6	341	2	S31571	cinamyl-alcohol d
884	28	59.6	238	1	I38016	957	28	59.6	343	2	T15346	hypothetical prote
885	28	59.6	238	1	JC2297	958	28	59.6	344	2	I51330	androgen receptor
886	28	59.6	238	1	S43511	959	28	59.6	346	2	T31263	xylene monooxygena
887	28	59.6	239	2	F64382	960	28	59.6	348	1	H64657	probable cinamyl-
888	28	59.6	244	2	H84853	961	28	59.6	348	1	S77598	cytochrome-c oxida
889	28	59.6	245	2	G84853	962	28	59.6	350	2	B37316	ferredoxin-NAD red
890	28	59.6	246	2	S38950	963	28	59.6	350	2	S47292	phenol 2-monooxyg
891	28	59.6	247	2	T43136	964	28	59.6	350	2	A71857	zinc-dependent alc
892	28	59.6	254	2	B31790	965	28	59.6	352	2	I51282	TRP-1 - axolotl (f
893	28	59.6	255	2	T36778	966	28	59.6	353	2	A95312	probable dioxigena
894	28	59.6	257	2	C84890	967	28	59.6	354	2	C95381	probable oxidoredu
895	28	59.6	260	2	D64419	968	28	59.6	357	2	T09141	cinamyl-alcohol d
896	28	59.6	263	2	AD0590	969	28	59.6	362	2	S45094	cinamyl-alcohol d
897	28	59.6	270	2	G96914	970	28	59.6	364	2	B69131	tryptophan-tRNA li
898	28	59.6	270	2	T32007	971	28	59.6	366	2	G82970	probable ferredoxi
899	28	59.6	273	2	PC4153	972	28	59.6	370	2	B83191	alcohol dehydrogen
900	28	59.6	274	2	T02797	973	28	59.6	370	2	F64476	tryptophan-tRNA li
901	28	59.6	274	2	T39703	974	28	59.6	371	1	D90192	alcohol dehydrogen
902	28	59.6	275	2	G64368	975	28	59.6	373	1	A33419	alcohol dehydrogen
903	28	59.6	280	2	S26831	976	28	59.6	373	1	DERTA	alcohol dehydrogen
904	28	59.6	287	2	T44961	977	28	59.6	373	1	S68061	alcohol dehydrogen
905	28	59.6	288	2	S27842	978	28	59.6	374	1	A56643	alcohol dehydrogen

979 28 59.6 374 1 DEHUC2 alcohol dehydrogen
980 28 59.6 374 2 D72477 probable cryptocop
981 28 59.6 376 1 JC4967 alcohol dehydrogen
982 28 59.6 376 1 S51187 alcohol dehydrogen
983 28 59.6 376 2 UC7759 alcohol dehydrogen
984 28 59.6 377 2 AB0183 alcohol dehydrogen
985 28 59.6 378 2 C85431 alcohol dehydrogen
986 28 59.6 379 2 AF3320 flavohemoprotein
987 28 59.6 379 2 H69512 hypochemical prote
988 28 59.6 381 1 JN0447 alcohol dehydrogen
989 28 59.6 385 2 C75020 cryptophanyl-ERNA
990 28 59.6 386 1 S31140 alcohol dehydrogen
991 28 59.6 387 2 H72299 hypochemical prote
992 28 59.6 393 2 T41211 hypochemical wcf1
993 28 59.6 394 2 A97244 moaA/Nitrf family F
994 28 59.6 399 1 G2MSAM Ig gamma-2a chain
995 28 59.6 399 2 AE3148 glycosyltransferas
996 28 59.6 399 2 F98139 sqdx protein (impo
997 28 59.6 401 2 E88969 protein F15E11.7
998 28 59.6 403 2 JC5269 neuron-specific si
999 28 59.6 404 2 G69332 heterodisulfide re
1000 28 59.6 405 1 G2MSBM Ig gamma-2b chain

ALIGNMENTS

RESULT 1
E84409
thioredoxin (imported) - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revise 02-Feb-2001 #text_change 05-Oct-2004
C:Accession: E84409
R:Ng, W.V.; Kennedy, S.P.; Mainatis, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leichauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabluc Jung, K.H.; Alam, M.; Fretla, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84409
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: UNIPROT:Q9HMD0; UNIPARC:UPI000063B9A; GB:AE004437; NID:g10581982; F C:Genetics:
A:Gene: trxA2
C:Superfamily: thioredoxin

Query Match 100.0%; Score 47; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 12 WCGPCK 17

RESULT 2
G64213
thioredoxin - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revise 16-Aug-1996 #text_change 05-Oct-2004
C:Accession: G64213

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.; C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64800; MUID:96026346; PMID:7569993
A:Accession: G64213
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-102 <TIGR>
A:Cross-references: UNIPROT:P47370; UNIPARC:UPI0000136E89; GB:U39691; GB:L43967; NID:g10 A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-90/Domain: thioredoxin homology <THR>
F:30-33/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 3
S73896
thioredoxin - Mycoplasma pneumoniae (strain ATCC 29342)
N:Alternate names: hypothetical protein A65_off102
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C>Date: 27-Feb-1997 #sequence_revise 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S73896
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73896
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <HM>
A:Cross-references: UNIPROT:P75512; UNIPARC:UPI0000136E8A; EMBL:AE000056; GB:U00089; NIC A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: thioredoxin; thioredoxin homology
F:9-90/Domain: thioredoxin homology <TXN>

Query Match 100.0%; Score 47; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 4
B71503
probable thioredoxin - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revise 13-Sep-1998 #text_change 05-Oct-2004
C:Accession: B71503
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: B71503
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <ARN>
A:Cross-references: UNIPROT:O84544; UNIPARC:UPI0000136E75; GB:AE001344; GB:AE001273; NIT A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 27 WCGPCK 32

RESULT 5

C81660

thioredoxin TC0826 [imported] - Chlamydia muridarum (strain Nigg)

C.Species: Chlamydia muridarum, Chlamydia trachomatis Mopn

C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004

C.Accession: C81660

R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A.Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A.Reference number: A81500; MUID:20150255; PMID:10684935

A.Accession: C81660

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-102 <TET>

A.Cross-references: UNIPROT:Q9PJK3, UNIPARC:UPI0000057A90; GB:AE002349; GB:AE002160; NID

A.Experimental source: strain Nigg (Mopn)

C.Genetics:

A.Gene: TC0826

C.Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 27 WCGPCK 32

RESULT 6

TYB2

thioredoxin II - yeast (Saccharomyces cerevisiae)

N.Alternate names: protein L1933; protein YLR043c

C.Species: Saccharomyces cerevisiae

C.Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004

C.Accession: S15048; A39847; S15360; S64870; B38669

R.Gan, Z. R.

J. Biol. Chem. 266, 1692-1696, 1991

A.Title: Yeast thioredoxin genes.

A.Reference number: A38669; MUID:91107668; PMID:1988444

A.Accession: S15048

A.Molecule type: DNA

A.Residues: 1-103 <GAN>

A.Cross-references: UNIPROT:P22217, UNIPARC:UPI000004F943; EMBL:M59169; NID:G173027; PID

R.Muller, E.G.D.

J. Biol. Chem. 266, 9194-9202, 1991

A.Title: Thioredoxin deficiency in yeast prolongs S phase and shortens the G1 interval

A.Reference number: A39847; MUID:91225027; PMID:2026619

A.Accession: A39847

A.Molecule type: DNA

A.Residues: 1-103 <MU>

A.Cross-references: UNIPARC:UPI000004F943; GB:M62647; NID:G173047; PIDN:AAA5177.1; PID:

R.Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.

Eur. J. Biochem. 23, 328-335, 1971

A.Title: Yeast thioredoxin. Amino-acid sequence around the active-center disulfide of th

A.Reference number: S05793; MUID:72100583; PMID:4945270

A.Accession: S15360

A.Molecule type: protein

A.Residues: 26-34 <HAL>

A.Cross-references: UNIPARC:UPI0000171E21

R.Koetter, P.; Rose, M.; Entian, K.D.

submitted to the Protein Sequence Database, May 1996

A.Reference number: S64870

A.Accession: S64870

A.Molecule type: DNA

A.Residues: 1-103 <KOE>
 A.Cross-references: UNIPARC:UPI000004F943; EMBL:Z73215; NID:G1360372; PIDN:CAA97572.1; I

A.Note: experimental_source strain S288C

C.Genetics:

A.Gene: SGD:TRX1; TR-II; MIPS:YLR043c

A.Cross-references: SGD:S0004033; MIPS:YLR043c

A.Map position: 12R

C.Superfamily: thioredoxin; thioredoxin homology

C.Keywords: redox-active disulfide

F/2-103/Product: thioredoxin II #status predicted <MAT>

F/9-90/Domain: thioredoxin homology <THR>

F/30-33/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 7

T39085

thioredoxin II - fission yeast (Schizosaccharomyces pombe)

N.Alternate names: thioredoxine 2

C.Species: Schizosaccharomyces pombe

C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C.Accession: T39085; T46567

R.Gentles, S.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1997

A.Reference number: Z21826

A.Accession: T39085

A.Status: preliminary

A.Molecule type: translated from GB/EMBL/DBJ

A.Residues: 1-103 <GEN>

A.Cross-references: UNIPROT:O14463; UNIPARC:UPI000016205F; EMBL:Z99532; PIDN:CAB16724.1,

A.Experimental source: strain 972h-; cosmid C7D4

R.Lenaers, G.; Perret, E.; Bonin, O.; Picard, A.; Caput, D.

submitted to the EMBL Data Library, October 1997

A.Description: TRX2, a fission yeast stress protein.

A.Reference number: Z23075

A.Accession: T46567

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-103 <LEN>

A.Cross-references: UNIPARC:UPI000016205F; EMBL:AJ003819; PIDN:CAA06033.1

A.Experimental source: strain 972(-)

C.Genetics:

A.Gene: trx2; SPACTD4.07c

A.Map position: 1

C.Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 8

A28086

thioredoxin - rabbit

C.Species: Oryctolagus cuniculus (domestic rabbit)

C.Date: 30-Jun-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C.Accession: A28086

R.Johnson, R.S.; Mathews, W.R.; Bismann, K.; Hopper, S.

J. Biol. Chem. 263, 9589-9597, 1988

A.Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined

A.Reference number: A28086; MUID:88257078; PMID:3164311

A.Accession: A28086

A.Molecule type: protein
A.Residues: 1-104 <JON>
A.Cross-references: UNIPROT:P08628; UNIPARC:UPI0000136E96
C.Species: Bacillus subtilis
C.Date: 31-Jan-1992 #sequence revision 26-May-1994 #text_change 05-Oct-2004
C.Keywords: redox-active disulfide
F/8-91/Domain: thioredoxin homology <THR>
F/31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 9

B37192
thioredoxin - Bacillus subtilis

C.Species: Bacillus subtilis

C.Date: 31-Jan-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C.Accession: B37192; H69726

R.Chen, N.Y.; Zhang, U.J.; Paulus, H.

J. Gen. Microbiol. 135, 2931-2940, 1989

A.Title: Chromosomal location of the Bacillus subtilis aspartokinase II gene and nucleot

A.Reference number: A37192; PMID:90132525; PMID:2559145

A.Accession: B37192

A.Molecule type: DNA

A.Residues: 1-104 <CHE>

A.Cross-references: UNIPROT:P14949; UNIPARC:UPI000006087B; GB:U03294; GB:M26384; NID:914

R.Kumai, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emerson, P.T.; Eutlian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.

Nature 390, 249-256, 1997

A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.

Koehler, P.; Koningstein, G.; Krog, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Maue

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,

A.Authors: Schleich, S.; Schroeter, R.; Scorfone, F.; Sekiguchi, J.; Sekowska, A.; Ser

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A.Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A.Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A.Reference number: A69580; PMID:9804033; PMID:9384377

A.Accession: H69726

A.Status: nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-104 <KUN>

A.Cross-references: UNIPARC:UPI000006087B; GB:Z99118; GB:AL009126; NID:92635200; PIDN:CA

A.Experimental source: strain 168

C.Genetics:

A.Gene: trxA

A.Map position: 70 min

C.Superfamily: thioredoxin; thioredoxin homology

C.Keywords: redox-active disulfide

F/8-90/Domain: thioredoxin homology <THR>

F/39-32/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 28 WCGPCK 33

RESULT 10

TXBY1
thioredoxin I - yeast (Saccharomyces cerevisiae)

N.Alternate names: protein G7746; protein YGR209c; thioredoxin 2

C.Species: Saccharomyces cerevisiae

C.Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 05-Oct-2004

C.Accession: S15049; B39847; S05793; S53932; S61947; S64531; S63858; A38669

R.Gan, Z. R.

J. Biol. Chem. 266, 1692-1696, 1991

A.Title: Yeast thioredoxin genes.

A.Reference number: A38669; PMID:91107668; PMID:1988444

A.Accession: S15049

A.Molecule type: DNA

A.Residues: 1-104 <GAN>

A.Cross-references: UNIPROT:P22803; UNIPARC:UPI000004F91C; GB:M59168; NID:9173025; PIDN:

R.Muller, E.G.D.

J. Biol. Chem. 266, 9194-9202, 1991

A.Title: Thioredoxin deficiency in yeast prolongs S phase and shortens the G1 interval o

A.Reference number: A39847; PMID:9125027; PMID:2026619

A.Accession: B39847

A.Molecule type: DNA

A.Residues: 1-104 <MUL>

A.Cross-references: UNIPARC:UPI000004F91C; GB:M62648; NID:9173049; PIDN:AAA5178.1; PID:

R.Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.

Eur. J. Biochem. 23, 328-335, 1971

A.Title: Yeast thioredoxin. Amino-acid sequence around the active-center disulfide of th

A.Reference number: S05793; PMID:72100583; PMID:4945270

A.Accession: S05793

A.Molecule type: protein

A.Residues: 2;27-43;98-104 <NAL>

A.Cross-references: UNIPARC:UPI000111EC95; UNIPARC:UPI000171E1F; UNIPARC:UPI000171E20

A.Note: the sequence from the summary and from Fig. 5 is inconsistent with that from pag

R.Guerreiro, P.; Barreiro, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pousa

submitted to the EMBL Data Library, April 1995

A.Description: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII

es, of the human.

A.Reference number: S53932

A.Accession: S53932

A.Molecule type: DNA

A.Residues: 1-104 <GUE>

A.Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:9790489; PIDN:CAA89002.1; P

A.Experimental source: strain S288C

R.Song, J.M.; Cheung, B.; Rabinowitz, J.C.

submitted to the EMBL Data Library, November 1995

A.Description: Analysis of the 15.6-kb fragment encompassing the ADE3 gene.

A.Reference number: S61947

A.Accession: S61947

A.Molecule type: DNA

A.Residues: 1-104 <SON>

A.Cross-references: UNIPARC:UPI000004F91C; EMBL:U40843; NID:91165213; PIDN:AAA85584.1; I

A.Experimental source: strain GRP88

R.Guerreiro, P.; Barreiro, T.; Cyrne, L.; Soares, H.; Maia e Silva, A.; Rodrigues-Pous

submitted to the Protein Sequence Database, May 1996

A.Reference number: S64531

A.Accession: S64531

A.Molecule type: DNA

A.Residues: 1-104 <GUM>

A.Cross-references: UNIPARC:UPI000004F91C; EMBL:Z72994; NID:91323374; PIDN:CAA97236.1;

A.Experimental source: strain S288C

R.Guerreiro, P.; Barreiro, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pous

Yeast 12, 273-280, 1996

A.Title: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII revea

terial electron-transferring flavoproteins (beta-chain) and of the Escherichia coli pho

A.Reference number: S63848; PMID:97060019; PMID:8904340

A.Accession: S63848

A.Molecule type: DNA

A.Residues: 1-104 <GUF>

A.Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:9790489; PIDN:CAA89002.1; P

A.Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

A.Gene: SGD:TRX2; TR-1; MIPS:YGR209C

A.Cross-references: SGD:S0003441; MIPS:YGR209C

A.Map position: 7R

C.Superfamily: thioredoxin; thioredoxin homology

C.Keywords: redox-active disulfide

F:2-104/Product: thioredoxin I #status experimental <MAT>
F:9-91/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 30 WCGPCK 35

RESULT 11

S77780

thioredoxin - Mycoplasma capricolum (fragment)

N/Alternate names: Protein WC064

C/Species: Mycoplasma capricolum

C/Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C/Accession: S77780; S46921

R/Bork, P.; Ouzounis, S.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;

Mol. Microbiol. 16, 955-967, 1995

A/Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology

A/Reference number: S77739; MUID:96059641; PMID:7476192

A/Accession: S77780

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-104 <BOR>

A/Cross-references: UNIPROT:Q48985; UNIPARC:UPI00000B3213; EMBL:Z33053; NID:9514449; PID

A/Experimental source: ATCC 27343

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

C/Genetics:

A/Genetic code: SGC3

C/Superfamily: thioredoxin; thioredoxin homology

C/Keywords: redox-active disulfide

F:13-93/Domain: thioredoxin homology <THR>

F:33-36/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 12

A59394

thioredoxin - Clostridium pasteurianum

C/Species: Clostridium pasteurianum

C/Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 05-Oct-2004

C/Accession: B59394; A59394

R/Reynolds, C.M.; Meyer, J.; Poole, L.B.

Biochemistry 41, 1990-2001, 2002

A/Title: NADH-dependent bacterial thioredoxin reductase-like protein, in conjunction with

A/Reference number: B59394

A/Accession: B59394

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-104 <REI>

A/Cross-references: UNIPARC:UPI0000174DEF

R/Reynolds, C.M.; Poole, L.B.; Hammel, K.E.; Made, K.; Buchanan, B.B.

submitted to the Protein Sequence Database, September 2001

A/Reference number: A59394

A/Accession: A59394

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-104 <RE2>

A/Cross-references: UNIPARC:UPI0000174DEF

R/Hammel, K.E.; Cornwell, K.L.; Buchanan, B.B.

Proc. Natl. Acad. Sci. USA 80, 3681-3685, 1983

A/Title: Ferredoxin/flavoprotein-linked pathway for the reduction of thioredoxin.

A/Reference number: A59432
A/Contents: annotation; purification and characterization of the protein
C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 27 WCGPCK 32

RESULT 13

B84037

thioredoxin trxA [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004

C/Accession: B84037

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: B84037

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <STO>

A/Cross-references: UNIPROT:Q9K8A8; UNIPARC:UPI00000C40CD; GB:AP001517; GB:BA000004; NIT

A/Experimental source: strain C-125

C/Genetics:

A/Gene: trxA

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 28 WCGPCK 33

RESULT 14

B89885

thioredoxin [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004

C/Accession: B89885

R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguni

C.; Shiba, T.; Hatori, M.; Ogatawara, N.; Hayashi, H.; Hiratazu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: B89885

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <KUR>

A/Cross-references: UNIPROT:Q9ZEH4; UNIPARC:UPI00000D78B6; GB:BA000018; PID:G13700945; P

A/Experimental source: strain N315

C/Genetics:

A/Gene: trxA

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 28 WCGPCK 33

RESULT 15

A30006
 A:Species: Gallus gallus (chicken)
 C:Date: 31-Mar-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: A30006
 R:Jones, S.W.; Luk, K.C.
 J:J Biol. Chem. 263, 9607-9611, 1988
 A:Title: Isolation of a chicken thioredoxin cDNA clone: thioredoxin mRNA is differential
 A:Reference number: A30006; MUID:88257080; PMID:2838473
 A:Accession: A30006
 A:Molecule type: mRNA
 A:Residues: 1-105 <ON>
 A:Cross-references: UNIPROT:P08629; UNIPARC:UPI00001713BC; GB:J03882; NID:g212765; PIDN:
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:9-92/Domain: thioredoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 16

JH0568
 A:Species: Homo sapiens (human)
 C:Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: JH0568; S04106; S44375; A31993; PT0079; A60749; A38922; S53453; A60870
 R:Tonnissen, K.F.; Wells, J.R.E.
 Gene 102, 221-228, 1991
 A:Title: Isolation and characterization of human thioredoxin-encoding genes.
 A:Reference number: JH0568; MUID:91340156; PMID:1874447
 A:Accession: JH0568
 A:Molecule type: DNA
 A:Residues: 1-105 <TON>
 A:Cross-references: UNIPROT:P10599; UNIPARC:UPI000011065C; EMBL:X54539; NID:g37455; PIDN:
 R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMO J. 8, 757-764, 1989
 A:Title: ATL-derived factor (ADF), an II-2 receptor/Trac inducer homologous to thioredoxin
 A:Reference number: S04106; MUID:89251607; PMID:2785919
 A:Accession: S04106
 A:Molecule type: mRNA
 A:Residues: 1-105 <TAG1>
 A:Cross-references: UNIPARC:UPI000011065C; GB:X77584; NID:g453963; PIDN:CAA54687.1; PID:
 A:Note: this sequence has been revised in reference S44375
 R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMO J. 13, 2244, 1994
 A:Reference number: S44375; MUID:94244626; PMID:8187776
 A:Accession: S44375
 A:Contents: extractum
 A:Molecule type: mRNA
 A:Residues: 1-105 <TRG2>
 A:Cross-references: UNIPARC:UPI000011065C; EMBL:X77584; NID:g453963; PIDN:CAA54687.1; PID:
 R:Wollman, E.B.; d'Amico, L.; Rimsky, L.; Shaw, A.; Jacquot, J.P.; Wingfield, P.; Grabe
 J. Biol. Chem. 263, 15506-15512, 1988
 A:Title: Cloning and expression of a cDNA for human thioredoxin.
 A:Reference number: A31993; MUID:89008454; PMID:3170555
 A:Accession: A31993
 A:Molecule type: mRNA
 A:Residues: 1-38, 'N', '40-73', 'T', '75-105 <MO>
 A:Cross-references: UNIPARC:UPI000003066B; GB:J04026; NID:g339648; PIDN:AAA74596.1; PID:
 R:Marlin, H.; Dean, M.
 Biochem. Biophys. Res. Commun. 175, 123-128, 1991
 A:Title: Identification of a thioredoxin-related protein associated with plasma membrane
 A:Reference number: PT0079; MUID:91151337; PMID:1998498
 A:Accession: PT0079

A:Molecule type: protein
 A:Residues: 2-13, 'X', '15 <MAR>
 A:Cross-references: UNIPARC:UPI0000171E19
 R:Silberstein, D.S.; Ali, M.H.; Baker, S.L.; David, J.R.
 J. Immunol. 143, 979-983, 1989
 A:Title: Human eosinophil cytotoxicity-enhancing factor. Purification, physical character
 A:Reference number: A60749; MUID:89309777; PMID:2745979
 A:Accession: A60749
 A:Molecule type: protein
 A:Residues: 2-12, 'K', '14-15', 'XX', '18-19', 'X', '21-22 <SL>
 A:Cross-references: UNIPARC:UPI0000171E1A
 A:Note: the abstract is inconsistent with figure 4 in having one undetermined residue at
 R:Rimsky, L.; Wakaugli, H.; Ferreira, P.; Robin, P.; Capdevielle, J.; Turaz, T.; Fradeliz
 J. Immunol. 136, 3304-3310, 1986
 A:Title: Purification to homogeneity and NH-2-terminal amino acid sequence of a novel in
 A:Reference number: A38922; MUID:86169664; PMID:3485686
 A:Accession: A38922
 A:Molecule type: protein
 A:Residues: 2-16 <WAK>
 A:Cross-references: UNIPARC:UPI0000171E1B
 R:Dean, M.F.; Marlin, H.; Sansom, P.A.
 Biochem. J. 304, 861-867, 1994
 A:Title: Characterization of a thioredoxin-related surface protein.
 A:Reference number: S53453; MUID:95118305; PMID:7818492
 A:Accession: S53453
 A:Molecule type: protein
 A:Residues: 1-21, 38-57 <DEA>
 A:Cross-references: UNIPARC:UPI00000353C5; UNIPARC:UPI0000171E1C
 A:Note: described to be a surface-associated thioredoxin
 R:Wakaugli, H.; Rimsky, L.; Mahe, Y.; Kamel, A.M.; Fradelizi, D.; Turaz, T.; Bertoglio,
 Proc. Natl. Acad. Sci. U.S.A. 84, 804-808, 1987
 A:Title: Epstein-Barr virus-containing B-cell line produces an interleukin 1 that it use
 A:Reference number: A60870; MUID:87118252; PMID:3027706
 A:Contents: annotation
 R:Reichsel, A.; Gadsdaka, J.R.; Powis, G.; Montfort, W.R.
 submitted to the Brookhaven Protein Data Bank, February 1996
 A:Reference number: A65533; PDB:1ERT
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, reduced form, residues 1-1
 R:Reichsel, A.; Gadsdaka, J.R.; Powis, G.; Montfort, W.R.
 submitted to the Brookhaven Protein Data Bank, December 1990
 A:Reference number: A65534; PDB:1ERU
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, oxidized form, residues 1-
 R:Forman-Kay, J.D.; Clore, G.M.; Gronenborn, A.M.
 submitted to the Brookhaven Protein Data Bank, December 1990
 A:Reference number: A50924; PDB:4TRX
 A:Contents: annotation; conformation by (1)H-NMR, residues 1-73, 'T', '75-105
 R:Forman-Kay, J.D.; Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
 Biochemistry 30, 2685-2698, 1991
 A:Title: High-resolution three-dimensional structure of reduced recombinant human thior
 A:Reference number: A38953; MUID:91159399; PMID:2001356
 A:Contents: annotation; conformation by (1)H- and (15)N-NMR
 C:Comment: This small ubiquitous protein functions in many intracellular biological pati

A:Gene: GDB:TXN
 A:Cross-references: GDB:120475; OMIM:187700
 A:Map position: 9q31-9q31
 A:Intons: 8/3; 43/3; 63/3; 85/3
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:2-105/Product: thioredoxin #status experimental <MAT>
 F:9-92/Domain: thioredoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 17

JS0667
 thioresoxin - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C>Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: JS0667
 R:An, G.; Wu, R.
 Biochem. Biophys. Res. Commun. 183, 170-175, 1992
 A>Title: Thioresoxin gene expression is transcriptionally up-regulated by retinol in mor
 A:Reference number: JS0667; MUID:9218138; PMID:1543487
 A:Accession: JS0667
 A:Molecule type: mRNA
 A:Residues: 1-105 <ANG>
 A:Cross-references: UNIPROT:P29451; UNIPARC:UPI000016C493; GB:M84643; NID:g342338; PIDN:
 C:Superfamily: thioresoxin; thioresoxin homology
 C:Keywords: redox-active disulfide
 F:9-32/Domain: thioresoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 31 WCGPCK 36

RESULT 18

S04107
 thioresoxin - mouse
 N:Alternate names: ATL-derived factor (ADF)
 C:Species: Mus musculus (house mouse)
 C>Date: 21-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 05-Oct-2004
 C:Accession: J04068; S44376; S04107
 R:Matsumi, M.; Taniguchi, Y.; Hirota, K.; Takeo, M.; Yodoi, J.
 Gene 152, 165-171, 1995
 A>Title: Structure of the mouse thioresoxin-encoding gene and its processed pseudogene.
 A:Reference number: J04068; MUID:95137382; PMID:7835695
 A:Accession: J04068
 A:Molecule type: DNA
 A:Residues: 1-105 <MAT>
 A:Cross-references: UNIPROT:P10639; UNIPARC:UPI0000163891; DDBJ:D21855; NID:g517128
 R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMO J. 13, 2244, 1994
 A:Reference number: S44375; MUID:94244626; PMID:8187776
 A:Contents: erratum
 A:Accession: S44376
 A:Molecule type: mRNA
 A:Residues: 1-105 <TAGI>
 A:Cross-references: UNIPARC:UPI0000163891; EMBL:X77585; NID:g453971; PIDN:GAA54688.1; PI
 R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMO J. 8, 757-764, 1989
 A>Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioresoxi
 A:Reference number: S04106; MUID:89251607; PMID:2785919
 A:Accession: S04107
 A:Molecule type: mRNA
 A:Residues: 1-93, 'N', '94-96', 'ALT', '100-104', 'S', <TAG2>
 A:Cross-references: UNIPARC:UPI000017181E; GB:X77585
 C:Comment: This small ubiquitous protein functions in many intracellular biological path
 C:Genetics:
 A:Gene: MGI:Txn
 A:Cross-references: MGI:36258
 A:Map position: 4:24.6
 A:Introns: 29/2; 44/1; 84/2
 C:Superfamily: thioresoxin; thioresoxin homology
 C:Keywords: redox-active disulfide
 F:9-32/Domain: thioresoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 31 WCGPCK 36

RESULT 19

S04352
 thioresoxin - rat
 N:Alternate names: thioresoxin-related surface protein SASP
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Mar-1990 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: S04352; S66372
 R:Tomsen, K.F.; Robins, A.J.; Wells, J.R.E.
 Nucleic Acids Res. 17, 3973, 1989
 A>Title: Nucleotide sequence of a cDNA encoding rat thioresoxin.
 A:Reference number: S04352; MUID:89282399; PMID:2734107
 A:Accession: S04352
 A:Molecule type: mRNA
 A:Residues: 1-105 <TON>
 A:Cross-references: UNIPROT:P11232; UNIPARC:UPI00003066A; EMBL:X14878; NID:g57385; PIDN
 R:Dean, M.F.; Martin, H.; Sansom, P.A.
 Biochem. J. 304, 861-867, 1994
 A>Title: Characterization of a thioresoxin-related surface protein.
 A:Reference number: S53453; MUID:95118305; PMID:7818492
 A:Accession: S66372
 A:Molecule type: protein
 A:Residues: 2-21 <DEA>
 A:Cross-references: UNIPARC:UPI0000171E1D
 A>Note: 12-Lys, 15-Gly, 16-Leu, 17-Gln, and 18-Leu were also found
 A>Note: described to be a surface-associated thioresoxin
 C:Superfamily: thioresoxin; thioresoxin homology
 C:Keywords: redox-active disulfide
 F:9-32/Domain: thioresoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 31 WCGPCK 36

RESULT 20

TXFX
 thioresoxin - corynebacterium bacterium ATCC1425
 C:Species: corynebacterium bacterium ATCC1425
 C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 05-Oct-2004
 C:Accession: A00281
 R:Meng, M.; Hogenkamp, H.P.C.
 J. Biol. Chem. 256, 9174-9182, 1981
 A>Title: Purification, characterization, and amino acid sequence of thioresoxin from Co.
 A:Reference number: A00281; MUID:81264365; PMID:7021558
 A:Accession: A00281
 A:Molecule type: protein
 A:Residues: 1-105 <MEN>
 A:Cross-references: UNIPROT:P00275; UNIPARC:UPI0000136069
 A>Note: the source was designated as Corynebacterium nephridii
 C:Comment: Thioresoxins are ubiquitous small hydrogen carrier proteins that participate
 C:Superfamily: thioresoxin; thioresoxin homology
 C:Keywords: redox-active disulfide
 F:8-91/Domain: thioresoxin homology <THR>
 F:30-33/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 21

B97700
thioredoxin [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004

C:Accession: B97700

R:Ogata, H.; Audic, S.; Rensero-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:1157893

A:Accession: B97700

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <NR>

A:Cross-references: UNIPROT:Q92JUR5; UNIPARC:UP10000136E9A; GB:AE006914; P1DN:AL02540.1;

C:Genetics:

A:Gene: trxA

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
29 WCGPCK 34

RESULT 22

D97279
thioredoxin [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004

C:Accession: D97279

R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: D97279

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <NR>

A:Cross-references: UNIPROT:Q9TEW7; UNIPARC:UP100000CA715; GB:AE001437; P1DN:AK81023.1;

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3083

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
29 WCGPCK 34

RESULT 23

S33357
thioredoxin - Streptomyces aureofaciens (fragment)

C:Species: Streptomyces aureofaciens

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S33357

R:Labidova, O.; Nemethova, M.; Turna, J.; Kollárová, M.

submitted to the EMBL Data Library, April 1993

A:Description: PCR cloning of a protein-coding part of the thioredoxin gene from Strept

A:Reference number: S33357

A:Accession: S33357

A:Molecule type: DNA

A:Residues: 1-106 <LAB>

A:Cross-references: UNIPROT:P3J391; UNIPARC:UP10000136E9D; EMBL:X72799; NID:G297872; P1D
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:31-34/Disulfide Bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
30 WCGPCK 35

RESULT 24

H64622
thioredoxin - Helicobacter pylori

C:Species: Helicobacter pylori

A:Variety: strains J99, 26695

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: H64622; C71890

R:Tomb, J.F.; White, O.; Kellavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D

Petersen, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatal, H.G.; Glodex, A.; McKenne

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Wathey, L

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: H64622

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-106 <ROM>

A:Cross-references: UNIPROT:P56430; UNIPARC:UP10000136E82; GB:AE000594; GB:AE000511; NIT

A:Experimental source: strain 26695

R:Ives, R.A.; Ling, L.S.L.; Mott, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.,

J. Biol. Chem. 269, 176-180, 1999

A:Title: Genetic sequence comparison of two unrelated isolates of the human gastric pat

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: C71890

A:Molecule type: DNA

A:Residues: 1-106 <ARN>

A:Cross-references: UNIPARC:UP10000136E82; GB:AE001507; GB:AE001439; NID:G4155326; P1DN

A:Experimental source: strain J99

C:Genetics:

A:Gene: trxA; HP0824

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
29 WCGPCK 34

RESULT 25

A49888
thioredoxin - Penicillium chrysogenum

C:Species: Penicillium chrysogenum

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 05-Oct-2004

C:Accession: A49888; S38886

R:Cohen, G.; Argaman, A.; Schneider, R.; Mislavati, M.; Aharonowitz, Y.

J. Bacteriol. 176, 973-984, 1994

A:Title: The thioredoxin system of Penicillium chrysogenum and its possible role in pen

A:Reference number: A49888; MUID:94148789; PMID:8106340

A:Accession: A49888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-106 <COH>

A:Cross-references: UNIPROT:P3J4723; UNIPARC:UP10000136E91; EMBL:X76120; NID:G426468; P1

C:Genetics:
A:Gene: trxA
A:Introns: 8/2
C:Superfamily: thioredoxin; thioredoxin homology
F:10-92/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 47; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 26

AG2579
thioredoxin C-1 trxa [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004

C:Accession: AG2579

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavyn, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AG2579

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-106 <KUR>

A:Cross-references: UNIPROT:G8U46; UNIPARC:UPI0000164451; GB:AE008668; PIDN:AAL41053.1;

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: trxA

A:Map position: circular chromosome

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 27

A26622
thioredoxin - Chromatium vinosum

C:Species: Chromatium vinosum

C:Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: A26622

R:Johnson, R.S.; Biemann, K.

Biochemistry 26, 1209-1214, 1987

A:Title: The primary structure of thioredoxin from Chromatium vinosum determined by high

A:Reference number: A26622; MUID:87185419; PMID:3567166

A:Accession: A26622

A:Molecule type: protein

A:Residues: 1-107 <JOH>

A:Cross-references: UNIPROT:P09857; UNIPARC:UPI0000136E76

A>Note: unidentified residues are Ile or Leu

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: heat-stable protein; redox-active disulfide

F:10-93/Domain: thioredoxin homology <THR>

F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 28

S47867

thioredoxin-like protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C:Accession: S47867

R:Salz, H.K.; Flickinger, T.W.; Mittenfior, E.; Pellicena-Palle, A.; Petschek, J.P.; Br

Genetics 136, 1075-1086, 1994

A:Title: The Drosophila maternal effect locus deadhead encodes a thioredoxin homolog rec

A:Reference number: S47867; MUID:94274010; PMID:7516301

A:Accession: S47867

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-107 <SAL>

A:Cross-references: UNIPROT:P47938; UNIPARC:UPI0000124A52; EMBL:L27072; NID:G435591; PII

C:Genetics:

A:Gene: FlyBase:dhd

A:Cross-references: FlyBase:FBgn0011761

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F:8-92/Domain: thioredoxin homology <THR>

F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 29

T02814

thioredoxin TRXRPI [imported] - Leishmania major (strain Friedlin)

C:Species: Leishmania major

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C:Accession: B81458; T02814

R:Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;

Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999

A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c

A:Reference number: B81455; MUID:99178987; PMID:10077609

A:Accession: B81458

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <PYI>

A:Cross-references: UNIPROT:Q25345; UNIPARC:UPI000007DADA; GB:AE001274; NID:G3264850; PI

A:Experimental source: strain RHOM/IL/81/Friedlin

C:Genetics:

A:Gene: TRXRPI

A:Map position: 1

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 30

AH3504

thioredoxin C-1 [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 05-Oct-2004

C:Accession: AH3504

R;DelVecchio, V.G.; Kaparatel, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goldsman, E.; Seikov, E.; Elser, P.H.; Hagius, S.; O'Callaghan, D.; Lelsg Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitens*

A;Reference number: AD3252; PMID:11756688

A;Accession: AH3504

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-107 <KUR>

A;Cross-references: UNIPROT:Q8F56; UNIPARC:UPI0000582C9; GB:AE008917;

A;Experimental source: strain 16M

A;Gene: BME12022

A;Map position: 1

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 30 WCGPCK 35

RESULT 31

B64047

thioredoxin - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

C;Accession: B64047

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kurlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Pile, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; PMID:95350630; PMID:7542800

A;Accession: B64047

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-107 <TIGR>

A;Cross-references: UNIPROT:P43785; UNIPARC:UPI0000136E81; GB:U32693; GB:L42023; NID:915

A;Note: named as homolog to a protein from *Anacyclus nidulans*

C;Superfamily: thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;10-93/Domain: thioredoxin homology <THR>

F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 31 WCGPCK 36

RESULT 32

G82991

thioredoxin PA5240 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: G82991

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mroguch, S.D.; Warren, P.; Hickey, M.D.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Harbig, K.; Llin, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A;Reference number: A82950; PMID:20437337; PMID:10984043

A;Accession: G82991

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <STO>

A;Cross-references: UNIPROT:Q9X2T1; UNIPARC:UPI0000136E95; GB:AE004936; GB:AE004091; NID

A;Experimental source: strain PA01

C;Genetics:

A;Gene: trxA; PA5240

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 32 WCGPCK 37

RESULT 33

AD0471

thioredoxin 1 [imported] - *Yersinia pestis* (strain CO92)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004

C;Accession: AD0471

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Taraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; PMID:21470413; PMID:11586360

A;Accession: AD0471

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <KUR>

A;Cross-references: UNIPROT:Q8ZAD9; UNIPARC:UPI00000DC68C; GB:AL590842; PIDN:CAC9336.1,

C;Genetics:

A;Gene: trxA

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 32 WCGPCK 37

RESULT 34

D82338

thioredoxin VC0306 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004

C;Accession: D82338

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamadevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers, I 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; PMID:20406833; PMID:10953301

A;Accession: D82338

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <HEI>

A;Cross-references: UNIPROT:Q9KV51; UNIPARC:UPI00000C2CE6; GB:AE004119; GB:AE003852; NI

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0306

A;Map position: 1

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37

RESULT 35

S35497

thioredoxin - Salmonella typhimurium

C:Species: Salmonella typhimurium

C:Date: 09-Dec-1993 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: S35497; A9917; S31928

R:Kotani, H.; Nakajima, K.

Nucleic Acids Res. 20, 1424, 1992

A:Title: Cloning and sequence of thioredoxin gene of Salmonella typhimurium LT2.

A:Reference number: S35497; MUID:92220625; PMID:1561103

A:Accession: S35497

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-109 <KOT>

A:Cross-references: UNIPROT:P00274; UNIPARC:UPI000003112A; EMBL:DI0015; NID:G217084; PID

A:Experimental source: strain LT2

A>Note: The nucleotide sequence was submitted to the EMBL Data Library, March 1992

R:Miloslo, M.; Limauro, D.; Alfano, P.; Rivellini, F.; Lavitola, A.; Gulletta, E.; Bruni

J. Bacteriol. 175, 8030-8037, 1993

A:Title: Characterization of the rho genes of *Neisseria gonorrhoeae* and *Salmonella typhi*

A:Reference number: A49917; MUID:94075245; PMID:8253691

A:Accession: A49917

A:Molecule type: DNA

A:Residues: 1-109 <MLT>

A:Cross-references: UNIPARC:UPI000003112A; GB:Z21789; NID:G49361; PIDN:CAA79851.1; PID:G

A>Note: submitted to the EMBL Data Library, February 1993

C:Genetics:

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F:11-94/Domain: thioredoxin homology <THR>

F:33-36/Disulfide bonds: redox-active #status predicted

Query Match	100.0%	Score 47	DB 1	Length 109
Best Local Similarity	100.0%	Fred. No. 1.1		
Matches	6	Conservative	0	Mismatches
			0	Indels
				Gaps
				0

OY 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37

RESULT 36

TXEC thioredoxin [validated] - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004

C:Accession: A91519; H5181; S30676; I54863; A91802; I52550; A91236; A00280; A22425; A24

R:Wallace, B.J.; Kushner, S.R.

Gene 32, 399-408, 1984

A:Title: Genetic and physical analysis of the thioredoxin (trxA) gene of *Escherichia coli*

A:Reference number: A91519; MUID:85155506; PMID:6099324

A:Accession: A91519

A:Molecule type: DNA

A:Residues: 'MLHQQRNQHARLIPVELY', 1-109 <MAL>

A:Cross-references: UNIPROT:P00274; UNIPARC:UPI0000165538; GB:K02845; NID:G147610; PIDN:

A>Note: The sequence represents translation from an upstream ATG triplet that seems not

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H65181

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 'MLHQQRNQHARLIPVELY', 1-109 <BLAT>

A:Cross-references: UNIPARC:UPI0000165538; GB:AE000454; GB:U00096; NID:G2367278; PIDN:AN

A:Experimental source: strain K-12, substrain MG1655

A>Note: the sequence represents translation from an upstream ATG triplet that seems not

R:Danielis, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.

Science 257, 771-778, 1992

A:Title: Analysis of the *Escherichia coli* genome. DNA sequence of the region from 84.5 t

A:Reference number: S30650; MUID:92358234; PMID:1379743

A:Accession: S30676

A:Molecule type: DNA

A:Residues: 'MLHQQRNQHARLIPVELY', 1-109 <DNAN>

A:Cross-references: UNIPARC:UPI0000165538; EMBL:M87049; NID:G836656; PIDN:AAA67582.1; PJ

A>Note: the sequence represents translation from an upstream ATG triplet that seems not

R:Matsumoto, Y.; Shigesada, K.; Hirano, M.; Imai, M.

J. Bacteriol. 166, 945-958, 1986

A:Title: Autogenous regulation of the gene for transcription termination factor rho in p

A:Reference number: 154863; MUID:86223816; PMID:2423505

A:Accession: 154863

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-109 <MAS>

A:Cross-references: UNIPARC:UPI00003112A; GB:M12779; NID:G148067; PIDN:AAA24694.1; PID:

R:Lim, C.J.; Geraghty, D.; Fuchs, J.A.

J. Bacteriol. 163, 311-316, 1985

A:Title: Cloning and nucleotide sequence of the trxA gene of *Escherichia coli* K-12.

A:Reference number: A91802; MUID:85234377; PMID:3891733

A:Accession: A91802

A:Molecule type: DNA

A:Residues: 1-109 <LIM>

A:Cross-references: UNIPARC:UPI000003112A; GB:M10424; NID:G147608; PIDN:AAA24533.1; PID

A:Experimental source: strain K12

R:Hoecy, J.

Biochim. Rep. 4, 917-923, 1984

A:Title: Nucleotide sequence of the thioredoxin gene from *Escherichia coli*.

A:Reference number: 152550; MUID:85123150; PMID:608320

A:Accession: 152550

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-109 <HOE>

A:Cross-references: UNIPARC:UPI000003112A; GB:M26133; NID:G148065; PIDN:AAA24693.1; PID

R:Holmgren, A.

Eur. J. Biochem. 6, 475-484, 1968

A:Title: Thioredoxin. 6. The amino acid sequence of the protein from *Escherichia coli* B

A:Reference number: A91236; MUID:69079993; PMID:4883076

A:Accession: A91236

A:Molecule type: protein

A:Residues: 2-16, 'LV', 19-71, 'IG', 74-109 <HOL>

A:Cross-references: UNIPARC:UPI0000171E22

A:Experimental source: strain B

R:Haeblerlein, I.

Eur. J. Biochem. 223, 473-479, 1994

A:Title: Structure requirements for disulfide bridge sulfolysis of oxidized *Escherichia*

A:Reference number: S45671; MUID:94333336; PMID:8055916

A:Contents: annotation; chemical activity of wild type and engineered sequence

R:Kati, S.K.; Lemaster, D.W.; Eklund, H.

submitted to the Brookhaven Protein Data Bank, March 1990

A:Reference number: A50900; PDB:2TRX

A:Contents: annotation; X-ray crystallography, 1.68 angstroms, residues 2-109

R:Kati, S.K.; Lemaster, D.W.; Eklund, H.

J. Mol. Biol. 212, 167-184, 1990

A:Title: Crystal structure of thioredoxin from *Escherichia coli* at 1.68 Angstroms resolu

A:Reference number: A58630; MUID:90204538; PMID:2181145

A:Contents: annotation; X-ray crystallography, 1.68 angstroms

R:Holmgren, A.; Soderberg, B.O.; Eklund, H.; Branden, C.I.

Proc. Natl. Acad. Sci. U.S.A. 72, 2305-2309, 1975

A:Title: Three-dimensional structure of *Escherichia coli* thioredoxin-S-2 to 2.8 angstrom

A:Reference number: A93800; MUID:75176330; PMID:1094461

A:Contents: annotation; X-ray crystallography, 2.8 angstroms

R:Dyson, H.J.; Gipeert, G.P.; Case, D.A.; Holmgren, A.; Wright, P.E.

submitted to the Brookhaven Protein Data Bank, January 1990

A:Reference number: A50871; PDB:1TRX

A:Contents: annotation; conformation by (1)H-NMR, reduced form, residues 2-109

R:Dyson, H.J.; Gipeert, G.P.; Case, D.A.; Holmgren, A.; Wright, P.E.

Biochemistry 29, 4129-4136, 1990

A:Title: Three-dimensional solution structure of the reduced form of *Escherichia coli* th

A:Reference number: A58631; MUID:90298180; PMID:2193685

A:Contents: annotation, conformation by (1)H-NMR
 R.Jeng, M.F.; Campbell, A.P.; Begley, T.; Holmgren, A.; Case, D.A.; Wright, P.E.; Dyson, R. submitted to the Brookhaven Protein Data Bank, November 1995
 A:Reference number: A66947; PDB:1XOA
 A:Contents: annotation, conformation by (1)H-, (15)N-NMR, oxidized form, residues 2-109
 R.Jeng, M.F.; Campbell, A.P.; Begley, T.; Holmgren, A.; Case, D.A.; Wright, P.E.; Dyson, R. submitted to the Brookhaven Protein Data Bank, November 1995
 A:Reference number: A66948; PDB:1XOB
 A:Contents: annotation, conformation by (1)H-, (15)N-NMR, reduced form, residues 2-109
 C:Genetics:
 A:Gene: trxA
 A:Map position: 85 min
 C:Function:
 A:Description: is reduced with NADPH by thioredoxin reductase (EC 1.6.4.5); the reduced
 C:Disulfide exchange reactions
 C:Superfamily: thioredoxin homology
 C:Keywords: redox-active disulfide
 F:2-109/Product: thioredoxin #status experimental <MAR>
 F:11-94/Domain: thioredoxin homology <THR>
 F:33-36/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37

RESULT 37

S27053
 thioredoxin - Emericella nidulans
 C:Species: Emericella nidulans, Aspergillus nidulans
 C:Date: 22-Nov-1993 #sequence_revision 01-sep-1995 #text_change 09-Jul-2004
 C:Accession: S27053
 R:Le Marchal, P.; Hoang, B.M.C.; Schmitter, J.M.; van Dorsselaer, A.; Decottignies, P.
 Eur. J. Biochem. 210, 421-429, 1992
 A:Title: Purification, properties and primary structure of thioredoxin from Aspergillus
 A:Reference number: S27053; PMID:93092975; PMID:1459127
 A:Accession: S27053
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-109 <MAR>
 A:Cross-references: UNIPROT:P29429; UNIPARC:UPI0000136E7E
 C:Superfamily: thioredoxin; thioredoxin homology
 F:13-95/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 47; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 34 WCGPCK 39

RESULT 38

AF0922
 thioredoxin [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AF0922
 R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; PMID:21534947; PMID:11677608
 A:Accession: AF0922
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-109 <PAR>
 A:Cross-references: UNIPARC:UPI000003112A; GB:AL513382; PIDN:CAD09400.1; PID:g16504518;
 C:Genetics:
 A:Gene: STY3639
 C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37

RESULT 39

A87688
 thioredoxin [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
 C:Accession: A87688
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Desoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; PMID:21173698; PMID:11259647
 A:Accession: A87688
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-110 <STO>
 A:Cross-references: UNIPROT:Q9A2L8; UNIPARC:UPI00000C7AF9; GB:AE005673; NID:g13425273; F
 C:Genetics:
 A:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

Query Match 100.0%; Score 47; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 40

C81090
 thioredoxin NMB1366 [imported] - Neisseria meningitidis (strain MCS8 serogroup B)
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
 C:Accession: C81090
 R:Nettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
 Hickey, R.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
 et al.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizsa, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
 A:Reference number: A81000; PMID:20175755; PMID:10710307
 A:Accession: C81090
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-110 <TER>
 A:Cross-references: UNIPROT:O9JYV9; UNIPARC:UPI00000C46C4; GB:AE002485; GB:AE002098; NLI
 C:Genetics:
 A:Gene: NMB1366
 C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 33 WCGPCK 38

RESULT 41

E81850
 Chloredoxin I NMA1578 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
 C:Accession: E81850
 R:Parthill, J.; Achtmann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 R.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: E81850
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-110 <PAR>
 A:Cross-references: UNIPROT:O9JTV5; UNIPARC:UPI00000C4C16; GB:AL162756; GB:AL157959; NID
 C:Genetics:
 A:Gene: trxA; NMA1578
 C:Superfamily: thioedoxin; thioedoxin homology

Query Match 100.0%; Score 47; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 33 WCGPCK 38

RESULT 42

S57775
 Chloredoxin h, cytosolic [validated] - Chlamydomonas reinhardtii
 C:Species: Chlamydomonas reinhardtii
 C:Date: 27-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 05-Oct-2004
 C:Accession: S57775; S57799; S54868; S16090; S54870
 R:Stein, M.; Jacquot, J.P.; Jeanette, E.; Decottignies, P.; Hodges, M.; Lancelin, J.M.;
 Plant Mol. Biol. 28, 487-503, 1995
 A:Title: Chlamydomonas reinhardtii thioedoxins: structure of the genes coding for the c
 on and biochemical properties.
 A:Reference number: S57774; MUID:95359406; PMID:7632918
 A:Accession: S57775
 A:Molecule type: DNA
 A:Residues: 1-113 <STB>
 A:Cross-references: UNIPROT:P80028; UNIPARC:UPI000016D37; EMBL:X80887; NID:9840742; PID
 A:Accession: S57799
 A:Molecule type: protein
 A:Residues: 2-15 <STW>
 A:Cross-references: UNIPARC:UPI0000171E26
 R:Stein, M.; Hodges, M.; Jeanette, E.; Lancelin, J.M.; Jacquot, J.P.
 submitted to the EMBL Data Library, April 1994

A:Description: Chlamydomonas reinhardtii thioedoxins I : cDNA and amino acid deduced se
 A:Reference number: S54844
 A:Accession: S54868
 A:Molecule type: mRNA
 A:Residues: 1-113 <STP>
 A:Cross-references: UNIPARC:UPI000016D37; EMBL:X78822; NID:9840740; PIND:CA55399.1; PI
 R:Decottignies, P.; Schmitter, J.M.; Dutka, S.; Jacquot, J.P.; Miginiac-Maslow, M.
 Eur. J. Biochem. 198, 505-512, 1991
 A:Title: Characterization and primary structure of a second thioedoxin from the green a
 A:Reference number: S16090; MUID:91249849; PMID:2040309
 A:Accession: S16090
 A:Molecule type: protein
 A:Residues: 2-112 <MG>
 A:Cross-references: UNIPARC:UPI0000171E27
 R:Mittard, V.; Blackledge, M.J.; Stein, M.; Jacquot, J.P.; Marion, D.; Lancelin, J.M.
 submitted to the Brookhaven Protein Data Bank, May 1996
 A:Reference number: A66748; PDB:1TOR

A:Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR, residues 2-113
 R:Mittard, V.; Morelle, N.; Brutscher, B.; Smorre, J.P.; Marion, D.; Stein, M.; Jacquot
 Eur. J. Biochem. 229, 473-485, 1995
 A:Title: (1)H, (13)C, (15)N-NMR resonance assignments of oxidized thioedoxin h from th
 R spectroscopy and computer-assisted backbone assignment.
 A:Reference number: A58618; MUID:95262711; PMID:7744070
 A:Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR
 C:Genetics:
 A:introns: 27/3; 35/3; 69/3
 C:Superfamily: thioedoxin; thioedoxin homology

C:Keywords: redox-active disulfide
 F:2-113/Product: thioedoxin h #status experimental <MAT>
 F:15-98/Domain: thioedoxin homology <THR>
 F:37-40/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 36 WCGPCK 41

RESULT 43

T29044
 hypothetical protein B0228.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29044
 R:Leimbach, D.
 submitted to the EMBL Data Library, March 1995
 A:Description: The sequence of C. elegans coemid B0228.
 A:Reference number: Z18324
 A:Accession: T29044
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-115 <LEI>
 A:Cross-references: UNIPROT:O09433; UNIPARC:UPI000013667; EMBL:U23168; PIND:AA038808.1;
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:B0228.5
 A:introns: 69/3; 93/3
 C:Superfamily: thioedoxin; thioedoxin homology

Query Match 100.0%; Score 47; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 38 WCGPCK 43

RESULT 44

B70851
 probable tyrc protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Oct-2004
 C:Accession: B70851
 R:Coile, S.T.; Brosch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
 R.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, R.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: B70851
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-116 <COL>
 A:Cross-references: UNIPROT:P52229; UNIPARC:UPI0000165202; GB:AL021426; GB:AL123456; NID
 A:Experimental source: strain H37RV

C:Genetics:
A:Gene: trxC
C:Superfamily: thioredoxin; thioredoxin homology
F:15-98/Domain: thioredoxin homology <TRN>

Query Match 100.0%; Score 47; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 36 WCGPCK 41

RESULT 45

E70107

thioredoxin (trxA) homolog - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Oct-2004

C:Accession: E70107

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Iathigra, R.; White

son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; PMID:98065943; PMID:9403685

A:Accession: E70107

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-117 <LUE>

A:Cross-references: UNIPROT:O51088; UNIPARC:UPI00005732A; GB:AE001119; GB:AE000783; NID

A:Experimental source: strain B31

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 39 WCGPCK 44

RESULT 46

S34812

thioredoxin h2 - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004

C:Accession: S34812

R:Brugidou, C.; Marty, I.; Chartier, Y.; Meyer, Y.

Mol. Gen. Genet. 238, 285-293, 1993

A>Title: The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin genes which at

A:Reference number: S34812; PMID:93241165; PMID:8479434

A:Accession: S34812

A:Molecule type: DNA

A:Residues: 1-118 <BRU>

A:Cross-references: UNIPROT:Q07090; UNIPARC:UPI0000136D63; EMBL:Z11803; NID:G297518; PID

C:Genetics:

A:Introns: 29/3; 70/3

C:Superfamily: thioredoxin; thioredoxin homology

F:17-99/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 47; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 38 WCGPCK 43

RESULT 47

T39387
thioredoxin ii - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39387

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.

Submitted to the EMBL Data Library, January 1999

A:Reference number: 221850

A:Accession: T39387

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-121 <LNY>

A:Cross-references: UNIPROT:O94504; UNIPARC:UPI000006BFB2; EMBL:AL035085; PTDN:CAA22661.

A:Experimental source: strain 972h; cosmid cl2D12

C:Genetics:

A:Gene: SPDB:SPBC12D12.07C

A:Map position: 2

A:Introns: 33/2

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 46 WCGPCK 51

RESULT 48

S19498

thioredoxin homolog YCR083w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C:Accession: S19498

R:Feldmann, H.; Mannhaupt, G.; Vetter, I.

Submitted to the Protein Sequence Database, March 1992

A:Reference number: S19429

A:Accession: S19498

A:Molecule type: DNA

A:Residues: 1-127 <FEU>

A:Cross-references: UNIPROT:P25372; UNIPARC:UPI00001376B7; EMBL:X59720; NID:G1907116; PJ

C:Genetics:

A:Gene: SGD:TRX3; MIPS:YCR083W

A:Cross-references: SGD:S0000679

A:Map position: 3R

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F:34-115/Domain: thioredoxin homology <THR>

F:55-58/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 54 WCGPCK 59

RESULT 49

B91218

thioredoxin 1 [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004

C:Accession: B91218

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

gaesawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A:Reference number: A99629; PMID:21156231; PMID:11258796

A:Accession: B91218

A:Status: preliminary

A.Molecule type: DNA
A.Residues: 1-127 <HAY>
A.Cross-references: UNIPARC:UPI0000165538; GB:BA000007; PIDN:BAR38137.1; PID:g13364189;
A.Experimental source: strain O157:H7, substrain RMD 0509552
C.Genetics:
A.Gene: EC64714
C.Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
50 WCGPCK 55

RESULT 50

Ch86064
thioredoxin 1 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004

C.Accession: C86064
R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobbeck, B.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A.Reference number: A85480; MUID:21074935; PMID:11206551

A.Accession: C86064

A.Status: Preliminary

A.Molecule type: DNA

A.Residues: 1-127 <STO>

A.Cross-references: UNIPARC:UPI0000165538; GB:AE005174; NID:g12518641; PIDN:AGS8975.1;
A.Experimental source: strain O157:H7, substrain EDL933

C.Genetics:

A.Gene: trxA

C.Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
50 WCGPCK 55

RESULT 51

B96621
probleme thioredoxin F23H1.5 [imported] - Arabidopsis thaliana

C.Species: Arabidopsis thaliana (mouse-ear cress)

C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004

C.Accession: B96621

R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference number: A86141; MUID:21016719; PMID:11130712

A.Accession: B96621

A.Status: Preliminary

A.Molecule type: DNA

A.Residues: 1-129 <STO>

A.Cross-references: UNIPROT:Q9XIF4; UNIPARC:UPI0000008FOA; GB:AE005173; NID:g5080807; PI

C.Genetics:

A.Gene: F23H1.5

A.Map position: 1

C.Superfamily: thioredoxin

Query Match 100.0%; Score 47; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
54 WCGPCK 59

RESULT 52

T08084
dynein light chain, 14K, outer arm - Chlamydomonas reinhardtii

N.Alternate names: thioredoxin homolog

C.Species: Chlamydomonas reinhardtii

C.Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 31-Dec-2004

C.Accession: T08084

R.Patel-King, R.S.; Benashaki, S.E.; Harrison, A.; King, S.M.

J. Biol. Chem. 271, 6283-6291, 1996

A.Title: Two functional thioredoxins containing redox-sensitive vicinal dithiols from the

A.Reference number: Z16342; MUID:96198089; PMID:8626422

A.Accession: T08084

A.Status: Preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-129 <PAT>

A.Cross-references: UNIPROT:Q39591; UNIPARC:UPI0000129A19; EMBL:U43609; NID:g1163185; PI

A.Experimental source: strain 1132D

C.Comment: Seems to be associated with the intermediate chains at the base of the solid]

Query Match 100.0%; Score 47; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
33 WCGPCK 38

RESULT 53

D17107
thioredoxin (trxa) RP002 - Rickettsia prowazekii

C.Species: Rickettsia prowazekii

C.Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 05-Oct-2004

C.Accession: D17107

R.Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Slichteritz-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A.Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A.Reference number: A71630; MUID:99039499; PMID:9823893

A.Accession: D17107

A.Status: Preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-130 <AND>

A.Cross-references: UNIPARC:UPI0000164C06; GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:

A.Experimental source: strain Madrid E

C.Genetics:

A.Gene: trxa; RP002

C.Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
54 WCGPCK 59

RESULT 54

F97361
thioredoxin c-1 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C.Species: Agrobacterium tumefaciens

C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004

C.Accession: F97361

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
A:Reference number: A97359; MIMD:21608551; PMID:11743194
A:Accession: F97361
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KUR>
A:Cross-references: UNIPROT:Q8UUA6; UNIPARC:UPI00000D1691; GB:AB007869; PIDN:AAK85847.1; C:Genetics: AGK_C_37
A:Gene: AGK_C_37
A:Map position: circular chromosome
C:Superfamily: thioredoxin, thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 57 WCGPCK 62

RESULT 55
S70356
thioredoxin C3 - coryneform bacterium
C:Species: coryneform bacterium
C:Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 11-Jun-1999
C:Accession: S70356
R:Lim, C.J.; Sa, J.H.; Fuchs, J.A. Biochim. Biophys. Acta 1307, 13-16, 1996
A:Title: Identification of a third thioredoxin gene from *Corynebacterium nephridii*.
A:Reference number: S70356; MIMD:96254056; PMID:8652661
A:Accession: S70356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <LIM>
A:Cross-references: UNIPARC:UPI0000136D7A; EMBL:U43655; NID:G1165238; PIDN:AA06490.1; F A:Note: the source is designated as *Corynebacterium nephridii*
C:Superfamily: thioredoxin, thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 64 WCGPCK 69

RESULT 56
B96721
probable thioredoxin T17F3.9 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: B96721
R:Theologis, A.; Exeter, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; anen, N.R.; Hughes, B.; Huizar, U. Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MIMD:21016719; PMID:11130712
A:Accession: B96721
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <STO>
A:Cross-references: UNIPROT:Q9CASI; UNIPARC:UPI00000C0CF3; GB:AE005173; NID:G6358805; PI

C:Genetics: A:Gene: T17F3.9
A:Map position: 1
C:Superfamily: thioredoxin

Query Match 100.0%; Score 47; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 70 WCGPCK 75

RESULT 57
T08086
dynein light chain, 16K, outer arm - *Chlamydomonas reinhardtii*
N:Alternate names: thioredoxin homolog
C:Species: *Chlamydomonas reinhardtii*
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08086
R:Patel-King, R.S.; Benashaki, S.E.; Harrison, A.; King, S.M. J. Biol. Chem. 271, 6283-6291, 1996
A:Title: Two functional thioredoxins containing redox-sensensitive vicinal dithiols from the
A:Reference number: Z16342; MIMD:96198089; PMID:8626422
A:Accession: T08086
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-156 <PAT>
A:Cross-references: UNIPROT:Q93592; UNIPARC:UPI0000129A1A; EMBL:U43610; NID:G1163187; PI A:Experimental source: strain 1132D
C:Comment: Seems to interact directly with the a dynein heavy chain.
C:Superfamily: thioredoxin, thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 36 WCGPCK 41

RESULT 58
T09495
thioredoxin m - rape chloroplast
C:Species: chloroplast *Brassica napus* (rape)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T09495
R:Duek, P.D.; Mora Garcia, S.; Wolosinski, R.A. submitted to the EMBL Data Library, October 1996
A:Reference number: Z16696
A:Accession: T09495
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-177 <DUE>
A:Cross-references: UNIPROT:Q9XG50; UNIPARC:UPI000009E914; EMBL:U76831; NID:G1943719; P A:Genome: chloroplast
C:Superfamily: thioredoxin, thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:79-162/Domain: thioredoxin homology <TXN>

Query Match 100.0%; Score 47; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 100 WCGPCK 105

RESULT 59

T00893
thioredoxin F21B7.7 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00893
R:Shim, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Coe, J. R.
submitted to the EMBL Data Library, January 1998
A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
A:Reference number: Z14208
A:Accession: T00893
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-179 <SH1>
A:Cross-references: UNIPROT:048737; UNIPARC:UPI000000C325; EMBL:AC002560; NID:92618677;
C:Genetics:
A:Gene: ATSP:F21B7.7
A:Map position: 1
A:Introns: 76/1
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:82-165/Domain: thioredoxin homology <TXN>
F:104-107/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 103 WCGPCK 108

RESULT 60
TXSPM
thioredoxin m precursor - spinach
C:Species: Spinacia oleracea (spinach)
C>Date: 30-Sep-1988 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C:Accession: S20496; J00023; E20273
R:Wedel, N.; Clausmeyer, S.; Herrmann, R.G.; Gardet-Salvi, L.; Schuermann, P.
Plant Mol. Biol. 18, 527-533, 1992
A>Title: Nucleotide sequence of cDNAs encoding the entire precursor polypeptide for thioredoxin
A:Reference number: S20496; MUID:92163017; PMID:1536927
A:Accession: S20496
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-181 <MED>
A:Cross-references: UNIPROT:P07591; UNIPARC:UPI0000136E67; GB:X51462; GB:S84848; NID:921
R:Maeda, K.; Tsuniga, A.; Dalzoppo, D.; Vilbois, F.; Schurmann, P.
Eur. J. Biochem. 154, 197-203, 1986
A>Title: Further characterization and amino acid sequence of m-type thioredoxins from spinach
A:Reference number: A91159; MUID:86108311; PMID:3510868
A:Accession: J00023
A:Molecule type: Protein
A:Residues: 68-82; 'G', '84-89', 'Q', '91', 'SE', '94', 'S', '96-127', 'T', '129-164', 'D', '166', 'S', '168', 'YQ', '1
A:Cross-references: UNIPARC:UPI0000171E25
C:Comment: This enzyme has amino-terminal heterogeneity. Thioredoxin m activates malate
C:Comment: Arg-145 and Gly-164 are both essential for thioredoxin to interact with thior
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:1-67/Domain: transit peptide (chloroplast) #status predicted <TMP>
F:68-171/Product: thioredoxin mb #status experimental <PRB>
F:69-171/Product: thioredoxin mc #status experimental <PRC>
F:70-171/Product: thioredoxin md #status experimental <PRD>
F:82-165/Domain: thioredoxin homology <THR>
F:104-107/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 103 WCGPCK 108

RESULT 61
T07837
thioredoxin f precursor - rape
C:Species: Brassica napus (rape)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07837
R:Moita-Garcia, S.E.F.; Rodriguez-Suarez, R.U.; Molosik, R.A.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z16164
A:Accession: T07837
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-182 <MOD>
A:Cross-references: UNIPROT:048997; UNIPARC:UPI0000136DB6; EMBL:AF018174; NID:92921093;
A:Experimental source: 30-day old green leaves
C:Genetics:
A:Gene: TRXF
A:Genome: nuclear
C:Function:
A:Description: activates fructose 1,6-bisphosphatase during photosynthesis
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:79-163/Domain: thioredoxin homology <TXN>

Query Match 100.0%; Score 47; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 101 WCGPCK 106

RESULT 62
S20929
thioredoxin f precursor - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S20929
R:Leplanc, L.; Hodges, M.; Gadal, P.; Cretin, C.
Plant Mol. Biol. 18, 1023-1025, 1992
A>Title: Isolation, characterization and nucleotide sequence of a full-length pea cDNA e
A:Reference number: S20929; MUID:92256804; PMID:1581563
A:Accession: S20929
A:Molecule type: mRNA
A:Residues: 1-182 <LEP>
A:Cross-references: UNIPROT:P29450; UNIPARC:UPI0000136DE9; EMBL:X63537; NID:920906; PIDN
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:1-74/Domain: transit peptide (chloroplast) #status predicted <TMP>
F:75-182/Product: thioredoxin f #status predicted <MAT>
F:83-167/Domain: thioredoxin homology <THR>
F:106-109/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 105 WCGPCK 110

RESULT 63
E96539
hypothetical protein F143.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: E96539
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huzar, L.
Nature 408, 816-820, 2000
A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani, R.; Rooney, T.; Rowley, D.; Sakano, H.
A:Author: Salzberrg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96539
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-182 <STO>
A:Cross-references: UNIPROT:Q9SX49; UNIPARC:UPI00000AC075; GB:AE005173; NID:G5734774; P
C:Genetics:
A:Gene: F1413.8
A:Map position: 1

Query Match 100.0%; Score 47; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 98 WCGPCK 103

RESULT 64
D95115
Chlorodoxin family protein [imported] - *Streptococcus pneumoniae* (strain TIGR4)
C:Species: *Streptococcus pneumoniae*
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: D95115
R:Etcelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
son, J.D.; Umayam, L.A.; White, O.; Salzberrg, S.L.; Lewis, M.R.; Radue, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
A:Author: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: D95115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <KUR>
A:Cross-references: UNIPROT:Q97R36; UNIPARC:UPI0000051693; GB:AE005672; PIDN:AA75117.1;
A:Experimental source: Strain TIGR4
C:Genetics:
A:Gene: SPI000

Query Match 100.0%; Score 47; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 80 WCGPCK 85

RESULT 65
F85044
probable M-type chlorodoxin [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: F85044
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-186 <STO>

A:Cross-references: UNIPROT:Q9SEU8; UNIPARC:UPI0000001768; GB:NC_001268; NID:G7270675; P
C:Genetics:
A:Gene: AT4G03520
A:Map position: 4
C:Superfamily: chlorodoxin; chlorodoxin homology

Query Match 100.0%; Score 47; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 109 WCGPCK 114

RESULT 66
S04661
Chlorodoxin f precursor - spinach
C:Species: *Spinacia oleracea* (spinach)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: S04661; A20273
R:Ramo, M.; Tsugita, A.; Wiesner, C.; Wedel, N.; Bartling, D.; Herrmann, R.G.; Aguilar,
Eur. J. Biochem. 182, 315-322, 1989
A:Title: Primary structure of spinach-chloroplast chlorodoxin f. Protein sequencing and
A:Reference number: S04661; MUID:89289715; PMID:2737203
A:Accession: S04661
A:Molecule type: mRNA
A:Residues: 1-190 <KAW>
A:Cross-references: UNIPROT:P09856; UNIPARC:UPI0000136D8A; EMBL:X14959; NID:G21343; PIDN
A:Note: part of this sequence was confirmed by protein sequencing
R:Tsugita, A.; Maeda, K.; Schuermann, P.
Biochem. Biophys. Res. Commun. 115, 1-7, 1983
A:Title: Spinach chloroplast chlorodoxins in evolutionary drift.
A:Reference number: A20273; MUID:83308759; PMID:6351859
A:Accession: A20273

A:Molecule type: protein
A:Residues: 106-119, 'NGDKCATQHLGVQA', 120 <TSU>
A:Cross-references: UNIPARC:UPI0000174DE8
A:Note: this sequence has been revised in reference S04661
C:Comment: chlorodoxin f activates fructose 1,6-bisphosphatase during photosynthesis.
C:Superfamily: chlorodoxin; chlorodoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:1-77/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:78-190/Product: chlorodoxin f #status predicted <MAT>
F:91-175/Domain: chlorodoxin homology <THR>
F:114-117/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 113 WCGPCK 118

RESULT 67
T12261
chlorodoxin f precursor - common ice plant
C:Species: *Mesembryanthemum crystallinum* (common ice plant)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12261
R:Michalowski, C.B.; Bohner, H.J.,
submitted to the EMBL Data Library, June 1998
A:Description: A cDNA for chlorodoxin f precursor from the common ice plant.
A:Reference number: Z17478
A:Accession: T12261
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-191 <MIC>
A:Cross-references: UNIPROT:O81332; UNIPARC:UPI0000136D88; EMBL:AF069314; NID:G3202021;
C:Function:
A:Description: activates fructose 1,6-bisphosphatase during photosynthesis

C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:92-176/Domain: thioredoxin homology <TXN>

Query Match 100.0%; Score 47; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 114 WCGPCK 119

RESULT 68
H97984

conserved hypothetical protein spr0904 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: H97984
R:Hosts: J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; H
e, R.; LeBlanc, D.J.; Lee, L.N.; Letkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
U. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekums, S.R.;
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H97984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <KUR>
A:Cross-references: UNIPROT:Q8DQ10; UNIPARC:UPI0000083552; GB:AE007317; PIDN:AAK99708.1;
C:Genetics:
A:Gene: spr0904

Query Match 100.0%; Score 47; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 86 WCGPCK 91

RESULT 69
T40552

thioredoxin-like protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40552
R:Lyne, M.H.; Rajadream, M.A.; Barrell, B.G.; Xiang, Z.; Hunt, I.C.; Aves, S.J.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21936
A:Accession: T40552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-290 <LYN>
A:Cross-references: UNIPROT:Q9USR1; UNIPARC:UPI0000069A89; EMBL:AL110506; PIDN:CAB54816.
C:Genetics:
A:Gene: SPAC577.08c
A:Map position: 2
A:Introns: 75/2

Query Match 100.0%; Score 47; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 30 WCGPCK 35

RESULT 70

AH3011

thioredoxin trxA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AH3011
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
i Kar, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH3011
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-322 <KUR>
A:Cross-references: UNIPROT:Q8U9M8; UNIPARC:UPI0000164857; GB:AE008689; PIDN:AAL44510.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: trxA
A:Map position: linear chromosome

Query Match 100.0%; Score 47; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 63 WCGPCK 68

Search completed: February 23, 2006, 00:42:33
Job time : 32.5 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:11:42 ; Search time 146.5 Seconds

(without alignments)
28.895 Million cell updates/sec

Title: US-10-660-118a-3

Perfect score: 47

Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	80	Q4T7B7_TETNG	Q4T7B7 tetrads n
2	47	100.0	84	Q60744_HUMAN	Q60744 homo sapien
3	47	100.0	85	Q5T936_HUMAN	Q5T936 homo sapien
4	47	100.0	88	Q5V032_HALMA	Q5V032 haloarcula
5	47	100.0	89	Q9HMD0_HALMA	Q9HMD0 haloarcula
6	47	100.0	91	THIO_THIRO	THIO_THIRO
7	47	100.0	95	Q4XKV3_PLACH	Q4XKV3 plasmidum
8	47	100.0	96	Q4Z518_PLABE	Q4Z518 plasmidum
9	47	100.0	98	Q5IB12_BACFN	Q5IB12 bacteroides
10	47	100.0	98	Q64R91_BACFR	Q64R91 bacteroides
11	47	100.0	99	Q8AB91_BACTN	Q8AB91 bacteroides
12	47	100.0	100	THIO_MYCGA	THIO_MYCGA
13	47	100.0	100	Q9JN64_MYCGA	Q9JN64 mycoplasma
14	47	100.0	101	THIO1_CHLTR	THIO1 chlorobium
15	47	100.0	101	Q6K1E7_MYCMO	Q6K1E7 mycoplasma
16	47	100.0	102	THIO_CHLTV	THIO_CHLTV
17	47	100.0	102	THIO_CHLMU	THIO_CHLMU
18	47	100.0	102	THIO_CHLTR	THIO_CHLTR
19	47	100.0	102	THIO_MYCGE	THIO_MYCGE
20	47	100.0	102	THIO_MYCPN	THIO_MYCPN
21	47	100.0	102	THIO_SCHPO	THIO_SCHPO
22	47	100.0	102	TRX1_YEAST	TRX1_YEAST
23	47	100.0	102	Q5L731_CHLAB	Q5L731 chlamydia
24	47	100.0	102	Q6F1T8_MESFL	Q6F1T8 mesoplasma
25	47	100.0	102	Q6MUG0_MYCMS	Q6MUG0 mycoplasma
26	47	100.0	103	THIO_BACSV	THIO_BACSV
27	47	100.0	103	TRX2_YEAST	TRX2_YEAST
28	47	100.0	103	Q75C00_ASHGO	Q75C00 ashya goos
29	47	100.0	103	Q6FND5_CANGA	Q6FND5 candida gla
30	47	100.0	103	Q6BJ80_DEBHA	Q6BJ80 debaromyce
31	47	100.0	103	Q5ACN1_CANAL	Q5ACN1 candida alb

32	47	100.0	103	Q7P4W8_FUSNV	Q7P4W8 fusobacteri
33	47	100.0	103	Q5FLW1_LACAC	Q5FLW1 lactobacilli
34	47	100.0	103	Q6RH23_FUSNC	Q6RH23 fusobacteri
35	47	100.0	103	Q74K07_LACUO	Q74K07 lactobacilli
36	47	100.0	104	THIO_BOVIN	THIO_BOVIN
37	47	100.0	104	THIO_CALTA	THIO_CALTA
38	47	100.0	104	THIO_CHICK	THIO_CHICK
39	47	100.0	104	THIO_HORSE	THIO_HORSE
40	47	100.0	104	THIO_HUMAN	THIO_HUMAN
41	47	100.0	104	THIO_MACMU	THIO_MACMU
42	47	100.0	104	THIO_MOUSE	THIO_MOUSE
43	47	100.0	104	THIO_OPHNA	THIO_OPHNA
44	47	100.0	104	THIO_PIG	THIO_PIG
45	47	100.0	104	THIO_RABIT	THIO_RABIT
46	47	100.0	104	THIO_RAT	THIO_RAT
47	47	100.0	104	THIO_SHEEP	THIO_SHEEP
48	47	100.0	104	THIO_STAM	THIO_STAM
49	47	100.0	104	THIO_STAN	THIO_STAN
50	47	100.0	104	THIO_STAR	THIO_STAR
51	47	100.0	104	THIO_STAS	THIO_STAS
52	47	100.0	104	THIO_STAU	THIO_STAU
53	47	100.0	104	THIO_STAM	THIO_STAM
54	47	100.0	104	THIO_STAP	THIO_STAP
55	47	100.0	104	Q6CN03_KULIA	Q6CN03 kulyveromyc
56	47	100.0	104	Q6C399_YARLI	Q6C399 yarrowia li
57	47	100.0	104	Q5KK55_CRYNE	Q5KK55 cryptococcus
58	47	100.0	104	Q5W38_CRYNE	Q5W38 cryptococcus
59	47	100.0	104	Q5N1R2_PLAFA	Q5N1R2 plasmidum
60	47	100.0	104	Q5NFK9_PLAFA	Q5NFK9 plasmidum
61	47	100.0	104	Q7RH10_PLAYO	Q7RH10 plasmidum
62	47	100.0	104	Q7KOL8_PLAF7	Q7KOL8 plasmidum
63	47	100.0	104	Q6B963_SCHMA	Q6B963 schistosoma
64	47	100.0	104	Q5DAY8_SCHTA	Q5DAY8 schistosoma
65	47	100.0	104	Q4B985_MYCCA	Q4B985 mycoplasma
66	47	100.0	104	Q4HNM5_CAMUP	Q4HNM5 campylobact
67	47	100.0	104	Q7M0Y9_CLOPA	Q7M0Y9 clostridium
68	47	100.0	104	Q5LHJ1_BACFN	Q5LHJ1 bacteroides
69	47	100.0	104	Q4L5F0_STRAHJ	Q4L5F0 staphylococ
70	47	100.0	104	Q817L8_BACCR	Q817L8 bacillus ce
71	47	100.0	104	Q9K8A8_BACCH	Q9K8A8 bacillus ha
72	47	100.0	104	Q8XHX1_CLOPE	Q8XHX1 clostridium
73	47	100.0	104	Q8EP16_OCEIH	Q8EP16 oceanobacilli
74	47	100.0	104	Q8A5L0_BACTN	Q8A5L0 bacteroides
75	47	100.0	104	Q7Z2M0_BACCL	Q7Z2M0 bacillus ce
76	47	100.0	104	Q6HYD4_BACFK	Q6HYD4 bacillus th
77	47	100.0	104	Q64Y66_BACFR	Q64Y66 bacteroides
78	47	100.0	104	Q633S0_BACG2	Q633S0 bacillus ci
79	47	100.0	104	Q5WEK7_BACSK	Q5WEK7 bacillus ce
80	47	100.0	104	Q5HQZ9_STRAEQ	Q5HQZ9 staphylococ
81	47	100.0	104	Q5HG79_STRAAC	Q5HG79 staphylococ
82	47	100.0	104	Q8IL73_BACAN	Q8IL73 bacillus an
83	47	100.0	104	Q65G89_BACLD	Q65G89 bacillus li
84	47	100.0	105	THIO1_CONNE	THIO1 conne
85	47	100.0	105	THIO_PONPY	THIO_PONPY
86	47	100.0	105	THIO_RICCN	THIO_RICCN
87	47	100.0	105	THIO_RICCR	THIO_RICCR
88	47	100.0	105	Q5T937_HUMAN	Q5T937 homo sapien
89	47	100.0	105	Q7PAB0_RICSTI	Q7PAB0 rickettsia
90	47	100.0	105	Q6HY00_RICTY	Q6HY00 rickettsia
91	47	100.0	105	Q9TEM7_CLOAB	Q9TEM7 clostridium
92	47	100.0	105	Q8XMF0_CLOPE	Q8XMF0 clostridium
93	47	100.0	105	Q52KC4_MOUSE	Q52KC4 mus musculu
94	47	100.0	105	Q802D7_MELUD	Q802D7 melopitrac
95	47	100.0	105	Q6GQ64_XENLA	Q6GQ64 xenopus lae
96	47	100.0	106	THIO2_DROYA	THIO2 drosophila
97	47	100.0	106	THIO_HELPY	THIO_HELPY
98	47	100.0	106	THIO_HELPY	THIO_HELPY
99	47	100.0	106	THIO_PENCH	THIO_PENCH
100	47	100.0	106	THIO_STRAU	THIO_STRAU
101	47	100.0	106	Q9U5I5_MANSE	Q9U5I5 manuca sex
102	47	100.0	106	Q963B4_AEDAE	Q963B4 aedes aegypt
103	47	100.0	106	Q8T9N5_SCHMA	Q8T9N5 schistosoma
104	47	100.0	106	Q9UBF3_SCHTA	Q9UBF3 schistosoma

105	47	100.0	106	2	Q5VAN9_RHET	Q5van9 rhizobium e	178	47	100.0	110	2	Q4WV97_AS PFU	Q4wv97 aspergillus
106	47	100.0	106	2	Q4TMB6_9SPHN	Q4tmb6 erythrobact	179	47	100.0	110	2	Q6QUK5_PAXIN	Q6quk5 paxillus in
107	47	100.0	106	2	Q8KYV0_9PROT	Q8kyv0 uncultured	180	47	100.0	110	2	Q5BHI0_EMENT	Q5bhi0 aspergillus
108	47	100.0	106	2	Q8UJA6_AGR75	Q8uja6 agrobacteri	181	47	100.0	110	2	Q6ZYI0_9METZ	Q6zyi0 suberites f
109	47	100.0	106	2	Q8EWM2_MYCPB	Q8ewm2 mycoplasma	182	47	100.0	110	2	Q5FRV8_NETG1	Q5frv8 netseria f
110	47	100.0	106	2	Q5LLP8_SILPO	Q5llp8 silicibacte	183	47	100.0	110	2	Q9A2I8_CAUCR	Q9a2i8 caulobacter
111	47	100.0	106	2	Q4SOR5_TETNG	Q4sor5 tetraodon n	184	47	100.0	110	2	Q9JYV9_NEIMB	Q9jyv9 neisseria m
112	47	100.0	107	1	THIO1_DROME	THIO1 drosophila	185	47	100.0	110	2	Q9JYV5_NEIMA	Q9jyv5 neisseria m
113	47	100.0	107	1	THIO1_DROYA	P6226 drosophila	186	47	100.0	110	2	Q88ZK9_LACPL	Q88zk9 lactobacill
114	47	100.0	107	1	THIO_CHRVI	P09857 chromatiu	187	47	100.0	110	2	Q5YMS6_NOCFA	Q5yms6 nocardia fa
115	47	100.0	107	1	THIO_BCHGR	O17486 echinococcu	188	47	100.0	111	2	Q5EUN4_9ENTR	Q5eun4 buchnera ap
116	47	100.0	107	1	THIO_HAEIN	P43785 haemophilus	189	47	100.0	112	1	THIO_MFCM	THIO mycobacteri
117	47	100.0	107	2	Q7RXV8_NEUCR	Q7rxv8 neutrospora	190	47	100.0	112	1	TRXH_CHLRE	TRXH chlamydomon
118	47	100.0	107	2	Q9CILI_NEUCR	Q9cili neutrospora	191	47	100.0	112	2	Q5YB1_9CHLO	Q5yb1 helicospori
119	47	100.0	107	2	Q7PMZ6_ANOGA	Q7pmz6 anophelae g	192	47	100.0	112	2	Q7MGPE_VIBVY	Q7mgpe vibrio vuln
120	47	100.0	107	2	Q9NGZ1_ANOGA	Q9ngz1 anophelae g	193	47	100.0	112	2	Q6LLI6_PHOPR	Q6lli6 photobacter
121	47	100.0	107	2	Q9NGZ3_TRYBB	Q9ngz3 trypanosoma	194	47	100.0	113	2	Q4UPY4_XANCP	Q4upy4 xanthomonas
122	47	100.0	107	2	Q25345_LEIMA	Q25345 leishmania	195	47	100.0	113	2	Q5GUR7_XANOR	Q5gur7 xanthomonas
123	47	100.0	107	2	Q6B343_TRYCR	Q6b343 trypanosoma	196	47	100.0	113	2	Q8PFZ2_XANAC	Q8pfz2 xanthomonas
124	47	100.0	107	2	Q5S1X7_IXOSC	Q5s1x7 ixodes scap	197	47	100.0	113	2	Q8F4D3_XANCP	Q8f4d3 xanthomonas
125	47	100.0	107	2	Q57AF5_BRUAB	Q57af5 bruceella ab	198	47	100.0	113	2	Q879Y5_XYLFT	Q879y5 xyella fas
126	47	100.0	107	2	Q5FGA3_EHRBG	Q5fga3 ethiopia r	199	47	100.0	114	1	THIO2_DROME	THIO2 drosophila
127	47	100.0	107	2	Q9AJR5_ACTAC	Q9ajr5 actinobacil	200	47	100.0	114	2	Q51FHE_ENTHI	Q51fhe entamoeba h
128	47	100.0	107	2	Q6M1C7_CORGL	Q6m1c7 corynebacte	201	47	100.0	114	2	Q7YZF7_CABEL	Q7yzf7 caenorhabdi
129	47	100.0	107	2	Q4QPG1_HAB18	Q4qpg1 haemophilus	202	47	100.0	115	2	THIO1_CABEL	THIO1 mycobacteri
130	47	100.0	107	2	Q6NEA2_CORDI	Q6nea2 corynebacte	203	47	100.0	115	1	THIO_MYCBO	THIO mycobacteri
131	47	100.0	107	2	Q9ZTCS_RHIME	Q9ztc5 rhizobium m	204	47	100.0	115	1	THIO_MYCBO	THIO mycobacteri
132	47	100.0	107	2	Q6G1B7_BAROU	Q6g1b7 bartonella	205	47	100.0	116	2	Q4WB53_AS PFU	Q4wb53 aspergillus
133	47	100.0	107	2	Q6G588_BABBE	Q6g588 bartonella	206	47	100.0	116	2	Q6UB83_PABBR	Q6ub83 paracoccidi
134	47	100.0	107	2	Q8RXY9_BRUSU	Q8rxy9 bruceella bu	207	47	100.0	116	2	Q4ZZP9_PESBY	Q4zzp9 pseudomonas
135	47	100.0	107	2	Q98CM9_RHIL0	Q98cm9 rhizobium l	208	47	100.0	117	1	THIO_BORBU	THIO borreliella bu
136	47	100.0	107	2	Q73GQ5_WOLPM	Q73gq5 wolbachia p	209	47	100.0	117	2	Q6E2V3_BORGA	Q6e2v3 borreliella ga
137	47	100.0	107	2	Q8YB56_BRUME	Q8yb56 bruceella me	210	47	100.0	117	2	Q93AQ3_MYCPA	Q93aq3 mycobacteri
138	47	100.0	107	2	Q8RSM0_CORBP	Q8rsm0 corynebacte	211	47	100.0	118	1	TRXH2_TOBAC	TRXH2 nicotiana t
139	47	100.0	107	2	Q5NPF9_FRAAT	Q5nfp9 francisella	212	47	100.0	121	2	Q945D4_SCHPO	Q945d4 schistosach
140	47	100.0	107	2	Q5HAC8_EHRBW	Q5hac8 ethiopia r	213	47	100.0	123	2	Q61CC9_CABBR	Q61cc9 caenorhabdi
141	47	100.0	108	1	THIO_ECOLI	P00274 escherichia	214	47	100.0	123	2	Q4USG8_CORJK	Q4usg8 corynebacte
142	47	100.0	108	1	THIO_PSEAE	Q9x2t1 pseudomonas	215	47	100.0	124	2	Q8NLS6_CORGL	Q8nls6 corynebacte
143	47	100.0	108	1	THIO_THIPE	P52233 thlobacillu	216	47	100.0	126	2	Q8RGH7_PODAN	Q8rgh7 podospira a
144	47	100.0	108	2	Q41OD7_9BIVA	Q41od7 chlamys far	217	47	100.0	126	2	Q685T8_9SCOR	Q685t8 mesobuthus
145	47	100.0	108	2	Q5TY47_ANOGA	Q5ty47 anophelae g	218	47	100.0	126	2	Q685V4_9SCOR	Q685v4 mesobuthus
146	47	100.0	108	2	Q61VR6_9GAMM	Q61vr6 uncultured	219	47	100.0	126	2	Q685V4_9SCOR	Q685v4 mesobuthus
147	47	100.0	108	2	Q7BAF7_PRR01	Q7baf7 gamma-prote	220	47	100.0	126	2	Q685X1_9SCOR	Q685x1 mesobuthus
148	47	100.0	108	2	Q4LH05_9BURX	Q4lh05 burkholderi	221	47	100.0	126	2	Q685X8_9SCOR	Q685x8 mesobuthus
149	47	100.0	108	2	Q4J018_AZCVI	Q4j018 azotobacter	222	47	100.0	126	2	Q685Y8_9SCOR	Q685y8 mesobuthus
150	47	100.0	108	2	Q6Q926_9GAMM	Q6q926 uncultured	223	47	100.0	126	2	Q685Y8_9SCOR	Q685y8 mesobuthus
151	47	100.0	108	2	Q5SB04_VIRB1	Q5sbu4 vibrio fusc	224	47	100.0	126	2	Q685Y9_BURBU	Q685y9 buthus eupe
152	47	100.0	108	2	Q4F072_9GAMM	Q4f072 psychrobact	225	47	100.0	126	2	Q685X3_9SCOR	Q685x3 mesobuthus
153	47	100.0	108	2	Q7MYL3_PHOLL	Q7myl3 photorhabd	226	47	100.0	126	2	Q685W5_9SCOR	Q685w5 mesobuthus
154	47	100.0	108	2	Q8ZAD9_YERPE	Q8zad9 yerinia pe	227	47	100.0	127	1	THIO_NEUCR	THIO neutrospora
155	47	100.0	108	2	Q66G18_YERPS	Q66g18 yerinia ps	228	47	100.0	127	1	TRX3_YEAST	TRX3 yeast
156	47	100.0	108	2	Q6CZB0_ERMCT	Q6czb0 erwinia car	229	47	100.0	127	1	TXNDB_MOUSE	TXNDB mouse
157	47	100.0	108	2	Q5FT93_GLUOX	Q5fte93 glucinobact	230	47	100.0	127	1	TXNDB_RAT	TXNDB rat
158	47	100.0	108	2	Q9KX51_VIRCH	Q9kx51 vibrio chol	231	47	100.0	129	1	DYI4_CHLRE	DYI4 chlamy
159	47	100.0	108	2	Q8Y056_RALSO	Q8y056 ralsstonia s	232	47	100.0	129	2	Q9XIF4_ARATH	Q9xif4 arabidopsi
160	47	100.0	108	2	Q8BJ06_SHEON	Q8bj06 shewanella	233	47	100.0	130	2	Q8GUR6_PEA	Q8gur6 plum sativ
161	47	100.0	108	2	Q8BDN7_VIBVU	Q8bdn7 vibrio vuln	234	47	100.0	133	2	Q7D2B9_AGR75	Q7d2b9 agrobacteri
162	47	100.0	108	2	Q87KH6_VIRBA	Q87kh6 vibrio para	235	47	100.0	134	2	Q9RD25_STRCO	Q9rd25 streptomyce
163	47	100.0	108	2	Q7NKP2_CHRVO	Q7nkp2 chromobacte	236	47	100.0	135	2	Q6PVP4_SOYBN	Q6pvp4 glycine max
164	47	100.0	108	2	Q6A034_DESPS	Q6a034 desulfotale	237	47	100.0	135	2	Q57HT5_SALCH	Q57ht5 salmone
165	47	100.0	108	2	Q63U09_BURPS	Q63u09 burkholderi	238	47	100.0	136	2	Q5UWAE_HALMA	Q5uwa6 halotaculla
166	47	100.0	108	2	Q62JU6_BURMA	Q62ju6 burkholderi	239	47	100.0	137	2	Q4PLX7_IXOSC	Q4plx7 ixodes scap
167	47	100.0	108	2	Q5QYF9_IDILO	Q5qyf9 idiomaticina	240	47	100.0	137	2	Q4NH78_9MICO	Q4nh78 archibacte
168	47	100.0	108	2	Q5PIK8_AZOSE	Q5pik8 azotobacter	241	47	100.0	137	2	Q5UR29_MITIV	Q5ur29 mitivulus
169	47	100.0	108	2	Q5NKG7_FRAAT	Q5nkg7 azotobacter	242	47	100.0	138	2	Q6Z4I3_ORYSA	Q6z4i3 oryza sativ
170	47	100.0	109	1	THIO_EMENT	P29429 emeticella	243	47	100.0	139	2	Q6CKI8_KULUA	Q6cki8 kluyvetomyc
171	47	100.0	109	2	Q4WZ14_AS PFU	Q4wz14 aspergillus	244	47	100.0	139	2	Q7NZ16_CHRVO	Q7nz16 chromobacte
172	47	100.0	109	2	Q4K3Z3_PSEFF	Q4k3z3 pseudomonas	245	47	100.0	140	2	Q9C9Y6_ARATH	Q9c9y6 arabidopsi
173	47	100.0	109	2	Q5PRK3_SALPA	Q5prk3 salmonella	246	47	100.0	140	2	Q8BJL1_SHEON	Q8bjl1 shewanella
174	47	100.0	109	2	Q88CG6_PSEBP	Q88cg6 pseudomonas	247	47	100.0	140	2	Q5ZJY6_CHICK	Q5zjy6 gallus gall
175	47	100.0	109	2	Q87UQ3_PSSSM	Q87uq3 pseudomonas	248	47	100.0	141	2	Q6FTV1_CANGA	Q6ftv1 candida gla
176	47	100.0	109	2	Q6OCPB_METCA	Q6ocpb methylococc	249	47	100.0	141	2	Q7MHH7_BORBR	Q7mhh7 bordecella
177	47	100.0	109	2	Q4SOR6_TETNG	Q4sor6 tetraodon n	250	47	100.0	141	2	Q7W990_BORPA	Q7w990 bordecella

251	47	100.0	141	2	QVYP8 BORPE	Q7VYP8 bordelella	324	47	100.0	301	2	Q63W5 BURPS	Q63W5 burkholderi
252	47	100.0	142	2	Q6F74 ACIAD	Q6F74 acinetobact	325	47	100.0	304	2	Q5LM9 SILPO	Q5LM9 silicibacte
253	47	100.0	141	2	Q5ZFA4 PLAMJ	Q5ZFA4 plantago ma	326	47	100.0	305	2	Q4TRI0 9SPHN	Q4TRI0 erythrobact
254	47	100.0	143	2	Q6VB16 IPQBA	Q6VB16 ipomoea bat	327	47	100.0	306	2	Q6ND42 RHOPA	Q6ND42 rhodospendo
255	47	100.0	144	2	Q51010 ENTHI	Q51010 entameoba h	328	47	100.0	313	2	Q4INX3 GIBZE	Q4INX3 gibzelella
256	47	100.0	144	2	Q41UJ1 AZOVI	Q41UJ1 azotobacter	329	47	100.0	313	2	Q89WT4 BRUJA	Q89WT4 bradyrhizob
257	47	100.0	144	2	Q4KJF7 PSERF5	Q4KJF7 pseudomonas	330	47	100.0	317	2	Q5FSW0 GIUOX	Q5FSW0 gluconobact
258	47	100.0	144	2	Q88CW1 PSERPX	Q88CW1 pseudomonas	331	47	100.0	322	2	Q8U9M8 AGRTS	Q8U9M8 agrobacteri
259	47	100.0	145	1	THIO3 CORNE	P52228 corynebacte	332	47	100.0	324	2	Q6C3W5 YARLI	Q6C3W5 yarrowia li
260	47	100.0	145	2	Q84XR3 CHLRE	Q84XR3 chlamydomon	333	47	100.0	324	2	Q6FVRO BRUSU	Q6FVRO bruceella su
261	47	100.0	146	2	Q802D6 MELUD	Q802D6 melopsittac	334	47	100.0	326	2	Q5GX15 XANOR	Q5GX15 xanthomonas
262	47	100.0	147	2	Q58HK3 SCHEMA	Q58HK3 schistosoma	335	47	100.0	329	2	Q579B4 BRUAB	Q579B4 bruceella ab
263	47	100.0	148	2	Q9CASI ARATH	Q9CASI arabidopsis	336	47	100.0	329	2	Q8YCX7 BRUME	Q8YCX7 bruceella me
264	47	100.0	149	2	Q988U5 RHILIO	Q988U5 rhizobium l	337	47	100.0	330	2	TXNDS HUMAN	Q86XW9 homo saplen
265	47	100.0	150	2	Q5DPA0 SCJJA	Q5DPA0 schistosoma	338	47	100.0	330	2	Q92L96 RHIME	Q92L96 rhizobium m
266	47	100.0	152	2	Q4UOW0 NTCAL	Q4UOW0 nicotiana a	339	47	100.0	331	2	Q7CT41 AGRTS	Q7CT41 agrobacteri
267	47	100.0	153	2	Q4UNK3 RICEFE	Q4UNK3 rickettsia	340	47	100.0	332	2	Q4NWV9 9BELT	Q4NWV9 anaeromyxob
268	47	100.0	156	1	DYLS5 CHLRE	Q39592 chlamydomon	341	47	100.0	333	2	Q4WPP6 ASPPU	Q4WPP6 aspergillus
269	47	100.0	157	1	THIO7 DROME	Q81FW4 dirosophila	342	47	100.0	335	2	Q98E31 RHILIO	Q98E31 rhizobium l
270	47	100.0	157	2	Q8A7R8 BACTN	Q8A7R8 bacteroides	343	47	100.0	385	2	Q75FP6 ASHGO	Q75FP6 ashbya goos
271	47	100.0	160	2	Q64CW9 9ARCH	Q64CW9 uncultured	344	47	100.0	416	2	TXXB MYCIE	P4843 mycobacteri
272	47	100.0	160	2	Q4P051 USTMA	Q4P051 ustilago ma	345	47	100.0	458	2	Q75JMG DICDI	P4843 mycobacteri
273	47	100.0	161	2	Q87G10 PODAN	Q87G10 podospira a	346	47	100.0	540	2	Q75JMG DICDI	Q75JMG dictyosteli
274	47	100.0	161	2	Q5LXB8 BACFN	Q5LXB8 bacteroides	347	47	100.0	586	1	TXNDS MOUSE	Q715T0 mus musculi
275	47	100.0	161	2	Q64SV7 BACFR	Q64SV7 bacteroides	348	47	100.0	587	2	Q4R719 MACPA	Q4R719 macaca fasc
276	47	100.0	163	2	Q8D6F4 VIBVU	Q8D6F4 vibrio vuln	349	47	100.0	588	2	Q4R6Y0 MACPA	Q4R6Y0 macaca fasc
277	47	100.0	163	2	Q7MDA8 VIBVY	Q7MDA8 vibrio vuln	350	47	100.0	601	2	Q6IRCS XENLA	Q6IRCS xenopus lae
278	47	100.0	166	1	THIOW BOVIN	Q95108 bos taurus	351	47	100.0	625	2	Q4HZP6 GIBZE	Q4HZP6 gibzelella
279	47	100.0	166	1	THIOW HUMAN	Q99757 homo saplen	352	47	100.0	709	2	Q8A213 BACTN	Q8A213 bacteroides
280	47	100.0	166	1	THIOW MOUSE	P97493 mus musculi	353	47	100.0	870	2	Q4P5N4 USTMA	Q4P5N4 ustilago ma
281	47	100.0	166	2	Q6FH60 HUMAN	P97615 rattus norv	354	47	100.0	952	2	Q41011 GIBZE	Q41011 gibzelella
282	47	100.0	166	2	Q5K553 9BACT	Q5K553 uncultured	355	47	100.0	989	2	Q584R0 9RRYP	Q584R0 trypanosoma
283	47	100.0	166	2	Q545D5 MOUSE	Q545D5 mus musculi	356	47	100.0	999	2	Q8C922 ARATH	Q8C922 arabidopsi
284	47	100.0	166	2	Q6P131 BRREA	Q6P131 brachydanio	357	47	93.6	87	2	THIO2 DICDI	P23446 dictyosteli
285	47	100.0	170	2	Q7ZY6G XENLA	Q7ZY6G xenopus lae	358	47	93.6	88	1	Q8PZQ6 METMA	Q8PZQ6 methanosarc
286	47	100.0	170	2	Q641J6 XENTR	Q641J6 xenopus tro	359	47	93.6	88	2	Q8ETL30 METAC	Q8ETL30 methanosarc
287	47	100.0	173	2	Q84XR8 CHLRE	Q84XR8 chlamydomon	360	47	93.6	93	2	Q8GM51 ARATH	Q8GM51 arabidopsi
288	47	100.0	173	2	Q6H7B4 ORYSA	Q6H7B4 oryza sativ	361	47	93.6	96	2	Q6KIE8 MYCWO	Q6KIE8 mycoplasma
289	47	100.0	177	1	TRXM BRANA	Q9X980 brabsella na	362	47	93.6	100	2	Q22031 CYACA	Q22031 cyanidium c
290	47	100.0	178	1	TRXF1 ARATH	Q9X980 arabidopsi	363	47	93.6	101	2	THIO CHLPN	Q9X7P5 chlamydia p
291	47	100.0	179	1	TRXM1 ARATH	Q48737 arabidopsi	364	47	93.6	102	1	THIO CYAME	Q22022 cyanidiosch
292	47	100.0	180	2	Q7X8R5 ORYSA	Q7X8R5 oryza sativ	365	47	93.6	103	1	THIO LISIN	P04413 listeria in
293	47	100.0	181	1	TRXM SPICL	P07591 spinacia ol	366	47	93.6	103	1	THIO LISMO	P04413 listeria mo
294	47	100.0	182	1	TRXF BRANA	Q48897 bisessica na	367	47	93.6	103	1	Q88V17 LACPL	Q88V17 lactobacilli
295	47	100.0	182	1	TRXF PBA	P29450 pisum sativ	368	47	93.6	103	2	Q720U6 LISMF	Q720U6 listeria mo
296	47	100.0	182	1	TRXF ARATH	Q97436 streptococc	369	47	93.6	104	1	THIO RHORU	P10473 rhodospirill
297	47	100.0	185	2	Q97R36 STRPN	Q97R36 streptococc	370	47	93.6	104	1	Q88V17 LACPL	Q88V17 lactobacilli
298	47	100.0	185	2	Q97R36 STRPN	Q97R36 streptococc	371	47	93.6	104	1	THIO LISIN	P10473 rhodospirill
299	47	100.0	186	1	TRXM2 ARATH	Q98608 arabidopsi	372	47	93.6	104	1	Q9544 PASHE	Q9544 fasciola he
300	47	100.0	186	2	Q81GZ6 ARATH	Q81GZ6 arabidopsi	373	47	93.6	104	2	Q962B7 BRABE	Q962B7 brachyosio
301	47	100.0	186	2	Q56Y64 ARATH	Q56Y64 arabidopsi	374	47	93.6	104	2	Q4HFK4 CAMCO	Q4HFK4 campylobact
302	47	100.0	187	2	Q8S091 ORYSA	Q8S091 oryza sativ	375	47	93.6	104	2	Q4HJN3 CAMLA	Q4HJN3 campylobact
303	47	100.0	190	1	TRXF SPICL	P09856 spinacia ol	376	47	93.6	104	2	Q8DNP9 STRR6	Q8DNP9 streptococc
304	47	100.0	191	1	TRXF MESCR	Q84132 mesembryant	377	47	93.6	104	2	Q9PIYO CAMJE	Q9PIYO campylobact
305	47	100.0	191	2	Q8DIO1 STRR6	Q8DIO1 streptococc	378	47	93.6	104	2	Q9CF37 LACPA	Q9CF37 lactococcus
306	47	100.0	195	2	Q5YTO5 9ASPA	Q5YTO5 hyacinthus	379	47	93.6	104	2	Q7P68 STRPN	Q7P68 streptococc
307	47	100.0	195	2	Q6C4U8 YARLI	Q6C4U8 yarrowia li	380	47	93.6	104	2	Q8NZ17 STRPN	Q8NZ17 streptococc
308	47	100.0	199	2	Q4HX91 GIBZE	Q4HX91 gibzelella	381	47	93.6	104	2	Q99Y75 STRPY	Q99Y75 streptococc
309	47	100.0	211	2	Q5AT09 EMENTI	Q5AT09 aspergillus	382	47	93.6	104	2	Q8E3J7 STRR3	Q8E3J7 streptococc
310	47	100.0	217	2	Q7S153 NEUCR	Q7S153 neurospora	383	47	93.6	104	2	Q8DXX8 STRR5	Q8DXX8 streptococc
311	47	100.0	222	2	Q64EO3 9ARCH	Q64EO3 uncultured	384	47	93.6	104	2	Q835H2 ENTBA	Q835H2 enterococcu
312	47	100.0	232	2	Q4V8P5 RAT	Q4V8P5 rattus norv	385	47	93.6	104	2	Q7MKW5 PORGI	Q7MKW5 porphyromon
313	47	100.0	254	2	Q61WM2 CAEBR	Q61WM2 caenorhabdi	386	47	93.6	104	2	Q7CET1 STRP3	Q7CET1 streptococc
314	47	100.0	282	2	Q4LIU3 9BURK	Q4LIU3 burkholderi	387	47	93.6	104	2	Q720Y0 LEPIC	Q720Y0 leptospira
315	47	100.0	283	2	Q617G4 CAEBR	Q617G4 caenorhabdi	388	47	93.6	104	2	Q5HX18 CAMUR	Q5HX18 campylobact
316	47	100.0	284	2	Q9NZK6 CAEBL	Q9NZK6 caenorhabdi	389	47	93.6	104	2	THIO1 DICDI	THIO1 dictyosteli
317	47	100.0	285	2	Q4UMIO XANCP	Q4UMIO xanthomonas	390	47	93.6	105	1	THIO RHOSH	THIO rhodocacter
318	47	100.0	285	2	Q8B7I9 XANCP	Q8B7I9 xanthomonas	391	47	93.6	105	1	Q519H9 ENTHI	Q519H9 entameoba h
319	47	100.0	286	2	Q8PIW2 XANAC	Q8PIW2 xanthomonas	392	47	93.6	105	2	Q54KN7 DICDI	Q54KN7 dictyosteli
320	47	100.0	287	2	Q7KMR7 DROME	Q7KMR7 dirosophila	393	47	93.6	105	2	Q890T2 CLOTE	Q890T2 clostridium
321	47	100.0	287	2	Q9VRP3 DROME	Q9VRP3 schizosacch	394	47	93.6	105	2		
322	47	100.0	287	2			395	47	93.6	105	2		
323	47	100.0	290	2	Q9USR1_SCHPO		396	47	93.6	105	2		

397	44	93.6	105	2	Q7YKR2_HABDU	Q7VIR2_haemophilus	470	44	93.6	120	2	Q6SKK3_ARTAU	Q6KE3_arthrobacte
398	44	93.6	105	2	Q7US34_SYNPX	Q7UB34_synchococc	471	44	93.6	121	2	Q6FRF3_ORYSA	Q6FRF3_oryza sativ
399	44	93.6	105	2	Q5XWG6_GEOXA	Q5XWG6_geobacillus	472	44	93.6	121	2	Q6L4X5_ORYSA	Q6L4X5_oryza sativ
400	44	93.6	106	1	THIO1_AMASO	P0412_anabaena sp	473	44	93.6	122	1	TRXH_ORYSA	Q4243_oryza sativ
401	44	93.6	106	1	THIO1_AMASP	P0411_anabaena sp	474	44	93.6	122	2	Q7EZK7_ORYSA	Q7EZK7_oryza sativ
402	44	93.6	106	1	THIO1_SYNP7	P12243_synchococc	475	44	93.6	122	2	Q7AZK2_HORVD	Q7AZK2_hordeum vul
403	44	93.6	106	1	THIO_COPCM	Q9UW02_coplinus co	476	44	93.6	122	2	Q4WIF6_AMAIZE	Q4WIF6_zea mays (m
404	44	93.6	106	1	THIO_PASMU	Q9C409_pasteurella	477	44	93.6	123	2	Q7XJG6_ARYTH	Q7XJG6_arabidopsis
405	44	93.6	106	1	THIO_SYNP3	P52231_synchocyst	478	44	93.6	123	2	Q6VBI4_IPOBA	Q6VBI4_ipomoea bat
406	44	93.6	106	2	Q5NNI9_ZYMMO	P52319_zymomonas m	479	44	93.6	123	2	Q7U005_MYCBO	Q7U005_mycobacteri
407	44	93.6	106	2	Q6NND2_RHOJA	P52319_synchocyst	480	44	93.6	123	2	Q7D8E1_MYCTU	Q7D8E1_mycobacteri
408	44	93.6	106	2	Q89MD9_BRJJA	Q89MD9_bradynizob	481	44	93.6	123	2	Q6G4Z3_BIFLO	Q6G4Z3_bifidobacte
409	44	93.6	106	2	Q8DGN0_SYNEL	Q8DGN0_synchococc	482	44	93.6	124	2	Q6KJZ7_CAPAN	Q6KJZ7_capsicum an
410	44	93.6	106	2	Q7MSG6_WOISL	Q7MSG6_wolfinella s	483	44	93.6	124	2	Q6M1N0_CORGL	Q6M1N0_corynebacte
411	44	93.6	106	2	Q6ME96_PARUM	Q6ME96_parchallamyd	484	44	93.6	124	2	Q5YLL7_NOCFA	Q5YLL7_nocardia fa
412	44	93.6	107	1	THIO_CFACA	P51295_cyanidium c	485	44	93.6	125	1	TRXH_PICMA	Q65049_picea maria
413	44	93.6	107	1	THIO_PORPU	P51295_porphyras pu	486	44	93.6	125	1	Q9LDX4_WHEAT	Q9LDX4_triticum ae
414	44	93.6	107	1	THIO_PORPE	P50254_porphyras ye	487	44	93.6	126	1	TRXH1_TOBAC	P29449_nicotiana t
415	44	93.6	107	1	THIO_STRCL	Q05739_streptomyce	488	44	93.6	126	1	TRXH_WHEAT	Q64394_triticum ae
416	44	93.6	107	2	Q5EN23_MAGGR	Q5EN23_magnaporthe	489	44	93.6	127	2	Q6NEB0_CORDI	Q6NEJ0_corynebacte
417	44	93.6	107	2	Q51V99_MAGGR	Q51V99_magnaporthe	490	44	93.6	127	2	Q7W1J3_BORBR	Q7W1J3_bordecella
418	44	93.6	107	2	Q79N44_SYNP7	Q79N44_synchococc	491	44	93.6	127	2	Q7W665_BORPA	Q7W665_bordecella
419	44	93.6	107	2	Q8DKP7_SYNEL	Q8DKP7_synchococc	492	44	93.6	127	2	Q7YXN6_BORPE	Q7YXN6_bordecella
420	44	93.6	107	2	Q7VBF6_PROMA	Q7VBF6_prochloroco	493	44	93.6	129	2	Q82SV1_STRAM	Q82SV1_streptomyce
421	44	93.6	107	2	Q7V6M6_PRODM	Q7V6M6_prochloroco	494	44	93.6	130	2	Q64395_TRITU	Q64395_triticum ae
422	44	93.6	107	2	Q7V126_PROMP	Q7V126_prochloroco	495	44	93.6	130	2	Q7PTJ2_WHEAT	Q7PTJ2_triticum ae
423	44	93.6	107	2	Q7U898_SYNPX	Q7U898_synchococc	496	44	93.6	131	2	Q9SMG5_SECCB	Q9SMG5_secale cere
424	44	93.6	107	2	Q72B01_DESVH	Q72B01_deuslofivibr	497	44	93.6	131	2	Q9SMG4_LOLPR	Q9SMG4_lolium pere
425	44	93.6	107	2	Q6SS27_MANSM	Q6SS27_mannheimia	498	44	93.6	131	2	Q9SMG6_HORBU	Q9SMG6_hordeum bul
426	44	93.6	107	2	Q5MZK6_SYNP6	Q5MZK6_synchococc	499	44	93.6	131	2	Q8H6X0_WHEAT	Q8H6X0_triticum ae
427	44	93.6	108	2	Q4WMD4_ASPEU	Q4WMD4_aspergillus	500	44	93.6	131	2	Q8GZK4_HORVD	Q8GZK4_hordeum vul
428	44	93.6	108	2	Q5JRY2_HUMAN	Q5JRY2_homo sapien	501	44	93.6	131	2	Q84X91_YPOLV	Q84X91_leymus chin
429	44	93.6	108	2	Q6VBI5_IPOBA	Q6VBI5_ipomoea bat	502	44	93.6	131	2	Q9AS75_ORYSA	Q9AS75_oryza sativ
430	44	93.6	108	2	Q4NK10_9M1CC	Q4NK10_arthrobacte	503	44	93.6	131	2	Q9S753_9POLA	Q9S753_phalaris co
431	44	93.6	108	2	Q8YVH9_NANSP	Q8YVH9_anabaena sp	504	44	93.6	132	2	Q4WTT9_9DELT	Q4WTT9_anacromyob
432	44	93.6	108	2	Q82VNZ_NITTEU	Q82VNZ_nitrosomonas	505	44	93.6	132	2	Q8H6K4_ORYSA	Q8H6K4_oryza sativ
433	44	93.6	108	2	Q7UJ35_RHDBA	Q7UJ35_rhodospirilli	506	44	93.6	133	1	TRXH2_ARYTH	Q38679_arabidopsis
434	44	93.6	108	2	Q6MKD2_BDEBA	Q6MKD2_bdellovibri	507	44	93.6	133	2	Q8G6X5_MAIZE	Q8G6X5_zea mays (m
435	44	93.6	108	2	Q6ABM1_LEIXX	Q6ABM1_leifsonia x	508	44	93.6	133	2	Q8GZT3_BRACM	Q8GZT3_brasileia ca
436	44	93.6	108	2	Q5ZRE7_LEGPH	Q5ZRE7_legionella	509	44	93.6	134	2	Q8L9AC_ARYTH	Q8L9AC_arabidopsis
437	44	93.6	108	2	Q5XKU3_LEGPA	Q5XKU3_legionella	510	44	93.6	134	2	Q8S1R5_ORYSA	Q8S1R5_oryza sativ
438	44	93.6	108	2	Q5MSL4_LEGPL	Q5MSL4_legionella	511	44	93.6	136	2	Q9JWZ3_PRUPE	Q9JWZ3_prunus pers
439	44	93.6	109	1	THIO2_SYNP3	P73613_synchocyst	512	44	93.6	139	1	THIO2_ECOLI	P33636_escherichia
440	44	93.6	109	1	THIO_CHIAU	P73613_chloroflexu	513	44	93.6	139	2	Q57L52_SALCH	Q57L52_salmonella
441	44	93.6	109	1	THIO_GRIPA	P50338_griffithsia	514	44	93.6	139	2	Q5LBI1_BACFN	Q5LBI1_bacteroides
442	44	93.6	110	1	THIO_STRCO	P52230_streptomyce	515	44	93.6	139	2	Q8Z4J6_SALTI	Q8Z4J6_salmonella
443	44	93.6	110	2	Q4H9D7_9DEIO	Q4H9D7_deinococcus	516	44	93.6	139	2	Q8ZMX4_SALTY	Q8ZMX4_salmonella
444	44	93.6	110	2	Q879K6_STRP3	Q879K6_streptococc	517	44	93.6	139	2	Q5PID7_SALPA	Q5PID7_salmonella
445	44	93.6	110	2	Q8YVY7_ANASP	Q8YVY7_anabaena sp	518	44	93.6	139	2	Q67747_AQUAE	Q67747_aquifex aeo
446	44	93.6	110	2	Q82FE7_STRAM	Q82FE7_streptomyce	519	44	93.6	139	2	Q605Y8_METCA	Q605Y8_methyllococc
447	44	93.6	110	2	Q7NM87_GLOVI	Q7NM87_gloeobacter	520	44	93.6	140	1	TRXM_CHLRE	P23400_chlamydomon
448	44	93.6	111	2	Q9ALA7_SYNP7	Q9ALA7_synchococc	521	44	93.6	140	2	Q72IL5_THHET2	Q72IL5_thermus the
449	44	93.6	111	2	Q5N062_SYNP6	Q5N062_synchococc	522	44	93.6	140	2	Q5S193_THHET8	Q5S193_thermus the
450	44	93.6	112	2	Q67LQ7_SYNP6	Q67LQ7_synbiobacte	523	44	93.6	141	2	Q4H6T8_9DEIO	Q4H6T8_deinococcus
451	44	93.6	113	2	Q68BP1_GRAUL	Q68BP1_gracilaria	524	44	93.6	141	2	Q5LMAO_SILPO	Q5LMAO_silicibacte
452	44	93.6	113	2	Q8GUR9_PEA	Q8GUR9_pisum sativ	525	44	93.6	142	2	Q9RVS8_DEIRA	Q9RVS8_deinococcus
453	44	93.6	114	1	TRXH1_ARYTH	P29448_arabidopsis	526	44	93.6	142	2	Q61985_CABEL	Q61985_cannorhabdi
454	44	93.6	114	1	Q67SM1_SYMTH	Q67SM1_symbiobacte	527	44	93.6	142	2	Q9RYY9_DEIRA	Q9RYY9_deinococcus
455	44	93.6	115	2	Q75ID5_ASHGO	Q75ID5_ashbya goss	528	44	93.6	143	2	Q8S312_9ROSI	Q8S312_populus tre
456	44	93.6	115	2	Q5MZN0_SYNP6	Q5MZN0_synchococc	529	44	93.6	144	2	Q7UPJ1_RHOBA	Q7UPJ1_rhodopirelli
457	44	93.6	116	1	TRXH_FAGES	Q96419_fagopyrum e	530	44	93.6	145	2	Q6NCUE_RHOPA	Q6NCUE_rhodospelo
458	44	93.6	117	1	Q74OZ6_MYCPA	Q74OZ6_mycobacteri	531	44	93.6	145	2	Q8ZBM4_YERPE	Q8ZBM4_yersinia pe
459	44	93.6	118	1	TRXH_RICCO	Q43636_ricinus com	532	44	93.6	145	2	Q6E640_YERPS	Q6E640_yersinia ps
460	44	93.6	118	2	Q9JXZ4_PEA	Q9JXZ4_pisum sativ	533	44	93.6	145	2	Q7NOC1_CHRVO	Q7NOC1_chromobacte
461	44	93.6	118	2	Q8GVD3_WHEAT	Q8GVD3_triticum ae	534	44	93.6	145	2	Q5P2H5_AZOSE	Q5P2H5_azarocae sp
462	44	93.6	118	2	Q7XZK3_HORVD	Q7XZK3_hordeum vul	535	44	93.6	147	2	Q8J164_BRJJA	Q8J164_bradynizob
463	44	93.6	118	2	Q5XAS7_STRP6	Q5XAS7_streptococc	536	44	93.6	148	2	Q5M1S6_AEDAL	Q5M1S6_aedes albop
464	44	93.6	119	2	Q9SP36_SECCB	Q9SP36_secale cere	537	44	93.6	149	2	Q8N1G6_CORGL	Q8N1G6_corynebacte
465	44	93.6	119	2	Q5ZF48_PIAMU	Q5ZF48_plantago ma	538	44	93.6	150	2	Q84XS0_CHLRE	Q84XS0_chlamydomon
466	44	93.6	120	2	Q8F4W0_LEPIN	Q8F4W0_leptospira	539	44	93.6	151	2	Q8Z6F1_STRAM	Q8Z6F1_streptomyce
467	44	93.6	120	2	Q5URY3_HUMAN	Q5URY3_homo sapien	540	44	93.6	152	2	Q8H6X3_TOBAC	Q8H6X3_nicotiana t
468	44	93.6	120	2	Q9AR82_PEA	Q9AR82_pisum sativ	541	44	93.6	153	2	Q7XY47_GRIPA	Q7XY47_griffithsia
469	44	93.6	120	2	Q4NLS3_9M1CC	Q4NLS3_arabidopsis	542	44	93.6	153	2	Q9FYJ3_ARYTH	Q9FYJ3_arabidopsis

543	44	93.6	154	2	Q4K890_PSEF5	Q4K890_pseudomonas	616	44	93.6	512	2	Q4SEJ5_TETNG	Q4sej5_tetradon n
544	44	93.6	154	2	Q88MC7_PSEPK	Q88mc7_pseudomonas	617	44	93.6	515	1	TXND2_MOUSE	Q6902 mus musculus
545	44	93.6	154	2	Q8AB92_BACTN	Q8ab92_bacteroides	618	44	93.6	543	1	OSIAW9_BACFN	OSIAW9 bacteroides
546	44	93.6	155	2	Q4ZQ39_PSESY	Q4zq39_pseudomonas	619	44	93.6	543	2	Q64R8C_BACFR	Q64r8c bacteroides
547	44	93.6	155	2	Q8EF86_SHEON	Q8ef86_shewanella	620	44	93.6	550	1	TXND2_RAT	Q5hx6 ratuus norv
548	44	93.6	155	2	Q88523_PSESM	Q88523_pseudomonas	621	44	93.6	553	1	TXND2_HUMAN	Q86vq3 homo sapien
549	44	93.6	155	2	Q6ARG0_BACFR	Q6arg0_bacteroides	622	44	93.6	569	2	Q7YOE8_ORYSA	Q7Yoe8 oryza sativ
550	44	93.6	157	2	Q4NJ44_9MICC	Q4nj44_arthrobacter	623	44	93.6	581	2	Q4RON5_TETNG	Q4rns tetradon n
551	44	93.6	158	2	Q94282_CABEL	Q94282_caenorhabdi	624	44	93.6	588	1	TXND3_HUMAN	Q84427 homo sapien
552	44	93.6	159	2	Q93VQ2_ARATH	Q93vq2_arabidopsis	625	44	93.6	596	2	Q6FW44_HUMAN	Q6fw44 homo sapien
553	44	93.6	160	2	P95355_NEIGO	P95355_neisseria g	626	44	93.6	602	2	Q6WNE3_CABER	Q6wne3 caenorhabdi
554	44	93.6	160	2	Q5F5K1_NEIGB1	Q5f5k1_neisseria g	627	44	93.6	605	2	Q7IG53_BRARE	Q7IG53 brachydantio
555	44	93.6	160	2	Q9K1R4_NEIBM	Q9k1r4_neisseria m	628	44	93.6	606	2	Q9TW67_CABEL	Q9tw67 caenorhabdi
556	44	93.6	167	1	TXMXC8_PORGI	TXMXC8 zea mays (m	629	44	93.6	610	2	Q7IG52_BRARE	Q7IG52 brachydantio
557	44	93.6	169	2	Q7MXC8_PORGI	Q7MXC8 porphyromon	630	44	93.6	619	1	TF7L2_HUMAN	Q9qnb0 homo sapien
558	44	93.6	170	2	Q8KDH8_CHLTE	Q8kdh8_chlorobium	631	44	93.6	633	2	Q5L8Y4_BACFN	Q5l8y4 bacteroides
559	44	93.6	172	1	TXMX_ORYSA	Q92p20 oryza sativ	632	44	93.6	633	2	Q64P47_BACFR	Q64p47 bacteroides
560	44	93.6	172	1	TXMX_PEA	P48384 plium sativ	633	44	93.6	634	2	Q8A0X4_BACTN	Q8A0x4 bacteroides
561	44	93.6	173	1	TXMX3_ARATH	Q9seu7 arabidopsis	634	44	91.5	98	2	Q25549_NAEFO	Q25549 naegleria f
562	44	93.6	173	2	Q681Y9_ARATH	Q681y9_arabidopsis	635	43	91.5	105	1	THIO1_SYNY3	THIO1 SYNY3
563	44	93.6	173	2	Q67ZH7_ARATH	Q67zh7_arabidopsis	636	43	91.5	105	2	Q5XGB5_XENTR	Q5Xgb5 xenopus tro
564	44	93.6	173	2	Q67XN4_ARATH	Q67xn4_arabidopsis	637	43	91.5	105	2	Q5U566_XENLA	Q5U566 xenopus lae
565	44	93.6	173	2	Q4NX02_9BELT	Q4nx02_aeaeomyxob	638	43	91.5	105	2	THIO GEOCY	Q96952 geodia cydo
566	44	93.6	174	2	Q623W5_CABER	Q623w5_caenorhabdi	639	43	91.5	106	1	THIO_ICTPU	Q9cgl3 ictalurus p
567	44	93.6	175	1	TXMX_WHEAT	Q91y12 arabidopsis	640	43	91.5	107	2	Q9TXH8_CABEL	Q9txh8 caenorhabdi
568	44	93.6	175	2	Q9LV12_ARATH	Q9lv12_arabidopsis	641	43	91.5	107	2	Q617H0_CABER	Q617h0 caenorhabdi
569	44	93.6	175	2	Q5NDAC_TRTTU	Q5ndac_triticum tu	642	43	91.5	107	2	Q6DG16_BRARE	Q6dg16 brachydantio
570	44	93.6	177	2	Q7MS25_BRECH	Q7ms25_brevibacill	643	43	91.5	107	2	Q7ZU14_BRARE	Q7zu14 brachydantio
571	44	93.6	180	2	Q95AH9_PEA	Q95ah9_plium sativ	644	43	91.5	108	2	Q84XS1_CHIRE	Q84xs1 chlamydomon
572	44	93.6	180	2	Q7XKD0_ORYSA	Q7xkd0_oryza sativ	645	43	91.5	109	2	THIO2 ANASP	P20857 anabaena sp
573	44	93.6	184	2	Q8FLQ6_CORER	Q8flq6_corynebacte	646	43	91.5	110	1	Q8IEV4_TRIVA	Q8IEV4 trichomonas
574	44	93.6	185	2	Q9RXM6_DEIRA	Q9rxm6_deinococcus	647	43	91.5	112	2	Q6IVS9_TRIVA	Q6IVS9 trichomonas
575	44	93.6	189	2	Q655X0_ORYSA	Q655x0_oryza sativ	648	43	91.5	112	2	Q6IVS8_TRIVA	Q6IVS8 trichomonas
576	44	93.6	192	2	Q4HB83_9DEIO	Q4hb83_deinococcus	649	43	91.5	112	2	THIO2_CABEL	Q17424 caenorhabdi
577	44	93.6	193	1	TXMX4_ARATH	Q9seu6 arabidopsis	650	43	91.5	119	1	Q5V6K7_HALMA	Q5V6k7 haloarcula
578	44	93.6	194	2	Q64764_ARATH	Q64764_arabidopsis	651	43	91.5	119	2	Q64709_HALSA	Q64709 haloabacteri
579	44	93.6	197	2	Q6ZN00_HUMAN	Q6zn00_homo sapien	652	43	91.5	119	2	Q6AMH7_PROAC	Q6amh7 propionibac
580	44	93.6	197	2	Q73S01_MYCPA	Q73s01_mycobacteri	653	43	91.5	121	2	Q5JMR9_ORYSA	Q5jmr9 oryza sativ
581	44	93.6	202	2	Q4J5Y3_CORJX	Q4j5y3_corynebacte	654	43	91.5	123	2	Q5QZV7_IDILO	Q5qzv7 idiomarina
582	44	93.6	207	2	Q5UR15_HUMAN	Q5ur15_homo sapien	655	43	91.5	142	2	Q6J277_CABER	Q6j277 caenorhabdi
583	44	93.6	208	2	Q7OK47_9ACTO	Q7ok47_gordonia we	656	43	91.5	145	2	Q6SRD7_ARATH	Q6srd7 arabidopsis
584	44	93.6	211	2	Q67LA9_SYWTH	Q67la9_symbiobacte	657	43	91.5	151	2	Q84XS2_CHIRE	Q84xs2 chlamydomon
585	44	93.6	212	2	Q6XN29_RHOER	Q6xn29_rhodococcus	658	43	91.5	152	2	Q9JMT2_MIRIA	Q9jmt2 neisseria m
586	44	93.6	212	2	Q5YPM1_NOCPA	Q5ypm1_nocardia fa	659	43	91.5	160	2	Q8TIA1_METAC	Q8tia1 methanosarc
587	44	93.6	216	2	Q49816_MYCLE	Q49816_mycobacteri	660	43	91.5	161	2	Q8PY73_METMA	Q8py73 methanosarc
588	44	93.6	216	2	Q7UIU8_MYCBO	Q7uiu8_mycobacteri	661	43	91.5	165	2	Q8L7S9_ARATH	Q8l7s9 arabidopsis
589	44	93.6	216	2	Q06392_MYCTU	Q06392_mycobacteri	662	43	91.5	167	2	Q6MLM7_BDEBA	Q6mlm7 bdellovibri
590	44	93.6	220	2	Q9CB61_MYCLB	Q9cb61_nocardia fa	663	43	91.5	169	2	Q6NPP9_ARATH	Q6npp9 arabidopsis
591	44	93.6	222	2	Q9CB61_MYCLB	Q9cb61_mycobacteri	664	43	91.5	172	2	Q73AC8_BACCI	Q73ac8 bacillus ce
592	44	93.6	266	2	Q7XQO2_ORYSA	Q7xqo2_oryza sativ	665	43	91.5	184	2	Q81F76_BACCR	Q81f76 bacillus ce
593	44	93.6	268	2	Q8KD40_CHLTE	Q8kd40_chlorobium	666	43	91.5	184	2	Q81F76_BACCR	Q81f76 bacillus ce
594	44	93.6	280	2	Q811B1_RALISO	Q811b1_ralstonia s	667	43	91.5	184	2	Q81F76_BACCR	Q81f76 bacillus ce
595	44	93.6	286	2	Q7PNL3_ANGOA	Q7pnl3_anopheles g	668	43	91.5	184	2	Q8HSG7_BACCH	Q8hsg7 bacillus th
596	44	93.6	299	2	Q9ABW0_CAUCR	Q9abw0_caulobacter	669	43	91.5	184	2	Q6HFG7_BACCH	Q6hfg7 bacillus th
597	44	93.6	317	2	Q6ES52_ORYSA	Q6es52_oryza sativ	670	43	91.5	184	2	Q63D26_BACCE	Q63d26 bacillus ce
598	44	93.6	328	2	Q7MUAO_PORGI	Q7muao_porphyromon	671	43	91.5	191	2	Q6AMH0_BACCE	Q6amh0 bacillus ce
599	44	93.6	333	2	Q5DBJ3_SCHUA	Q5dbj3_schistosoma	672	43	91.5	191	2	Q733M6_BACCI	Q733m6 bacillus ce
600	44	93.6	340	2	Q91B43_CHICK	Q91b43_gallus gall	673	43	91.5	191	2	Q81AF8_BACCR	Q81af8 bacillus ce
601	44	93.6	355	2	Q5PU93_BRARE	Q5pu93_birachydantio	674	43	91.5	191	2	Q81AF8_BACCR	Q81af8 bacillus ce
602	44	93.6	358	2	Q7MWH7_PORGI	Q7mwh7_porphyromon	675	43	91.5	191	2	Q6HFI7_BACCH	Q6hfi7 bacillus th
603	44	93.6	361	2	Q5LAX1_BACFN	Q5lax1_bacteroides	676	43	91.5	191	2	Q637L5_BACCE	Q637l5 bacillus th
604	44	93.6	361	2	Q64R88_BACFR	Q64r88_bacteroides	677	43	91.5	242	2	Q9XIG4_ARATH	Q9xig4 arabidopsis
605	44	93.6	364	2	Q7T264_XENTR	Q7t264_xenopus lae	678	43	91.5	248	2	Q4N8K0_TREPA	Q4n8k0 theileria p
606	44	93.6	364	2	Q7T265_XENTR	Q7t265_xenopus tro	679	43	91.5	254	2	Q9N357_CABEL	Q9n357 caenorhabdi
607	44	93.6	366	2	Q8A882_BACTN	Q8a882_bacteroides	680	43	91.5	277	2	Q8NC82_HUMAN	Q8nc82 homo sapien
608	44	93.6	367	2	Q5LIB3_BACFN	Q5lib3_bacteroides	681	43	91.5	327	2	Q5A915_CANAL	Q5a915 candida alb
609	44	93.6	367	2	Q64S05_BACFR	Q64s05_bacteroides	682	43	91.5	336	2	Q6BRN9_DEBHA	Q6brn9 debaryomyce
610	44	93.6	380	2	Q8LGS8_ARATH	Q8lgs8_arabidopsis	683	43	91.5	444	2	Q4S9P6_TETNG	Q4s9p6 tetradon n
611	44	93.6	380	2	Q8YMG7_ARATH	Q8ymg7_arabidopsis	684	43	91.5	464	2	Q53Q77_HUMAN	Q53q77 homo sapien
612	44	93.6	385	2	Q93X83_9ROSI	Q93x83_vitis labru	685	43	91.5	464	2	Q9N3Y6_HUMAN	Q9n3y6 homo sapien
613	44	93.6	386	2	Q8VZH4_TOBAC	Q8vzh4_nicotiana t	686	43	91.5	476	2	Q9JLV4_MOUSE	Q9jlv4 mus musculu
614	44	93.6	413	2	Q67T35_SYWTH	Q67t35_symbiobacte	687	43	91.5	578	2	Q81B68_ARATH	Q81b68 arabidopsis
615	44	93.6	433	2	Q4R6D4_MACFA	Q4r6d4_macaca faec	688	43	91.5	578	2	Q80763_ARATH	Q80763 arabidopsis

689	43	91.5	612	2	Q96K36_HUMAN	Q96K36 homo sapien	762	42	89.4	460	2	Q7URF7_RHOBA	Q7URF7 rhodopirell
690	43	91.5	706	2	Q9VYR5_DROME	Q9VYR5 drosophila	763	42	89.4	473	2	Q5L9C4_BACFN	Q5L9C4 bacteroides
691	43	91.5	706	2	Q6NPB8_DROME	Q6NPB8 drosophila	764	42	89.4	473	2	Q64PK8_BACFN	Q64PK8 bacteroides
692	43	91.5	747	2	Q8TD87_HUMAN	Q8TD87 homo sapien	765	42	89.4	477	2	Q7IG54_BRARE	Q7IG54 brachydanio
693	43	91.5	747	2	Q6UTZ6_HUMAN	Q6UTZ6 homo sapien	766	42	89.4	491	2	Q7UIG8_RHOBA	Q7UIG8 rhodopirell
694	43	91.5	768	2	Q96K54_HUMAN	Q96K54 homo sapien	767	42	89.4	506	2	Q6QUQ2_QUEBU	Q6QUQ2 quercus sub
695	43	91.5	781	2	Q614U3_CABER	Q614U3 caenorhabdi	768	42	89.4	506	2	Q8GTC2_QUEBU	Q8GTC2 quercus sub
696	43	91.5	788	2	Q9XWE1_CABER	Q9XWE1 caenorhabdi	769	42	89.4	517	2	Q7Q063_ANGSA	Q7Q063 anopheles g
697	43	91.5	792	2	Q86T61_HUMAN	Q86T61 homo sapien	770	42	89.4	534	1	ENV_FSVST	P03392 feline sarc
698	43	91.5	793	2	Q81XB1_HUMAN	Q81XB1 homo sapien	771	42	89.4	606	2	Q9VMF6_DROME	Q9VMF6 drosophila
699	43	91.5	793	2	Q96K38_HUMAN	Q96K38 homo sapien	772	42	89.4	653	1	TXND3_CIOIN	O954J5 ciona intes
700	43	91.5	793	2	Q96K44_HUMAN	Q96K44 homo sapien	773	42	89.4	662	1	ENV_FVLB	P11261 feline leuk
701	43	91.5	793	2	Q5R5L3_PONPY	Q5R5L3 pongo pygma	774	42	89.4	662	1	ENV_FSVGA	P03391 feline sarc
702	43	91.5	793	2	Q8CIB0_MOUSE	Q8CIB0 mus musculu	775	42	89.4	662	2	Q7LYT7_FLV	Q7LYT7 feline leuk
703	43	91.5	793	2	Q9DC23_MOUSE	Q9DC23 mus musculu	776	42	89.4	666	2	Q90AE9_FLV	Q90AE9 feline leuk
704	43	91.5	793	2	Q7LS84_MOUSE	Q7LS84 mus musculu	777	42	89.4	668	1	ENV_FLVG6	P21443 feline leuk
705	43	91.5	795	2	Q8CH78_MOUSE	Q8CH78 mus musculu	778	42	89.4	837	1	TXND3_ANNCR	P96666 anthocidari
706	43	91.5	796	2	Q6NRT6_XENLA	Q6NRT6 xenopus lae	779	42	89.4	1019	2	Q7UMF5_RHOBA	Q7UMF5 rhodopirell
707	43	91.5	1022	2	Q4Q7K2_LEIMA	Q4Q7K2 leishmania	780	42	89.4	1083	2	Q7UM78_RHOBA	Q7UM78 rhodopirell
708	42	89.4	77	2	Q8XHP3_CLOPE	Q8XHP3 clostridium	781	41	87.2	45	2	Q9VM82_DROME	Q9VM82 drosophila
709	42	89.4	89	2	Q4HCJ2_GDEIO	Q4HCJ2 deinococcus	782	41	87.2	100	2	Q4YUN1_PLABE	Q4YUN1 plasmodium
710	42	89.4	101	2	Q4NZX5_THBPA	Q4NZX5 theileria p	783	41	87.2	100	2	Q4FND3_9RICK	Q4FND3 candidatus
711	42	89.4	104	2	Q8DSD2_STRMU	Q8DSD2 streptococc	784	41	87.2	105	2	Q7VKX3_HELHP	Q7VKX3 helicobacte
712	42	89.4	104	2	Q5M2L2_STR12	Q5M2L2 streptococc	785	41	87.2	107	1	THIO2_CORRE	P07887 corynebacte
713	42	89.4	104	2	Q5LY08_STR11	Q5LY08 streptococc	786	41	87.2	108	1	THIO_BUCAL	P57853 buchnera ap
714	42	89.4	105	2	Q5CR91_CRYPV	Q5CR91 cryptospori	787	41	87.2	109	1	THIO_BUCAP	O51890 buchnera ap
715	42	89.4	108	1	THIO2_CHLFE	THIO2 chlorobium	788	41	87.2	108	1	Q741T5_GEOSL	Q741T5 geobacter s
716	42	89.4	108	1	THIO_CHLFT	P10472 chlorobium	789	41	87.2	109	2	Q81LNO_BUCPS	O81LNO buchnera ap
717	42	89.4	115	2	Q5PB59_ANAMM	Q5PB59 anaplasma m	790	41	87.2	110	2	Q6R877_ACTAD	O6R877 actinobact
718	42	89.4	121	2	Q81KL4_PLAFV	Q81KL4 plasmodium	791	41	87.2	112	2	Q6R877_ACTAD	O6R877 actinobact
719	42	89.4	121	2	Q7R8F6_PLAYO	Q7R8F6 plasmodium	792	41	87.2	113	2	Q9PA22_XYUFA	Q9PA22 xyella fas
720	42	89.4	121	2	Q4YYT5_PLABE	Q4YYT5 plasmodium	793	41	87.2	113	2	Q7VRM1_CANBF	Q7VRM1 candidatus
721	42	89.4	139	2	Q9VUG9_DROME	Q9VUG9 drosophila	794	41	87.2	117	2	Q812Q3_PLAF7	Q812Q3 plasmodium
722	42	89.4	139	2	Q6DID1_ERMCT	Q6DID1 erwinia car	795	41	87.2	120	2	Q5ZVM8_LEGPH	Q5ZVM8 legionella
723	42	89.4	139	2	Q743D8_MYCPA	Q743D8 mycobacteri	796	41	87.2	120	2	Q5X5F3_LEGPA	O5X5F3 legionella
724	42	89.4	140	2	Q9CHC8_MYCLE	Q9CHC8 mycobacteri	797	41	87.2	120	2	Q5MWT6_LBSPU	Q5MWT6 legionella
725	42	89.4	141	2	Q4UBR7_SULAC	Q4UBR7 sulfolobus	798	41	87.2	128	2	Q7IG48_PLAF7	Q7IG48 plasmodium
726	42	89.4	148	2	Q4US63_XANCP	Q4US63 xanthomonas	799	41	87.2	129	2	Q4HN70_CAMLA	Q4HN70 campylobact
727	42	89.4	148	2	Q5ZZA0_NOCFA	Q5ZZA0 nocardia fa	800	41	87.2	142	2	Q9W022_DROME	Q9W022 drosophila
728	42	89.4	148	2	Q8PMZ8_XANAC	Q8PMZ8 xanthomonas	801	41	87.2	159	2	Q6A5E3_PROAC	Q6A5E3 propionibac
729	42	89.4	148	2	Q8PBE2_XANPC	Q8PBE2 xanthomonas	802	41	87.2	184	2	Q4TKK5_9SPHN	Q4TKK5 erythrobact
730	42	89.4	160	2	Q604X8_METCA	Q604X8 methylcoccc	803	41	87.2	200	2	Q5CS14_CRYPV	O5CS14 cryptospori
731	42	89.4	160	2	Q63QP3_BURPS	Q63QP3 burkholderi	804	41	87.2	200	2	Q5CKF3_CRYHO	O5CKF3 cryptospori
732	42	89.4	172	2	Q50039_MYCLE	Q50039 mycobacteri	805	41	87.2	210	2	Q9A684_CAUCR	Q9A684 caulobacter
733	42	89.4	174	2	Q8XVP6_RALSO	Q8XVP6 ralestonia s	806	41	87.2	289	2	Q4IWM6_AZOVI	Q4IWM6 azotobacter
734	42	89.4	175	2	Q9LKW0_LYGCS	Q9LKW0 lycopersico	807	41	87.2	289	2	Q9HMM7_PSEAB	Q9HMM7 pseudomonas
735	42	89.4	181	2	Q6IR37_NICBE	Q6IR37 nicotiana b	808	41	87.2	290	2	Q4ZMX6_PSESY	Q4ZMX6 pseudomonas
736	42	89.4	181	2	Q6URF3_NICBE	Q6URF3 nicotiana b	809	41	87.2	290	2	Q4K589_PSEFS	Q4K589 pseudomonas
737	42	89.4	183	2	Q8LFA3_ARATH	Q8LFA3 arabidopsis	810	41	87.2	290	2	Q8BQ12_PSEPK	Q8BQ12 pseudomonas
738	42	89.4	183	2	Q9M7X9_ARATH	Q9M7X9 arabidopsis	811	41	87.2	336	2	Q8B9R3_PSESM	Q8B9R3 pseudomonas
739	42	89.4	186	2	Q6ZGX6_BURMA	Q6ZGX6 burkholderi	812	41	87.2	336	2	Q7WTC7_PORGI	Q7WTC7 porphyromon
740	42	89.4	187	2	Q8DTZ1_STRMU	Q8DTZ1 streptococc	813	41	85.1	136	2	Q9B810_RHTLO	Q9B810 rhizobium l
741	42	89.4	189	2	Q8H2V6_ORYSA	Q8H2V6 oryza sativ	814	40	85.1	136	2	Q7Q9B5_ANGSA	Q7Q9B5 anopheles g
742	42	89.4	197	2	Q6MJ38_BDEBA	Q6MJ38 bdellovibri	815	40	85.1	160	2	Q76877_DROME	Q76877 drosophila
743	42	89.4	207	2	Q4LLZ3_9BORK	Q4LLZ3 burkholderi	816	40	85.1	192	1	RESA_OEETH	O8CF53 cyanobacti
744	42	89.4	209	2	Q5Z300_NOCFA	Q5Z300 nocardia fa	817	40	85.1	4810	1	Q57X24_YTRYP	Q57X24 trypanosoma
745	42	89.4	216	2	Q8M2X9_ORYSA	Q8M2X9 oryza sativ	818	39	83.0	103	2	Q71Z58_LISMF	Q71Z58 listeria mo
746	42	89.4	241	2	Q9MSD4_CHLRE	Q9MSD4 chlamydomon	819	39	83.0	103	2	Q8Y6S4_LISMF	Q8Y6S4 listeria mo
747	42	89.4	273	1	ENV_FLTV1	P21444 feline leuk	820	39	83.0	103	2	Q9ZBA0_LISIN	Q9ZBA0 listeria in
748	42	89.4	273	1	Q9U054_FLV	Q9U054 feline leuk	821	39	83.0	104	2	Q8RKA7_OBNOE	O8RKA7 oenococcus
749	42	89.4	299	2	Q8C834_MOUSE	Q8C834 mus musculu	822	39	83.0	105	1	THIO_TREPA	O83889 treponema p
750	42	89.4	315	2	Q5U0E5_CRYNE	Q5U0E5 cryptococcu	823	39	83.0	105	2	Q971U3_CIOAB	Q971U3 clostridium
751	42	89.4	326	2	Q5K101_CRYNE	Q5K101 cryptococcu	824	39	83.0	107	2	Q5G528_WOLTR	Q5G528 wolbachia s
752	42	89.4	330	2	Q5BCU1_EMENT	Q5BCU1 aspergillus	825	39	83.0	109	2	Q87XC3_PSESM	Q87XC3 pseudomonas
753	42	89.4	336	2	Q8CA16_MOUSE	Q8CA16 mus musculu	826	39	83.0	110	2	Q97AL9_TREVO	Q97AL9 thermoplaem
754	42	89.4	370	2	Q41218_GIBRE	Q41218 gibberella	827	39	83.0	112	2	Q83A24_CORBU	Q83A24 coxiella bu
755	42	89.4	380	2	Q89SU4_BRALA	Q89SU4 bradyrhizob	828	39	83.0	113	2	Q9HUV7_TREAC	Q9HUV7 thermoplaem
756	42	89.4	386	2	Q8JHX2_CHICK	Q8JHX2 gallus gall	829	39	83.0	114	2	Q8S3L3_9ROSI	Q8S3L3 populus tre
757	42	89.4	402	2	Q7UNJ6_RHOBA	Q7UNJ6 rhodopirell	830	39	83.0	121	1	THIO_FUSCU	THIO fusarium cu
758	42	89.4	426	2	Q8JUY3_BRARE	Q8JUY3 brachydanio	831	39	83.0	121	2	Q4IK55_GIBZE	Q4IK55 gibberella
759	42	89.4	438	2	Q8JUY2_BRARE	Q8JUY2 brachydanio	832	39	83.0	123	2	Q84LP7_CITPA	Q84LP7 citrus para
760	42	89.4	451	2	Q7UD06_RHOBA	Q7UD06 rhodopirell	833	39	83.0	131	2	Q54NK3_DICDI	Q54NK3 dictyostell
761	42	89.4	459	1	TF7L2_MOUSE	Q92460 mus musculu	834	39	83.0	146	2	Q66542_AQUAE	Q66542 aquifex aeo

835	39	83.0	158	2	0623U3_CAEBR	0623U3 caenorthabdi	908	38	80.9	145	2	09V8Y6_DROME	09V8Y6 drosophila
836	39	83.0	163	2	06M1L5_BDEBA	06M1L5 bdellovibri	909	38	80.9	149	2	05C0B0_SCHJA	05C0B0 schistosoma
837	39	83.0	165	1	STOA_BACSU	031687 bacillus su	910	38	80.9	150	2	04NVD1_9BELT	04NVD1 anaeromyxob
838	39	83.0	165	2	08F3T9_LERPN	08F3T9 leptospira	911	38	80.9	151	2	08YJ16_BRUME	08YJ16 bruceella me
839	39	83.0	165	2	072RV9_LERPN	072RV9 leptospira	912	38	80.9	153	2	05YBC3_9CHLO	05YBC3 helicospori
840	39	83.0	168	2	07ZKX7_XENLA	07ZKX7 xenopus lae	913	38	80.9	154	2	091505_PSEAE	091505 pseudomonas
841	39	83.0	170	1	TXD12_MOUSE	09CQU0 mus musculu	914	38	80.9	156	2	041T42_AZOV1	041T42 azotobacter
842	39	83.0	170	1	05JYNI_MOUSE	05JYNI mus musculu	915	38	80.9	156	2	06GQZ1_XENLA	06GQZ1 xenopus lae
843	39	83.0	172	1	TXD12_MOUSE	09CQU0 mus musculu	916	38	80.9	171	2	04FNK2_9RICK	04FNK2 candidatus
844	39	83.0	172	1	05R9J5_BOVIN	05R9J5 bos taurus	917	38	80.9	172	2	06SXM9_CREID	06SXM9 ctenopharyx
845	39	83.0	172	2	0503D8_BRARE	0503D8 brachydanio	918	38	80.9	173	2	07W742_BORPA	07W742 bordetella
846	39	83.0	173	2	05KZP3_GEOXA	05KZP3 geobacillus	919	38	80.9	173	2	07W1P2_BORER	07W1P2 bordetella
847	39	83.0	173	2	05U4U7_XENLA	05U4U7 xenopus lae	920	38	80.9	175	2	051X14_PROWI	051X14 proteobacteria
848	39	83.0	177	2	065HX8_BACLD	065HX8 bacillus li	921	38	80.9	176	1	HEILX_RHOCA	HEILX rhodococcus
849	39	83.0	178	2	04PEU3_USITMA	04PEU3 usitlagu ma	922	38	80.9	179	2	033574_RHOSE	033574 rhodospirillum rubrum
850	39	83.0	178	2	06XVR3_CAEEL	06XVR3 caenorthabdi	923	38	80.9	179	2	051R18_SILPO	051R18 silicibacter
851	39	83.0	178	2	0628F4_CAEEL	0628F4 caenorthabdi	924	38	80.9	182	2	04XT52_PLACH	04XT52 plasmodium
852	39	83.0	179	1	RESA_BACSU	P35160 bacillus su	925	38	80.9	185	2	096C96_HUMAN	096C96 homo sapien
853	39	83.0	179	2	0950S7_CAEEL	0950S7 caenorthabdi	926	38	80.9	186	2	06JAC4_TRTTU	06JAC4 tritricum tu
854	39	83.0	182	2	04NS08_9BELT	04NS08 anaeromyxob	927	38	80.9	186	2	06NJT0_CORDI	06NJT0 corynebacter
855	39	83.0	185	2	07MAR8_WOLSU	07MAR8 wolfinella s	928	38	80.9	187	2	05LXCI_SILPO	05LXCI silicibacter
856	39	83.0	196	2	04KLD8_XENLA	04KLD8 xenopus lae	929	38	80.9	188	2	06TABS_WHEAT	06TABS tritricum tu
857	39	83.0	201	2	07ANQ4_BACCI	07ANQ4 bacillus ce	930	38	80.9	189	2	06JACS_TRTTU	06JACS tritricum tu
858	39	83.0	202	2	08CXG2_OCEIH	08CXG2 oceanobacill	931	38	80.9	189	2	06AAY6_PROAC	06AAY6 propionibac
859	39	83.0	222	2	057W40_9TRYP	057W40 trypanosoma	932	38	80.9	190	2	0810L8_DROME	0810L8 drosophila
860	39	83.0	222	2	09NS57_CAEEL	09NS57 caenorthabdi	933	38	80.9	192	2	098EAT_RHILLO	098EAT rhizobium l
861	39	83.0	260	2	0619U4_CAEER	0619U4 caenorthabdi	934	38	80.9	196	2	09FUR2_PPUAV	09FUR2 prunus aviu
862	39	83.0	283	2	050Y72_IDTIO	050Y72 idiomarina	935	38	80.9	198	2	095276_OSTOS	095276 oseretragia
863	39	83.0	318	2	09L2A3_STRCO	09L2A3 streptomyce	936	38	80.9	203	2	04M0U5_9BURI	04M0U5 burkholderi
864	39	83.0	328	2	082JCS_STRAW	082JCS streptomyce	937	38	80.9	207	2	08FSD2_COREF	08FSD2 corynebacter
865	39	83.0	351	2	041046_CHVPI	041046 paramecium	938	38	80.9	207	2	08NT71_CORGL	08NT71 corynebacter
866	39	83.0	358	2	084449_CHVPI	084449 paramecium	939	38	80.9	208	2	098G37_RHILLO	098G37 rhizobium l
867	39	83.0	372	2	064MVB_9ARCH	064MVB uncultured	940	38	80.9	210	2	08H703_PHTIN	08H703 phytophthor
868	39	83.0	392	2	05GMV1_ORISA	05GMV1 oryza sativ	941	38	80.9	211	2	04SYCS_TETNG	04SYCS tetradon n
869	39	83.0	392	2	08VZQ0_ARATH	08VZQ0 arabidopsis	942	38	80.9	212	2	05YMW1_NOCFA	05YMW1 nocardia fa
870	39	83.0	421	2	06D7Q8_ERWCT	06D7Q8 erwina car	943	38	80.9	214	2	06XN30_RHOER	06XN30 rhodococcus
871	39	83.0	498	2	0648T6_9ARCH	0648T6 uncultured	944	38	80.9	216	2	09LRP6_CHILO	09LRP6 chlorocella v
872	39	83.0	507	2	064CN9_9ARCH	064CN9 uncultured	945	38	80.9	223	2	05OKB1_EMITHU	05OKB1 emiliania h
873	39	83.0	508	2	064AW1_9ARCH	064AW1 uncultured	946	38	80.9	223	2	08RA15_THERTN	08RA15 thermotoga
874	39	83.0	508	2	064AR4_9ARCH	064AR4 uncultured	947	38	80.9	226	2	04XNK9_PLACH	04XNK9 plasmodium
875	39	83.0	616	2	051BS8_ENTHI	051BS8 entamoeba h	948	38	80.9	228	2	04V963_BRARE	04V963 brachydanio
876	39	83.0	622	2	050XV6_ENTHI	050XV6 entamoeba h	949	38	80.9	234	2	07RINO_GIALA	07RINO giardia lam
877	39	83.0	658	2	07UMQ6_RHOBA	07UMQ6 rhodospirill	950	38	80.9	235	2	097451_GIALA	097451 giardia lam
878	39	83.0	2567	2	090574_CHICK	090574 gallus gall	951	38	80.9	234	2	07XZ51_GRIJA	07XZ51 griffithsia
879	39	83.0	5825	2	082731_VICFA	082731 victoria faba	952	38	80.9	235	2	06PZEB_BRANA	06PZEB brassica na
880	39	83.0	26	2	09S880_SPTOL	09S880 spinacia ol	953	38	80.9	235	2	04J305_CORUK	04J305 corynebacter
881	38	80.9	63	2	07M1Q4_SOTBN	07M1Q4 glycine max	954	38	80.9	238	2	057AS4_BRUAB	057AS4 bruceella ab
882	38	80.9	76	2	06JAC2_WHEAT	06JAC2 tritricum ae	955	38	80.9	240	2	08FYAS_BRUSU	08FYAS bruceella su
883	38	80.9	100	2	09LXZ8_ARATH	09LXZ8 arabidopsis	956	38	80.9	248	2	05YBC2_9CHLO	05YBC2 helicospori
884	38	80.9	106	2	071VT1_LISMF	071VT1 listeria mo	957	38	80.9	242	2	04PLZ2_IXOSC	04PLZ2 ixodes scap
885	38	80.9	106	2	0926S8_LISIN	0926S8 listeria in	958	38	80.9	247	2	05F472_CHICK	05F472 gallus gall
886	38	80.9	106	2	08Y3KS_LISMO	08Y3KS listeria mo	959	38	80.9	249	2	08X1D2_COCIM	08X1D2 coccidioid
887	38	80.9	107	2	09GTJ2_HETGL	09GTJ2 heterodera	960	38	80.9	253	2	05AFB1_CCNAL	05AFB1 candida alb
888	38	80.9	108	2	07XYD7_WHEAT	07XYD7 tritricum ae	961	38	80.9	266	2	05COA7_SCHJA	05COA7 schistosoma
889	38	80.9	110	2	072HU9_THET2	072HU9 thermus the	962	38	80.9	271	2	0604D2_METCA	0604D2 methylococc
890	38	80.9	110	2	05SHI3_THET2	05SHI3 thermus the	963	38	80.9	287	2	07PT26_ANOGA	07PT26 anopheles g
891	38	80.9	111	2	093CWB_LACSK	093CWB lactobacill	964	38	80.9	298	2	09MB13_ORYSA	09MB13 oryza sativ
892	38	80.9	112	2	06TAB9_WHEAT	06TAB9 tritricum ae	965	38	80.9	318	1	MDP1_YEAST	MDP1 yeast
893	38	80.9	112	2	08D2Q0_WIGBR	08D2Q0 wigglewort	966	38	80.9	327	2	06PTP9_BRARE	06PTP9 brachyromy
894	38	80.9	116	2	07QX91_GIALA	07QX91 giardia lam	967	38	80.9	337	2	05XWD1_ENTHI	05XWD1 entamoeba h
895	38	80.9	116	2	09U015_GIALA	09U015 giardia lam	968	38	80.9	338	2	09PBH0_XYLFA	09PBH0 xyella fas
896	38	80.9	116	2	06MRB6_BDEBA	06MRB6 bdellovibri	969	38	80.9	341	2	06DH89_BRARE	06DH89 brachydanio
897	38	80.9	119	2	05OVME_ENTHI	05OVME entamoeba h	970	38	80.9	347	2	087C67_XYLFT	087C67 xyella fas
898	38	80.9	121	2	08BTLH_CORGL	08BTLH corynebacte	971	38	80.9	347	2	04UIS4_THEAN	04UIS4 theileria a
899	38	80.9	127	2	05U0U8_ENTHI	05U0U8 entamoeba h	972	38	80.9	354	2	09BK83_GIALA	09BK83 giardia lam
900	38	80.9	133	2	05CE99_CRYHO	05CE99 cryptospori	973	38	80.9	359	1	PD12_SCHPO	PD12 schistosoma
901	38	80.9	134	2	07XY30_GRIJA	07XY30 griffithsia	974	38	80.9	359	1	TTGA_ASPNG	TTGA aspergillus
902	38	80.9	134	2	028984_ARCFU	028984 archaeglob	975	38	80.9	359	2	04F7X2_SCHPO	04F7X2 schistosom
903	38	80.9	134	2	07OSG3_GIALA	07OSG3 giardia lam	976	38	80.9	359	2	P93358_TOBAC	P93358 nicotiana t
904	38	80.9	134	2	09NDB1_GIALA	09NDB1 giardia lam	977	38	80.9	360	2	086UY0_HUMAN	086UY0 homo sapien
905	38	80.9	135	2	0582J4_9TRYP	0582J4 trypanosoma	978	38	80.9	361	1	PD1K6_ARATH	PD1K6 arabidopsis
906	38	80.9	138	2	051X15_PROWI	051X15 proteobacteria	979	38	80.9	361	2	0546R3_ARATH	0546R3 arabidopsis
907	38	80.9	142	2	07QJ17_ANOGA	07QJ17 anopheles g	980	38	80.9	363	2	06EH23_HUMAN	06EH23 homo sapien

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981 38 80.9 363 2 0861A3_DICDI 0861A3_diccyostei1
982 38 80.9 363 2 015735_DICDI 015735_diccyostei1
983 38 80.9 364 1 PD1A6_MEDSA P38661_medicago aa
984 38 80.9 364 2 096W60_ASPTU 096W60_aspergillus
985 38 80.9 364 2 06CC54_YARLI 06CC54_yarrowia 11
986 38 80.9 364 2 095T75_DROME 095T75_drosophila
987 38 80.9 366 2 05C145_SCHJA 05C145_schistosoma
988 38 80.9 366 2 05EUD6_MAIZE 05EUD6_zea mays 1m
989 38 80.9 367 2 075M08_ORYSA 075M08_oryza sativ
990 38 80.9 367 2 05EUD7_MAIZE 05EUD7_zea mays 1m
991 38 80.9 368 2 05BHA5_EBMTU 05BHA5_aspergillus
992 38 80.9 368 2 04WT19_ASPTU 04WT19_aspergillus
993 38 80.9 368 2 050U17_ENTHI 050U17_entamoeba h
994 38 80.9 369 1 ERP38_NEUCR 092249_neurospora
995 38 80.9 369 2 091815_FUGRU 091815_fugu rubrip
996 38 80.9 371 2 05EMX2_MAGGR 05EMX2_magnaporthe
997 38 80.9 371 2 052C23_MAGGR 052C23_magnaporthe
998 38 80.9 371 2 0942L2_ORYSA 0942L2_oryza sativ
999 38 80.9 371 2 082WE2_NITEU 082WE2_nitrososoma
1000 38 80.9 376 2 09FEG4_TRITU 09FEG4_triticum tu

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ALIGNMENTS

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RESULT 1
04T7B7_TETNG
ID 04T7B7_TETNG PRELIMINARY; PRT; 80 AA.
AC 04T7B7;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF8161, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0005833001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxId=99883;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Benoit A.,
RA Nicand S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cartolico L., Poulain J., De Bernardis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Medirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Croillius H.;
RT "Genome duplication in the teleost fish Tetraodon nigriviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAPE01008161; CAP91215.1; -; Genomic_DNA.
FT NON TER 1 80
FT NON TER 1 80
SQ SEQUENCE 80 AA; 8611 MW; 64705ABEA4A5620B CRC64;

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Query Match 100.0%; Score 47; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 WCGPCK 6
Db 2 WCGPCK 7

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RESULT 2
060744_HUMAN
ID 060744_HUMAN PRELIMINARY; PRT; 84 AA.
AC 060744;
DT 01-ANG-1998 (TReMBLrel. 07, Created)
DT 01-ANG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Thioredoxin delta 3 (Fragment).
GN Name=TXN delta 3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OC NCBI_TaxId=9606;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Wang Y., Wang Y.G., Zhang Y., Yuan Y., Ma D.;
RT "An alternative splice variant of human thioredoxin.";
RL Chin. Sci. Bull. 43:292-295(1998).
DR EMBL; AF065241; AAC17430.1; -; mRNA.
DR HSSP; P10599; 1ERR.
DR SMR; 060744; 1-84.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR006663; Thioredox dom2.
DR InterPro; IPR012336; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF00085; Thioredoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Redox-active center.
FT NON TER 1 84
SQ SEQUENCE 84 AA; 9321 MW; 818FB84BA865721 CRC64;

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Query Match 100.0%; Score 47; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 WCGPCK 6
Db 30 WCGPCK 35

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RESULT 3
05T936_HUMAN
ID 05T936_HUMAN PRELIMINARY; PRT; 85 AA.
AC 05T936;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Thioredoxin.
GN Name=TXN; ORFNames=RP11-427L11.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OC NCBI_TaxId=9606;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Williams S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL158158; CAL14067.1; -; Genomic_DNA.
DR SMR; 05T936; 1-85.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.

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DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR012336; ThioRedoxin-1like.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Redox-active center.
SQ SEQUENCE 85 AA; 9452 MW; 3CC6254BD6A1D66F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 4
OSV0J2_HALMA PRELIMINARY; PRT; 88 AA.
ID OSV0J2_HALMA PRELIMINARY; PRT; 88 AA.
AC OSV0J2;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE ThioRedoxin.
GN Name=trxA3; OrderedLocuNames=trxA3;2110;
OS Halobacterium marismortui (Halobacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Halobacteriales;
OC NCB1 TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Borneau R., Facciotti M.T., Pan M., Gushman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Halobacterium marismortui: a halophilic archaeon from
RT the Dead Sea."
RL Genome Res. 14:2221-2234 (2004).
DR EMBL; AY596297; AAV46961.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR006663; ThioRedox_dom2.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR Complete proteome.
SQ SEQUENCE 88 AA; 10011 MW; CFE9B8FAC1F69857 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 12 WCGPCK 17

RESULT 5
OSV0J2_HALMA PRELIMINARY; PRT; 89 AA.
ID OSV0J2_HALMA PRELIMINARY; PRT; 89 AA.
AC OSV0J2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ThioRedoxin.
GN Name=trxA2; OrderedLocuNames=VNG2600G;
OS Halobacterium salinarum (Halobacterium salinarum).
OC Archaea; Euryarchaeota; Halobacteriales;

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OC Halobacteriaceae; Halobacterium.
OX NCB1 TaxID=2242;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sirogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonksi P.E., Krebs W.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freltas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
DR EMBL; AE005133; AAG20641.1; -; Genomic DNA.
DR PIR; E84409; E84409.
DR HSSP; P10599; 1BRV.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR006663; ThioRedox_dom2.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR Complete proteome.
SQ SEQUENCE 89 AA; 10019 MW; BDP97B3496F70BFF CRC64;

Query Match 100.0%; Score 47; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 12 WCGPCK 17

RESULT 6
THIO_THIRO
ID THIO_THIRO STANDARD; PRT; 91 AA.
AC P96132;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE ThioRedoxin (TRX) (Fragment).
GN Name=trxA;
OS Thiocapsa roseopersicina.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Thiocapsa.
OX NCB1 TaxID=1058;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ML;
RA Haverkamp T., Schwenn J.D.;
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (by
CC similarity).
CC -!- SIMILARITY: Belongs to the thioRedoxin family.
CC -!- SIMILARITY: Contains 1 thioRedoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U75512; AAB36882.1; -; Genomic DNA.
CC HSSP; P00274; 2TRX.

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DR InterPro: IPR006662; ThioRed.  
DR InterPro: IPR006663; ThioRedox dom2.  
DR InterPro: IPR005746; ThioRedoxin.  
DR InterPro: IPR012336; ThioRedoxin-like.  
DR InterPro: IPR012335; ThioRedoxin-fold.  
DR Pfam: PF00085; ThioRedoxin_1.  
DR PRINTS: PR00421; THIOREDOXIN.  
DR TIGRPFAM: TIGR01068; thioRedoxin; 1.  
DR PROSITE: PS00194; THIOREDOXIN; 1.  
KM Electron transport; Redox-active center; Transport.  
FT DISULFID 33 36 Redox-active (By similarity).  
FT NON_TER 91 91  
SQ SEQUENCE 91 AA; 10209 MW; 385DC641F42585D4 CRC64;  
  
Query Match 100.0%; Score 47; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 WCGPCK 6  
Db 32 WCGPCK 37  
  
RESULT 7  
Q4XKV3 PLACH  
ID Q4XKV3 PLACH PRELIMINARY; PRT; 95 AA.  
AC Q4XKV3;  
DT 13-SRP-2005 (TrEMBLrel. 31, Created)  
DT 13-SRP-2005 (TrEMBLrel. 31, Last sequence update)  
DE ThioRedoxin, putative (Fragment).  
GN ORFNames=PCJ30021.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI_TaxID=5825;  
RN NUCLEOTIDE SEQUENCE.  
RP Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses.";  
RT Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: CAJ01005024; CAH82459.1; -; Genomic_DNA.  
DR InterPro: IPR006662; ThioRed.  
DR InterPro: IPR006663; ThioRedox dom2.  
DR InterPro: IPR012336; ThioRedoxin-like.  
DR InterPro: IPR012335; ThioRedoxin-fold.  
DR Pfam: PF00085; ThioRedoxin_1.  
DR PRINTS: PR00421; THIOREDOXIN.  
DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN_1.  
KM Redox-active center.  
FT NON_TER 1 1  
SQ SEQUENCE 95 AA; 10666 MW; E144E16B1980C6C CRC64;  
  
Query Match 100.0%; Score 47; DB 2; Length 95;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 WCGPCK 6  
Db 20 WCGPCK 25  
  
RESULT 8  
Q4Z518 PLABE  
ID Q4Z518 PLABE PRELIMINARY; PRT; 96 AA.  
  
AC Q4Z518;  
DT 13-SRP-2005 (TrEMBLrel. 31, Created)  
DT 13-SRP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SRP-2005 (TrEMBLrel. 31, Last annotation update)  
DE ThioRedoxin, putative (Fragment).  
GN ORFNames=PB000593.00.0;  
OS Plasmodium berghei.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI_TaxID=5821;  
RN NUCLEOTIDE SEQUENCE.  
RP Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses.";  
RT Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: CAJ01000448; CAH94443.1; -; Genomic_DNA.  
DR InterPro: IPR006662; ThioRed.  
DR InterPro: IPR006663; ThioRedox dom2.  
DR InterPro: IPR012336; ThioRedoxin-like.  
DR InterPro: IPR012335; ThioRedoxin-fold.  
DR Pfam: PF00085; ThioRedoxin_1.  
DR PRINTS: PR00421; THIOREDOXIN.  
DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN_1.  
KM Redox-active center.  
FT NON_TER 1 1  
SQ SEQUENCE 96 AA; 10769 MW; FC08612C6FECSAAB9 CRC64;  
  
Query Match 100.0%; Score 47; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 WCGPCK 6  
Db 21 WCGPCK 26  
  
RESULT 9  
Q5LB12 BACEN  
ID Q5LB12 BACEN PRELIMINARY; PRT; 98 AA.  
AC Q5LB12;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Putative thioRedoxin.  
GN OrderdicusNames=BF3015;  
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).  
OC Bacteriia; Bacteroidetes; Bacteroidales;  
OC Bacteriia; Bacteroidetes; Bacteroidales (class); Bacteroidales;  
OX NCBI_TaxID=272559;  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RP PubMed=15746427; DOI=10.1126/science.1107008;  
RX Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,  
RA Abratt V., Leonard N., Poxton I., Duerden B., Harris B., Quail M.A.,  
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,  
RA Line A., Lord A., Noperczak H., Ormond D., Price C.,  
RA Rabinovitch E., Woodward J., Barrell B.G., Parkhill J.;  
RT "Extensive DNA inversions in the B. fragilis genome control variable  
RT gene expression.";  
RT Science 307:1463-1465(2005).  
RL EMBL: CR626927; CAH08710.1; -; Genomic_DNA.  
DR EMBL: IPR006662; ThioRed.  
DR InterPro: IPR006663; ThioRedox dom2.  
DR InterPro: IPR005746; ThioRedoxin-like.  
DR InterPro: IPR012336; ThioRedoxin-like.
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AC Q4Z518;  
DT 13-SRP-2005 (TrEMBLrel. 31, Created)  
DT 13-SRP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SRP-2005 (TrEMBLrel. 31, Last annotation update)  
DE ThioRedoxin, putative (Fragment).  
GN ORFNames=PB000593.00.0;  
OS Plasmodium berghei.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI_TaxID=5821;  
RN NUCLEOTIDE SEQUENCE.  
RP Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses.";  
RT Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: CAJ01000448; CAH94443.1; -; Genomic_DNA.  
DR InterPro: IPR006662; ThioRed.  
DR InterPro: IPR006663; ThioRedox dom2.  
DR InterPro: IPR012336; ThioRedoxin-like.  
DR InterPro: IPR012335; ThioRedoxin-fold.  
DR Pfam: PF00085; ThioRedoxin_1.  
DR PRINTS: PR00421; THIOREDOXIN.  
DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN_1.  
KM Redox-active center.  
FT NON_TER 1 1  
SQ SEQUENCE 96 AA; 10769 MW; FC08612C6FECSAAB9 CRC64;  
  
Query Match 100.0%; Score 47; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 WCGPCK 6  
Db 21 WCGPCK 26  
  
RESULT 9  
Q5LB12 BACEN  
ID Q5LB12 BACEN PRELIMINARY; PRT; 98 AA.  
AC Q5LB12;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Putative thioRedoxin.  
GN OrderdicusNames=BF3015;  
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).  
OC Bacteriia; Bacteroidetes; Bacteroidales;  
OC Bacteriia; Bacteroidetes; Bacteroidales (class); Bacteroidales;  
OX NCBI_TaxID=272559;  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RP PubMed=15746427; DOI=10.1126/science.1107008;  
RX Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,  
RA Abratt V., Leonard N., Poxton I., Duerden B., Harris B., Quail M.A.,  
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,  
RA Line A., Lord A., Noperczak H., Ormond D., Price C.,  
RA Rabinovitch E., Woodward J., Barrell B.G., Parkhill J.;  
RT "Extensive DNA inversions in the B. fragilis genome control variable  
RT gene expression.";  
RT Science 307:1463-1465(2005).  
RL EMBL: CR626927; CAH08710.1; -; Genomic_DNA.  
DR EMBL: IPR006662; ThioRed.  
DR InterPro: IPR006663; ThioRedox dom2.  
DR InterPro: IPR005746; ThioRedoxin-like.  
DR InterPro: IPR012336; ThioRedoxin-like.
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DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome.
SQ SEQUENCE 98 AA; 11253 MW; FA22303A85FC04D7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 22 WCGPCK 27

RESULT 10
O6ARG1_BACFR PRELIMINARY; PRT; 98 AA.
ID O6ARG1_BACFR PRELIMINARY; PRT; 98 AA.
AC O6ARG1_
RT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ThioRedoxin.
GN OrderedLocusNames=BF3175;
OS Bacteroides fragilis;
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;
EX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kunara S., Hattori M., Hayashi T., Ohnishi Y.,
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
DR EMBL; AP006841; BAD49920.1; -; Genomic_DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin; 1.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome.
KV Complete proteome.
SQ SEQUENCE 98 AA; 11253 MW; FA22303A85FC04D7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 22 WCGPCK 27

RESULT 11
O8AB91_BACTN PRELIMINARY; PRT; 99 AA.
ID O8AB91_BACTN PRELIMINARY; PRT; 99 AA.
AC O8AB91;
RT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE ThioRedoxin C-2.
GN OrderedLocusNames=BT0219;
OS Bacteroides thetaiotaomicron.

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OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VP1-5482 / ATCC 29148;
RA MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AE016926; AAO75326.1; -; Genomic_DNA.
DR HSSP; P80579; 1NM2.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR006663; ThioRedox dom2.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KV Complete proteome.
SQ SEQUENCE 99 AA; 11344 MW; 2037C6E75986C413 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 22 WCGPCK 27

RESULT 12
THIO_MYCGA STANDARD; PRT; 100 AA.
ID THIO_MYCGA STANDARD; PRT; 100 AA.
AC Q9REP9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE ThioRedoxin (Trx).
GN Name=trx; Synonyms=trx; OrderedLocusNames=MYCGA6330;
GN ORFNames=MGA_0452;
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A5969var.B;
RX MEDLINE=22830409; PubMed=12949158; DOI=10.1099/mic.0.26427-0;
RA Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F.,
RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
RT "The complete genome sequence of the avian pathogen Mycoplasma
RT gallisepticum strain R(10w).";
RL Microbiology 149:2307-2316(2003).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (by
CC similarity).
CC -!- SIMILARITY: Belongs to the thioRedoxin family.
CC -!- SIMILARITY: Contains 1 thioRedoxin domain.

```

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC EMBL; U35043; AAF1904.1; -; Genomic DNA.
CC EMBL; AE016969; AAP56983.1; ALT_INIT; Genomic DNA.
CC HSSP; P80579; 1QW.
CC InterPro; IPR006662; ThioRed.
CC InterPro; IPR006663; ThioRedox dom2.
CC InterPro; IPR005746; ThioRedoxin.
CC InterPro; IPR012336; ThioRedoxin-like.
CC InterPro; IPR012335; ThioRedoxin-fold.
CC InterPro; IPR011594; ThioRedoxin-like.
CC Pfam; PF00085; ThioRedoxin; 1.
CC PRINTS; PR00421; THIOREDOXIN.
CC PRODOM; PD003679; ThioRedoxin-like; 1.
CC TIGRFAms; TIGR01068; thioRedoxin; 1.
CC Complete proteome; Electron transport; Redox-active center; Transport.
CC DISULFID 29 32 Redox-active (By similarity).
CC CONFLICT 15 15 S -> T (in Ref. 1).
CC CONFLICT 74 74 V -> I (in Ref. 1).
CC CONFLICT 86 86 R -> I (in Ref. 1).
CC FT SEQUENCE 100 AA; 11549 MW; B2A8ADAC82BA3968 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGPCPK 6
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|
Db 28 WGPCPK 33

RESULT 13
QJUN64 MYCGA PRELIMINARY; PRT; 100 AA.
AC QJUN64;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-APR-2004 (TREMblrel. 26, Last annotation update)
DE ThioRedoxin.
DE Name=trx I;
GN Mycoplasma gallisepticum.
OS Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OC NCBI_TaxId=2096;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=AS969;
RC MEDLINE=92038016; PubMed=1718781; DOI=10.1016/0014-5793(91)81106-1;
RA Skarlov A.V., Bibilaashvili R.S.; 56 genome contains three regions
RT "Mycoplasma gallisepticum strain AS969 genome and
RT hybridizing with 16 S rRNA and two regions hybridizing with 23 S and 5
RT S rRNA."
RL FEBS Lett. 291:71-74(1991).
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=AS969;
RC MEDLINE=96320025; PubMed=8754006;
RA Skarlov A.V., Bibilaashvili R.Sh.;
RT "A physical map of Mycoplasma gallisepticum strain AS969 genome and
RT determination of its positions on certain genes."
RL Mol. Biol. (Mosk.) 30:585-594(1996).
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=AS969;
RC MEDLINE=96320025; PubMed=8754006;
RA Skarlov A.V., Bibilaashvili R.;
RT Submittal (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; U35043; AAP56983.1; -; Genomic DNA.
DR HSSP; P80579; 1QW2.
DR GO; GO:0005489; F:electron transporter activity; IEA.

DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin-fold.
DR InterPro; IPR011594; ThioRedoxin-like.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PRODOM; PD003679; ThioRedoxin-like; 1.
DR TIGRFAms; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR SEQUENCE 100 AA; 11577 MW; C2DFB426DBF3C8 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGPCPK 6
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|
Db 28 WGPCPK 33

RESULT 14
THIO1 CHLRE STANDARD; PRT; 101 AA.
AC Q8KEA4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE ThioRedoxin 1 (Trx-1).
GN Name=trx1; OrderedLocustNames=CT0785;
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobaculum.
OC NCBI_TaxId=1097;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=TLS / ATCC 49652 / DSM 12025;
RC MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.U., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolony D.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nieman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -!- SIMILARITY: Belongs to the thioRedoxin family.
CC -!- SIMILARITY: Contains 1 thioRedoxin domain.
CC CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE006470; AAM72022.1; -; Genomic DNA.
CC HSSP; P23400; 1DBY.
DR TIGR; CT0785; -;
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin-fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAms; TIGR01068; thioRedoxin; 1.

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DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 25 Redox-active (By similarity).
SQ SEQUENCE 101 AA, 11247 MW, BA78E511900B754 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 101;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 24 WCGPCK 29

RESULT 15
06KIE7_MYCMO PRELIMINARY; PRT; 101 AA.
AC 06KIE7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN Name=trxA; OrderedLocustNames=MMOB1430;
OS Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=163K / ATCC 43663;
RX PubMed=15289470; DOI=10.1101/gr.2674004;
RA Jaffe J.D., Strange-Thomann N., Smith C., Decaprio D., Fisher S.,
RA Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,
RA Kodira C.D., Major J., Wang S., Wilkinson J., Nicol R., Nussbaum C.,
RA Birren B., Berg H.C., Church G.M.;
RT "The complete genome and proteome of Mycoplasma mobile.";
RL Genome Res. 14:1447-1461(2004).
DR EMBL; AE017337; AAT27629.1; -; Genomic_DNA.
DR HSSP; P10599; IAUU.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioedoxin.
DR InterPro; IPR006663; Thioedoxin_dom2.
DR InterPro; IPR012336; Thioedoxin-like.
DR InterPro; IPR012335; Thioedoxin_fold.
DR Pfam; PF00085; Thioedoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Complete proteome.
SQ SEQUENCE 101 AA, 11700 MW, 8D3C45CCB4CAGFA4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 101;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 28 WCGPCK 33

RESULT 16
THIO_CHLVCV STANDARD; PRT; 102 AA.
ID THIO_CHLVCV
AC P52327;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioedoxin (TRX).
GN Name=trxA; Synonyms=trix; OrderedLocustNames=CCA00080;
OS Chlamydomonas reinhardtii.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonadales.
OX NCBI_TaxID=83357;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=GPIC;
RX MEDLINE=97090413; PubMed=8936321;
RA Roddy D.D., Chesbro B.B., Heinzen R.A., Hackett T.;
RT "A 28 kDa major immunogen of Chlamydia psittaci shares identity with
RT Mip proteins of Legionella spp. and Chlamydia trachomatis-cloning and
RT characterization of the C. psittaci mip-like gene.";
RL Microbiology 142:945-953(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J.F., Holtzapple E.K., Khouri H.M., Fedorova N.B.,
RA Carthy H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.J.,
RA White O., Salzberg S.L., Heia R.-C., McClarty G., Rank R.G.,
RA Bavoil P.M., Frazer C.M.;
RT "Genome sequence of Chlamydomonas reinhardtii (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiae.";
RL Nucleic Acids Res. 31:2134-2147(2003).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -!- SIMILARITY: Belongs to the thioedoxin family.
CC -!- SIMILARITY: Contains 1 thioedoxin domain.
CC -----
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CC removed.
CC -----
DR EMBL; I39892; AAB41348.1; -; Genomic_DNA.
DR EMBL; AE016994; AAP04832.1; -; Genomic_DNA.
DR HSSP; P80579; IQUM.
DR TIGR; CCA00080; -.
DR InterPro; IPR006662; Thioedoxin.
DR InterPro; IPR006663; Thioedoxin_dom2.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR012336; Thioedoxin-like.
DR InterPro; IPR012335; Thioedoxin_fold.
DR Pfam; PF00085; Thioedoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfam; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 28 Redox-active (By similarity).
SQ SEQUENCE 102 AA, 11159 MW, F1B57486973A6ED4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 27 WCGPCK 32

RESULT 17
THIO_CHLVCV STANDARD; PRT; 102 AA.
ID THIO_CHLVCV
AC O9PJK3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioedoxin (TRX).
GN Name=trxA; Synonyms=trix; OrderedLocustNames=TC0826;
OS Chlamydomonas reinhardtii.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonadales.
OX NCBI_TaxID=83357;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MoPh / N159;

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RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunnham R.C., Shen C., Gill S.R., Heideberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Uterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Knouti H.M., Craven B., Bowman C.,
RA Dodson R.U., Gwin M.L., Nelson W.C., Deboy R.T., Kolonay J.F.,
RA McCarty G., Salzberg S.L., Eisen J.A., Fraser C.M.,
RT "Genome sequences of Chlamydia trachomatis MOpn and Chlamydia
RT pneumoniae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -----
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
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CC removed.
CC -----
CC EMBL, AF002349; AAF39627.1; -; Genomic_DNA.
DR PIR: C81660; C81660.
DR HSSP: P80579; 1QW.
DR TIGR: TC0826; -.
DR InterPro: IPR006662; Thiored.
DR InterPro: IPR006663; Thioredox dom2.
DR InterPro: IPR005746; Thioredoxin.
DR InterPro: IPR012336; Thioredoxin-like.
DR InterPro: IPR012335; Thioredoxin_fold.
DR Pfam: PF00085; Thioredoxin_1.
DR PRINTS: PR00421; THIOREDOXIN.
DR TIGRFAMs: TIGR01068; thioredoxin; 1.
DR PROSITE: PS00194; THIOREDOXIN; 1.
DR Complete proteome; Electron transport; Redox-active center; Transport.
KM DISULFID 28 31 Redox-active (By similarity).
SQ SEQUENCE 102 AA; 1147 MW; C171B646D393428C CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 27 WCGPCK 32

RESULT 18
THIO_CHLTR STANDARD; PRT; 102 AA.
ID THIO_CHLTR
AC 084544;
DT 30-MAY-2000 (Rel. 39, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Thioredoxin (TRX).
GN Name=trx; OrderedLocustNames=CT539;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=UW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136; DOI=10.1126/science.282.5389.754;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Ollinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -----

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CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
CC EMBL, AE001324; AAC68141.1; -; Genomic_DNA.
DR PIR: B71503; B71503.
DR HSSP: P80579; 1QW.
DR PHCI-2DPAGE; 084544; -.
DR InterPro: IPR006662; Thiored.
DR InterPro: IPR006663; Thioredox dom2.
DR InterPro: IPR005746; Thioredoxin.
DR InterPro: IPR012336; Thioredoxin-like.
DR InterPro: IPR012335; Thioredoxin_fold.
DR Pfam: PF00085; Thioredoxin_1.
DR PRINTS: PR00421; THIOREDOXIN.
DR TIGRFAMs: TIGR01068; thioredoxin; 1.
DR PROSITE: PS00194; THIOREDOXIN; 1.
DR Complete proteome; Electron transport; Redox-active center; Transport.
KM DISULFID 28 31 Redox-active (By similarity).
SQ SEQUENCE 102 AA; 1197 MW; 8FAE022A5C980BE1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 27 WCGPCK 32

RESULT 19
THIO_MYCGE STANDARD; PRT; 102 AA.
ID THIO_MYCGE
AC P47370; Q49453;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioredoxin (Trx).
GN Name=trx; Synonyms=trx; OrderedLocustNames=MG124;
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxId=2097;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.W., Phillips C.A., Merrick J.N.,
RA Tomb J.F., Dougherty B.A., Bock K.F., Hu P.-C., Luster T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 1-21.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bock K.F., Hutchison C.A. III,
RA "A survey of the Mycoplasma genitalium genome by using random
RT sequencing."
RL J. Bacteriol. 175:7918-7930(1993).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----

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CC removed.
CC -----
DR EMBL; U39693; AAC71342.1; -; Genomic DNA.
DR EMBL; U01796; AAD12321.1; ALT_INIT; Genomic DNA.
DR PIR; G64213; G64213.
DR HSSP; P07591; 1F86.
DR TIGR; MG124; -.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 30 33 active (By similarity).
SQ SEQUENCE 102 AA; 11498 MW; FC08F02C4170EA2D CRC64;

Query Match 100.0%; Score 47; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 20
THIO_MYCPN STANDARD; PRT; 102 AA.
AC P75512;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE ThioRedoxin (TRX).
GN Name=trx; Synonyms=trx; OrderedLocustNames=MEN263; ORFNames=MP570;
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatetaceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97346047; PubMed=9202470;
RA Ben-Menachem G., Himmelreich R., Hermann R., Aharonowitz Y.,
RA Rotem S.;
RT "The thioRedoxin reductase system of mycoplasmas";
RN Microbiology 143:1933-1940(1997).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
RA Himmelreich R., Hilbert H., Plagens H., Firl E., Li B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae";
RN Nucleic Acids Res. 24:4420-4449(1996).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -!- SIMILARITY: Belongs to the thioRedoxin family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
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CC removed.
CC -----
DR EMBL; U51987; AAC45450.1; -; Genomic DNA.
DR EMBL; AE000056; AAB96218.1; -; Genomic DNA.
DR PIR; S73896; S73896.
DR HSSP; P23400; 1DBY.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 30 33 active (By similarity).
SQ SEQUENCE 102 AA; 11215 MW; 0D17B97E976FC144 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 21
THIO_SCHPO STANDARD; PRT; 102 AA.
AC O14463; P58265; Q9UTS9;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE ThioRedoxin (TR).
GN Name=trx1; Synonyms=trx2; ORFNames=SPAC7D4_07C;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21167391; PubMed=11267679; DOI=10.1016/S0167-4781(01)00176-2;
RA Cho Y.-W., Shin Y.H., Kim Y.-T., Kim H.-G., Lee Y.-J., Park E.-H.,
RA Fuchs J.A., Lim C.-U.;
RT "Characterization and regulation of Schizosaccharomyces pombe gene
RT encoding thioRedoxin";
RN Biochim. Biophys. Acta 1518:194-199(2001).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=972;
RA Lenaers G., Perret E., Bonin O., Picard A., Caput D.;
RT submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgourou J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltham J., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.U., Hunt S., Jagsels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volkart G., Aert R., Robben J., Gymnopoulos B.,
RA Weltjens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
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RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,
 RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
 RA Pohl T.M., Egger P., Zimmermann W., Wedler H., Wambutt R., Punnett B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelure V., Motter S.,
 RA Lucan M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Domiguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Ceruti L., Lowe T., McCombie W.R., Paulsen I., Porashkin J.,
 RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*."
 RL Nature 415:871-880(2002).
 CC -I- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC -I- SIMILARITY: Belongs to the thioredoxin family.
 CC -I- SIMILARITY: Contains 1 thioredoxin domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AF251279, AAF76881.1; -, Genomic_DNA.
 CC EMBL, AF192765, AAF05765.1; -, mRNA.
 CC EMBL, AJ003819, CAA06033.1; -, mRNA.
 CC EMBL, Z99532, CAB16724.1; -, Genomic_DNA.
 CC PIR, T39085, T39085.
 CC HSP, P80028, IEP7.
 CC DR GeneDB_Spmbe; SPAC7D4.07c; -.
 CC DR GO; GO:0005737; Cytoplasm; TAS.
 CC DR InterPro; IPR006662; Response to reactive oxygen species; IDA.
 CC DR InterPro; IPR006662; Thioredoxin.
 CC DR InterPro; IPR005746; Thioredoxin.
 CC DR InterPro; IPR012336; Thioredoxin-like.
 CC DR InterPro; IPR012335; Thioredoxin_fold.
 CC DR Pfam; PF00085; Thioredoxin; 1.
 CC DR PRINTS; PR00421; THIOREDOXIN.
 CC DR TIGRfams; TIGR01068; thioredoxin; 1.
 CC DR PROSITE; PS00194; THIOREDOXIN; 1.
 CC KW Complete proteome; Electron transport; Redox-active center; Transport.
 CC FT INIT MET 0 By similarity.
 CC FT ACT SITE 29 29 Nucleophile (By similarity).
 CC FT ACT SITE 32 32 Nucleophile (By similarity).
 CC FT SITE 23 23 Deprotonates C-terminal active site Cys
 CC FT SITE 30 30 (By similarity).
 CC FT SITE 31 31 Contributes to redox potential value (By
 CC FT SITE 31 31 similarity).
 CC FT DISULFID 29 32 Contributes to redox potential value (By
 CC FT CONFLICT 96 101 similarity).
 CC FT CONFLICT 101 101 Redox-active (By similarity).
 CC FT CONFLICT 101 101 ASIKAN -> VRUNRS (in ref. 1; AAF05765).
 CC SQ SEQUENCE 102 AA; 11166 MW; 7069F4ACDAC34595 CRC64;
 CC
 CC Query Match 100.0%; Score 47; DB 1; Length 102;
 CC Best Local Similarity 100.0%; Pred. No. 2.4;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 WCGPCK 6
 CC DB 28 WCGPCK 33
 CC
 CC RESULT 22
 CC TRX1 YEAST STANDARD; PRT; 102 AA.
 CC AC P22217;
 CC DT 01-AUG-1991 (Rel. 19, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 10-MAY-2005 (Rel. 47, Last annotation update)
 CC DE Thioredoxin I (TR-1) (Thioredoxin 2).

GN Name=TRX1; Synonyms=TRX2; Ordered locus names=YLR043C;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OK NCBI_TaxId=4932;
 RN
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=91107668; PubMed=1988444;
 RA Gan Z.-R.;
 RT "Yeast thioredoxin genes."
 RL J. Biol. Chem. 266:1692-1696 (1991).
 RN
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=91225027; PubMed=2026619;
 RA Muller E.G.D.;
 RT "Thioredoxin deficiency in yeast prolongs S phase and shortens the G1
 RT interval of the cell cycle."
 RL J. Biol. Chem. 266:9194-9202 (1991).
 RN
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=1561834;
 RA Muller E.G.D.;
 RT "Thioredoxin genes in *Saccharomyces cerevisiae*: map positions of TRX1
 RT and TRX2."
 RL Yeast 8:117-120 (1992).
 RN
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=S288C / AB972;
 RC MEDLINE=97133267; PubMed=9169871;
 RX Johnston M., Hillier L.W., Riles L., Albermann K., Andre B.,
 RA Ansorge W., Benes V., Brueckner M., Delius H., Dubois E.,
 RA Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U.,
 RA Heumann K., Heuss-Neltzel D., Hilbert H., Hilger F., Kleine K.,
 RA Keutter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T.,
 RA Moestl D., Mueller-Auer S., Nentwich U., Obermayer B., Piravandi E.,
 RA Pohl T.M., Portetelle D., Purnelle B., Reckmann S., Rieger M.,
 RA Rinke M., Rose M., Scharfe M., Scherens B., Scholler F., Schwager C.,
 RA Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M.,
 RA Verhaaselt P., Viereendeels F., Voet M., Volckaert G., Voss H.,
 RA Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A.,
 RA Hant U., Hobeisel J.D.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XII."
 RL Nature 387:87-90 (1997).
 RN
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP STRAIN=S288C;
 RC MARISCHEK G., Rolfs A., Richardson A., Kane M., Bagui M., Taycher E.,
 RA Hu Y., Vamberg F., Weger J., Kramer U., Moreira D., Kelley F.,
 RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
 RA Gonzalez L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
 RA Laber J.;
 RT "Creation of the YFLX clone resource: cloning of *Saccharomyces*
 RT cerevisiae ORFs in the Gateway recombinational cloning system."
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBS databases.
 RN
 RN PROTEIN SEQUENCE OF 1-12, AND TSA1 DEPENDENCE ON THIOREDOXIN.
 RP STRAIN=ATCC 200358 / YNN 295;
 RC MEDLINE=95050519; PubMed=7961686;
 RX Chae H.Z., Chung S.J., Rhee S.G.;
 RT "Thioredoxin-dependent peroxide reductase from yeast."
 RL J. Biol. Chem. 269:27670-27678 (1994).
 RN
 RN PROTEIN SEQUENCE OF 25-33.
 RX MEDLINE=72104597; PubMed=4333602;
 RA Hall D.B., Baldesten A., Holmgren A., Reichard P.;
 RT "The covalently-bound flavin of hepatic monooxygenase. 2.
 RT Identification and properties of cysteinyl riboflavin."
 RL Eur. J. Biochem. 24:328-335 (1971).
 RN
 RN FUNCTION, AND SUPPATE ASSIMILATION AND METHIONINE METABOLISM.
 RP PubMed=3060034; DOI=10.1007/BF00408300;
 RX Schwenn J.D., Krone F.A., Hismann K.;
 RT "Yeast PAPS reductase: properties and requirements of the purified

RT enzyme.";
 RL Arch. Microbiol. 150:313-319 (1988).
 RN [9]
 RP FUNCTION, AND LMA1 COMPLEX.
 RX PubMed=9015301; DOI=10.1083/jcb.136.2.299;
 RA Xu Z., Mayer A., Muller E.G.D., Wickner W.;
 RT "A heterodimer of thioredoxin and I(B)2 cooperates with Sec18p (NSF)
 RL to promote yeast vacuole inheritance.";
 RN J. Cell Biol. 136:299-306 (1997).
 RP FUNCTION, AND INTERACTION WITH SEC18.
 RX PubMed=9657146; DOI=10.1016/S0092-8674(00)81457-9;
 RA Xu Z., Sato K., Wickner W.;
 RT "LMA1 binds to vacuoles at Sec18p (NSF), transfers upon ATP hydrolysis
 RL Cell 93:1125-1134 (1998).
 RN [11]
 RP FUNCTION, AND DOT5 AND TSA2 DEPENDENCE ON THIOREDOXIN.
 RX PubMed=10681558; DOI=10.1074/jbc.275.8.5723;
 RA Park S.G., Cha M.K., Jeong W., Kim I.-H.;
 RT "Distinct physiological functions of thiol peroxidase isoenzymes in
 RL Saccharomyces cerevisiae.";
 RN J. Biol. Chem. 275:5723-5732 (2000).
 RP FUNCTION, AND REDUCTION OF AHP1.
 RX MEDLINE=99143107; PubMed=9988687; DOI=10.1074/jbc.274.8.4537;
 RA Lee J., Spector D., Godon C., Labarre J., Toledano M.B.;
 RT "A new antioxidant with alkyl hydroperoxide defense properties in
 RL yeast.";
 RN J. Biol. Chem. 274:4537-4544 (1999).
 RP FUNCTION, AND PROTECTION AGAINST REDUCING STRESS.
 RX PubMed=12410842;
 RA Trotter E.W., Grant C.M.;
 RT "Thioredoxins are required for protection against a reductive stress
 RL in the yeast Saccharomyces cerevisiae.";
 RN Mol. Microbiol. 46:869-878 (2002).
 RP FUNCTION, AND REGULATION OF HVR1/GPX3.
 RX PubMed=12437921; DOI=10.1016/S0092-8674(02)01048-6;
 RA Delaney A., Pflieger D., Barrault M.-B., Vinh J., Toledano M.B.;
 RT "A thiol peroxidase is an H2O2 receptor and redox-transducer in gene
 RL activation.";
 RN Cell 111:471-481 (2002).
 RP REVIEW, AND OXIDATIVE STRESS.
 RX PubMed=11018134; DOI=10.1146/annurev.micro.54.1.439;
 RA Carnel-Harel O., Storz G.;
 RT "Roles of the glutathione- and thioredoxin-dependent reduction systems
 RL in the Escherichia coli and Saccharomyces cerevisiae responses to
 oxidative stress.";
 RN Annu. Rev. Microbiol. 54:439-461 (2000).
 RP REVIEW, AND CELLULAR REDOX FUNCTIONS.
 RX PubMed=11169096;
 RA Grant C.M.;
 RT "Role of the glutathione/glutaredoxin and thioredoxin systems in yeast
 RL growth and response to stress conditions.";
 RN Mol. Microbiol. 39:533-541 (2001).
 RP REVIEW, AND VESICLE FUSION.
 RX PubMed=12914955; DOI=10.1016/S0167-4889(03)00086-7;
 RA Elazar Z., Scheetz-Shouval R., Shorer H.;
 RT "Involvement of LMA1 and GATE-16 family members in intracellular
 RL membrane dynamics.";
 RN Biochim. Biophys. Acta 1641:145-156 (2003).
 RP LEVEL OF PROTEIN EXPRESSION.
 RX PubMed=14562106; DOI=10.1038/nature02046;
 RA Dehaemaght S., Huu W.-K., Bower K., Howson R.W., Belle A.,
 RA Ghapure N., O'Shea E.K., Weissman J.S.;
 RT "Global analysis of protein expression in yeast.";
 RL Nature 425:737-741 (2003).

RN [19]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=22923954; PubMed=14562095; DOI=10.1038/nature02026;
 RA Huu W.-K., Falvo J.V., Gerke L.C., Carroll A.S., Howson R.W.,
 RA Weissman J.S., O'Shea E.K.;
 RT "Global analysis of protein localization in budding yeast.";
 RL Nature 425:686-691 (2003).
 RN [20]
 RP REDOX-ACTIVE DISULFIDE BOND.
 RX PubMed=4945270;
 RA Hall D.E., Baldesten A., Holmgren A., Reichard P.;
 RT "Yeast thioredoxin. Amino-acid sequence around the active-center
 RL disulfide of thioredoxin I and II.";
 RN Eur. J. Biochem. 23:328-335 (1971).
 CC -1- FUNCTION: Participates as a hydrogen donor in redox reactions
 CC through the reversible oxidation of its active center dithiol to a
 CC disulfide, accompanied by the transfer of 2 electrons and 2
 CC protons. It is involved in many cellular processes, including
 CC deoxyribonucleotide synthesis, repair of oxidatively damaged
 CC proteins, protein folding, sulfur metabolism, and redox
 CC homeostasis. Thioredoxin-dependent enzymes include
 CC phosphoadenosine-phosphosulfate reductase MPT16, alkyl-
 CC hydroperoxide reductase DOT5, thioredoxin peroxidases TSA1 and
 CC TSA2, alkyl hydroperoxide reductase AHP1, and peroxiredoxin HVR1.
 CC Thioredoxin is also involved in protection against reducing
 CC stress. As part of the LMA1 complex, it is involved in the
 CC facilitation of vesicle fusion such as homotypic vacuole and ER-
 CC derived COP1 vesicle fusion with the Golgi. This activity does
 CC not require the redox mechanism.
 CC -1- SUBUNIT: Part of the heterodimeric LMA1 complex together with the
 CC proteinase inhibitor PB12. LMA1 binds to the ATPase SEC18.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic, Golgi membrane associated, and
 CC nuclear.
 CC -1- PTM: Reversible disulfide bond formation between Cys-29 and Cys-
 CC 32, reverted by thioredoxin reductase TRX1 using NADPH as hydrogen
 CC donor.
 CC -1- MISCELLANEOUS: Present with 8579 molecules/cell.
 CC -1- MISCELLANEOUS: Yeast has two cytoplasmic thioredoxins, TRX1 and
 CC TRX2, and one mitochondrial, TRX3.
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC Query Match 100.0%; Score 47; DB 1; Length 102;
 CC Best Local Similarity 100.0%; Pred. No. 2.4;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 WGPCK 6
 CC |||||
 CC Db 28 WGPCK 33
 CC
 CC RESULT 23
 CC Q5L731 CHLAB PRELIMINARY; PRT; 102 AA.
 CC ID Q5L731-
 CC AC Q5L731-
 CC DT 01-FEB-2005 (TRENBLREL. 29, Created)
 CC DT 01-FEB-2005 (TRENBLREL. 29, Last sequence update)
 CC DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)
 CC DE Putative thioredoxin.
 CC GN Name=trxa; OrderedLocustNames=CAB082;
 CC OS Chlamydomonas abortus.
 CC CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonada.
 CC OK NCBI_Taxid=83555;
 CC RN (1)
 CC RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 CC STRAIN=S26/3;

RX PubMed=15837807; DOI=10.1101/gr.3684805;
 RA Thomson N.R., Yeates C., Bell K., Holden M.T.G., Bentley S.D.,
 RA Livingstone M., Cerdeno-Tarraga A.-M., Harris B., Doggett J.,
 RA Ormond D., Mungall K., Clarke K., Fellwell T., Hance Z., Sanders M.,
 RA Quail M.A., Price C., Barrell B.G., Parkhill J., Longbottom D.,
 RT "The Chlamydomonas reinhardtii genome sequence reveals an array of
 RT variable proteins that contribute to interspecies variation.";
 RL Genome Res. 15:629-640(2005).
 DR EMBL; CR848038; CAH63539.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 102 AA; 10989 MW; DA736F6B8223C35B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 27 WCGPCK 32

RESULT 24

Q6F1T8_MESFL PRELIMINARY; PRT; 102 AA.
 ID Q6F1T8_MESFL PRELIMINARY; PRT; 102 AA.
 AC Q6F1T8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Thioedoxin.
 GN OrderedLocNames=M1178;
 OS Mesoplasma florum (Acholeplasma florum).
 OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
 OC Entomoplasmataceae; Mesoplasma.
 OX NCBI_TaxId=2151;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RC STRAIN=11 / ATCC 33453;
 RA Birren B.W., Stange-Thomann N., Hafez N., Decaprio D., Fisher S.,
 RA Butler J., Elkins T., Kodira C.D., Major J., Wang S., Nicol R.,
 RA Nisham C.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A6017263; MAT5535.1; -; Genomic_DNA.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006662; Thioedoxin.
 DR InterPro; IPR005746; Thioedoxin.
 DR InterPro; IPR006663; Thioedoxin.
 DR Pfam; PF00085; Thioedoxin; 1.
 DR PRINTS; PR00421; THIOEDOXIN.
 DR TIGRFS; TIGR01068; thioedoxin; 1.
 KW Complete proteome.
 SQ SEQUENCE 102 AA; 11625 MW; 741401233DC8781 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 30 WCGPCK 35

RESULT 25

Q6MUG0_MYCMS PRELIMINARY; PRT; 102 AA.
 ID Q6MUG0_MYCMS PRELIMINARY; PRT; 102 AA.
 AC Q6MUG0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE THIOEDOXIN.
 GN Name=trxA; OrderedLocNames=MSC_0072;
 OS Mycoplasma mycoides (subsp. mycoides SC).

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxId=44101;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=RG1;
 RX PubMed=14762060; DOI=10.1101/gr.1673304;
 RA Westberg J., Persson A., Holmberg A., Gessmann A., Lundberg J.,
 RA Johansson K.-E., Petersson B., Uhlen M.;
 RT "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
 RT strain PGLT, the causative agent of contagious bovine pleuropneumonia
 RT (CBPP)";
 RL Genome Res. 14:221-227(2004).
 DR EMBL; BX842642; CAE76724.1; -; Genomic_DNA.
 DR HSSP; P10599; IADU.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006662; Thioedoxin.
 DR InterPro; IPR005746; Thioedoxin.
 DR InterPro; IPR006663; Thioedoxin.
 DR Pfam; PF00085; Thioedoxin; 1.
 DR PRINTS; PR00421; THIOEDOXIN.
 DR TIGRFS; TIGR01068; thioedoxin; 1.
 KW Complete proteome.
 SQ SEQUENCE 102 AA; 11576 MW; C6D7A9C9AAB5D83D CRC64;

Query Match 100.0%; Score 47; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 30 WCGPCK 35

RESULT 26

THIO_BACSU STANDARD; PRT; 103 AA.
 ID THIO_BACSU STANDARD; PRT; 103 AA.
 AC P14949; O07960; Q45687;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thioedoxin (TRX).
 GN Name=trxA; Synonyms=trx; OrderedLocNames=BSU28500;
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxId=1423;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=168;
 RX MEDLINE=97124191; PubMed=8969504;
 RA Wipac A., Carter N., Brignell C.S., Guy J.B., Piper K., Sanders J.,
 RA Emmerson P.T., Harwood C.R.;
 RT "The dnaB-pheA (256 degrees-240 degrees) region of the Bacillus
 RT subtilis chromosome containing genes responsible for stress responses,
 RT the utilization of plant cell walls and primary metabolism.";
 RL Microbiology 142:3067-3078(1996).
 RN [3]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=168;
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunet F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Besbieres P., Bolotin A., Borchert S.,
 RA Boriss R., Bourstier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Dentzot F., Devine K.M., Duesetoeft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gaileron N.,
 RA Ghim S.-Y., Glaser P., Goffeau A., Goldlighty E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.-F., Itaya M.,
 RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardinois S., Labber J.,
 RA Lazarevic V., Lee S.-W., Levine A., Liu H., Masuda S., Mauei C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogilwara A., Oudega B.,
 RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
 RA Prescott A.M., Presencan E., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
 RA Rose M., Sadate Y., Sato T., Scanlan E., Scheleth S., Schroeder R.,
 RA Scotione F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
 RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Takakoshi A., Tanaka T., Tempstra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
 RA Vassarotti A., Viari A., Wandut R., Wedler E., Wedler H.,
 RA Welzenegger T., Winters P., Wipac A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumbstein E.,
 RA Yoshikawa H., Danchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT subtilis".
 RT Nature 390:249-256(1997).
 RL [4]
 RN PROTEIN SEQUENCE OF 1-14.
 RP STRAIN=168 / JH642;
 RC MEDLINE=96345629; PubMed=8755892;
 RX Gramann P., Schroeder K., Schmid R., Marahiel M.A.,
 RA "Cold shock stress-induced proteins in *Bacillus subtilis*."
 RT J. Bacteriol. 178:4611-4619(1996).
 RL [5]
 RN NUCLEOTIDE SEQUENCE OF 1-7.
 RP STRAIN=168;
 RC Riechdorf S., Winkler A., Voelker U., Ernst H., Scharf C., Hecker M.,
 RA Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
 RL [1]
 CC FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC [1]
 CC SIMILARITY: Belongs to the thioredoxin family.
 CC [1]
 CC SIMILARITY: Contains 1 thioredoxin domain.
 CC [1]
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC [1]
 CC EMBL, J03294; AAA87315.1; -; Genomic DNA.
 DR EMBL, 275208; CA959577.1; -; Genomic DNA.
 DR EMBL, 299118; CAB14810.1; -; Genomic DNA.
 DR EMBL, X79976; CA56300.1; -; Genomic DNA.
 DR EMBL, X99275; CA67667.1; -; Genomic DNA.
 DR PIR, B37192; B37192.
 DR HSP, P23400; IDB1.
 DR Subtilisin, BG10348; trxa.
 DR InterPro: IPR006662; Thioredoxin.
 DR InterPro: IPR006663; Thioredoxin dom2.
 DR InterPro: IPR005746; Thioredoxin.
 DR InterPro: IPR012336; Thioredoxin-like.
 DR InterPro: IPR012335; Thioredoxin fold.
 DR InterPro: IPR011594; Thioredoxin-like.
 DR Pfam: PF00085; Thioredoxin; 1.
 DR PRINTS: PR00421; THIOREDOXIN.
 DR ProDom: PD003679; Thioredoxin-like; 1.
 DR TIGRfam: TIGR01068; thioredoxin; 1.
 DR PROSITE: PS00194; THIOREDOXIN; 1.
 KW Complete proteome; Direct protein sequencing; Electron transport;
 KW Redox-active center; Transport.

FT INIT MET 0 0
 FT DISTLFD 28 31 Redox-active.
 SQ SEQUENCE 103 AA: 11262 MW: 276B55D5B99F2D CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WGPCK 6
 Db 27 WGPCK 32
 RESULT 27
 ID TRX2 YEAST STANDARD; PRT; 103 AA.
 AC P22803;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioredoxin II (Trx-II) (Thioredoxin 1)
 GN Name=TRX2; Synonyms=TRX1; OrderedAccession=YGR209C; ORFNames=G7746;
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxId=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91107668; PubMed=1988444;
 RA Gan Z.-R.;
 RT "Yeast thioredoxin genes."
 RL J. Biol. Chem. 266:1692-1696(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91225027; PubMed=2026619;
 RA Muller E.G.D.;
 RT "Thioredoxin deficiency in yeast prolongs S phase and shortens the G1
 RT interval of the cell cycle."
 RL J. Biol. Chem. 266:9194-9202(1991).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=S288c / GRF8;
 RA Song J.M., Cheung E., Rabinowitz J.C.;
 RT "Analysis of the 15.6-kb fragment encompassing the ADE3 gene."
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=S288c;
 RX MEDLINE=97060019; PubMed=8904340;
 RX DOI=10.1002/(SICI)1097-0061(19960315)12:3<273::AID-YEAS898>3.3.CO;2-T;
 RA Guerrero I., Barreiro T., Soares H., Cyrne L., Maia e Silva A.,
 RA Rodrigues-Pousada C.;
 RT "Sequencing of a 17.6 kb segment on the right arm of yeast chromosome
 RT VII reveals 12 ORFs, including CCT, ADE3 and TR-I genes, homologues of
 RT the yeast PMT and EFG genes, of the human and bacterial electron-
 RT transferring flavoproteins (beta-chain) and of the *Escherichia coli*
 RT phosphoserine phosphohydrolase, and five new ORFs."
 RL Yeast 12:273-280(1996).
 RN [5]
 RN NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RP MEDLINE=97313265; PubMed=169869;
 RX Tettelin H., Agostoni-Carbone M.L., Albermann K., Albers M.,
 RA Arroyo J., Backes U., Barreiro T., Bertrani I., Bjourson A.J.,
 RA Bruckner M., Brusch C.V., Carignani G., Castagnoli L., Cerdan E.,
 RA Clemente M.L., Coblenz A., Cogillevina M., Coisac E., Detour E.,
 RA Del Bino S., Dellus H., Delneri D., de Wergifosse P., Dujon B.,
 RA Durand P., Entian K.-D., Eraso P., Escribano V., Fabiani L.,
 RA Farman B., Feroli F., Feuermann M., Froncaldi L., Garcia-Gonzalez M.,
 RA Garcia-Saez M.I., Goffeau A., Guerrero P., Hani J., Hansen M.,
 RA Hebling U., Hernandez K., Heumann K., Hilger F., Hofmann B.,
 RA Indge K.J., James C.M., Kilma R., Koetter P., Kramer W.,
 RA Launquin G., Leuther H., Louis E.J., Maillier E., Marconi A.,
 RA Martegani E., Mazon M.J., Mazzoni C., McReynolds A.D.K.,

RA Melchiorre P., Mewes H.-W., Minenkova O., Mueller-Auer S.,
RA Nawrocki A., Netter P., Neu R., Nombela C., Oliver S.G., Panzeri L.,
RA Paoluzzi S., Plevani P., Portetle D., Portillo P., Potier S.,
RA Purnelle B., Rieger M., Riles L., Rinaldi T., Robben J.,
RA Rodriguez-Ponsada C., Rodriguez-Belmonte E., Rodriguez-Torres A.M.,
RA Rose M., Ruzi M., Salto M., Sanchez-Perez M., Schaefer B.,
RA Schaefer M., Schaefer M., Schmidheini T., Schreier A., Stala J.,
RA Souciet J.-L., Steenma H.Y., Talla E., Thierry A., Vandenbol M.,
RA van der Aart O.J.M., Van Dyck L., Vanoni M., Verhasselt P., Voet M.,
RA Volckaert G., Wambut R., Watson M.D., Weber N., Wedler H.,
RA Wipfl F., Wolf K., Wright L.F., Zaccaria P., Zimmermann M.,
RA Zolner A., Kleine K.,
RA "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome VII.",
RL Nature 387:81-84(1997).
[16]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=S288c;
RA Marischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA Labaer J.,
RT "Creation of the YLEX clone resource: cloning of *Saccharomyces*
RT *cerevisiae* ORFs in the Gateway recombinational cloning system.",
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
[17]
RN PROTEIN SEQUENCE OF 1-12, AND TSA1 DEPENDENCE ON THIOREDOXIN.
RC STRAIN=ATCC 200358 / YNN 295;
RA MEDLINE=95050519; PubMed=7961686;
RA Chae H.Z., Chung S.J., Rhee S.G.,
RT "Thioredoxin-dependent peroxidase from yeast.",
RL J. Biol. Chem. 269:27670-27678(1994).
[18]
RN PROTEIN SEQUENCE OF 26-42.
RX MEDLINE=72104597; PubMed=4333602;
RA Hall D.E., Baldesten A., Holmgren A., Reichard P.,
RT "The covalently-bound flavin of hepatic monooxygenase. 2.
RT Identification and properties of cysteinyl riboflavin.",
RL Eur. J. Biochem. 24:328-335(1971).
[19]
RN FUNCTION, AND SULFATE ASSIMILATION AND METHIONINE METABOLISM.
RX PubMed=3060034; DOI=10.1007/BF00408300;
RA Schwann J.D., Krone F.A., Huemann K.,
RT "Yeast PAPS reductase: properties and requirements of the purified
RT enzyme.",
RL Arch. Microbiol. 150:313-319(1998).
[110]
RN FUNCTION, AND LMA1 COMPLEX.
RX PubMed=9015301; DOI=10.1083/jcb.136.2.299;
RA Xu Z., Mayer A., Muller E.G.D., Wickner W.,
RT "A heterodimer of thioredoxin and I(B)2 cooperates with Sec18p (NSF)
RT to promote yeast vacuole inheritance.",
RL J. Cell Biol. 136:299-306(1997).
[111]
RN FUNCTION, AND INTERACTION WITH SEC18.
RX PubMed=9657146; DOI=10.1016/S0092-8674(00)81457-9;
RA Xu Z., Sato K., Wickner W.,
RT "LMA1 binds to vacuoles at Sec18p (NSF), transfers upon ATP hydrolysis
RT to a t-SNARE (Vam3p) complex, and is released during fusion.",
RL Cell 93:1123-1134(1998).
[112]
RN FUNCTION, AND DOTS AND TSA2 DEPENDENCE ON THIOREDOXIN.
RX PubMed=16681558; DOI=10.1074/jbc.275.8.5723;
RA Park S.G., Cha M.K., Jeong W., Kim I.-H.,
RT "Distinct physiological functions of thiol peroxidase isoenzymes in
RT *Saccharomyces cerevisiae*.",
RL J. Biol. Chem. 275:5723-5732(2000).
[113]
RN FUNCTION, AND REDUCTION OF AHP1.
RX MEDLINE=99143107; PubMed=9988687; DOI=10.1074/jbc.274.8.4537;
RA Lee J., Spector D., Godon C., Labarre J., Tolédano M.B.,
RT "A new antioxidant with alkyl hydroperoxide defense properties in
RT yeast.",

RL J. Biol. Chem. 274:4537-4544(1999).
[114]
RN FUNCTION, AND REGULATION OF YAP1.
RX PubMed=11013218; DOI=10.1093/emboj/19.19.5157;
RA Delaunay A., Isnard A.D., Tolédano M.B.,
RT "H2O2 sensing through oxidation of the Yap1 transcription factor.",
RL EMBO J. 19:5157-5166(2000).
[115]
RN FUNCTION, AND REGULATION OF HYP1/GPX3.
RX PubMed=12437921; DOI=10.1016/S0092-8674(02)01048-6;
RA Delaunay A., Pflieger D., Barrault M.-B., Vinh J., Tolédano M.B.,
RT "A thiol peroxidase is an H2O2 receptor and redox-transducer in gene
RT activation.",
RL Cell 111:471-481(2002).
[116]
RN FUNCTION, AND PROTECTION AGAINST REDUCING STRESS.
RX PubMed=12410842;
RA Trotter E.W., Grant C.M.,
RT "Thioredoxins are required for protection against a reductive stress
RT in the yeast *Saccharomyces cerevisiae*.",
RL Mol. Microbiol. 46:869-878(2002).
[117]
RN REVIEW, AND OXIDATIVE STRESS.
RX PubMed=11018134; DOI=10.1146/annurev.micro.54.1.439;
RA Carmel-Harel O., Storz G.,
RT "Roles of the glutathione- and thioredoxin-dependent reduction systems
RT in the *Escherichia coli* and *Saccharomyces cerevisiae* responses to
RT oxidative stress.",
RL Annu. Rev. Microbiol. 54:439-461(2000).
[118]
RN REVIEW, AND CELLULAR REDOX FUNCTIONS.
RX PubMed=11169096;
RA Grant C.M.,
RT "Role of the glutathione/glutaredoxin and thioredoxin systems in yeast
RT growth and response to stress conditions.",
RL Mol. Microbiol. 39:533-541(2001).
[119]
RN REVIEW, AND VESICLE FUSION.
RX PubMed=12914955; DOI=10.1016/S0167-4889(03)00086-7;
RA Elazar Z., Scheerz-Shouval R., Shore H.,
RT "Involvement of LMA1 and GATE-16 family members in intracellular
RT membrane dynamics.",
RL Biochim. Biophys. Acta 1641:145-156(2003).
[120]
RN LEVEL OF PROTEIN EXPRESSION.
RX PubMed=14562106; DOI=10.1038/nature02046;
RA Chaemmagham S., Huh W.-K., Bower K., Howson R.W., Belle A.,
RT Dephure N., O'Shea E.K., Weissman J.S.,
RT "Global analysis of protein expression in yeast.",
RL Nature 425:737-741(2003).
[121]
RN SUBCELLULAR LOCATION.
RX MEDLINE=22923954; PubMed=14562095; DOI=10.1038/nature02026;
RA Huh W.-K., Falvo J.V., Gerke L.C., Carroll A.S., Howson R.W.,
RA Weissman J.S., O'Shea E.K.,
RT "Global analysis of protein localization in budding yeast.",
RL Nature 425:686-691(2003).
[122]
RN REDOX-ACTIVE DISULFIDE BOND.
RX PubMed=4945270;
RA Hall D.E., Baldesten A., Holmgren A., Reichard P.,
RT "Yeast thioredoxin. Amino-acid sequence around the active-center
RT disulfide of thioredoxin I and II.",
RL Eur. J. Biochem. 23:328-335(1971).
CC -1- FUNCTION: Participates as a hydrogen donor in redox reactions
CC through the reversible oxidation of its active center dithiol to a
CC disulfide, accompanied by the transfer of 2 electrons and 2
CC protons. It is involved in many cellular processes, including
CC deoxyribonucleotide synthesis, repair of oxidatively damaged

Query Match 100.0%; Score 47; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.4; Mismatches 0; Gaps 0;
Matches 6; Conservative 0; Indels 0;

Qy 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 28
 075C00 ASHGO PRELIMINARY; PRT; 103 AA.

AC 075C00-
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE "The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome."
 RT Science 304:304-307(2004).
 DR EMBL; AB016816; AAS51097.1; -; Genomic_DNA.
 DR HSSP; P10599; 1AUC.
 DR AGD; ACT131W; -.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRedox.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfams; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 103 AA; 11396 MW; 28B3A9A186540FE7 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 29
 06FND5 CANCA PRELIMINARY; PRT; 103 AA.

AC 06FND5;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE "Ordered locus names=CAGL0008035;
 Candida glabrata strain CBS138 chromosome K complete sequence.
 Ordered locus names=CAGL0008035;
 Candida glabrata (Yeast) (Torulopsis glabrata).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mltosporic Saccharomycetales; Candida.
 NCBI_Taxid=5478;
 [1]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 2001 / CBS 138;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boierame A., Boyer J., Catrolicco L., Confanioleri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.-M., Nikoleki M., Ozias S., Ozler-Kalogeropoulos O.,
 RA Pellens S., Pottier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpetti C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts."
 Nature 430:35-44(2004).
 DR EMBL; CR380957; CAG61220.1; -; Genomic_DNA.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRedox.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfams; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 103 AA; 11171 MW; DIA6EBA8B487712 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 30
 06B080 DEBHA PRELIMINARY; PRT; 103 AA.

AC 06B080;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DE "Similar to ep1p22217 Saccharomyces cerevisiae YLR043c TRX1 thioRedoxin
 1."
 GN OrderedLocusNames=DEBA0G05126g;
 OS Debaryomyces hanseni (Yeast) (Torulaspora hanseni).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetales; Debaryomyces.
 NCBI_Taxid=4959;
 [1]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 36239 / CBS 767;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boierame A., Boyer J., Catrolicco L., Confanioleri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.-M., Nikoleki M., Ozias S., Ozler-Kalogeropoulos O.,
 RA Pellens S., Pottier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpetti C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts."
 Nature 430:35-44(2004).

DR EMBL: CR382139; CAG90196.1; -; Genomic DNA.
 DR GO: GO:0005489; F:electron transporter activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR006662; ThioRed.
 DR InterPro: IPR006663; ThioRedox_dom2.
 DR InterPro: IPR005746; ThioRedoxin.
 DR InterPro: IPR012336; ThioRedoxin-like.
 DR InterPro: IPR012335; ThioRedoxin_fold.
 DR Pfam: PF00085; ThioRedoxin_1.
 DR PRINTS: PR00421; THIOREDOXIN.
 DR TIGRFAMs: TIGR01068; thioRedoxin; 1.
 DR PROSITE: PS00194; THIOREDOXIN; 1.
 DR Complete proteome.
 SQ SEQUENCE 103 AA; 11149 MW; 1F533CB671C532EC CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 29 WCGPCK 34

RESULT 31
 OSACN1 CANAL PRELIMINARY; PRT; 103 AA.
 ID OSACN1_1

AC OSACN1_1
 DT 10-MAY-2005 (TRENBLrel. 30, Created)
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
 DE Potential thioRedoxin.
 GN Name=TRX1; ORFNames=Ca019.7611;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Microsporitic Saccharomycetales; Candida.
 OX NCBI_Taxid=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federapfel N.A., Chidana H., Dungan J., Kalman S.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RT "The diploid genome sequence of Candida albicans";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
 RU [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
 RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
 RA Jones T., Scherer S., Agabian N.;
 RT "Annotation of the Genome of Candida albicans";
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AAC001000032; EAL00485.1; -; Genomic DNA.
 DR GO: GO:0005489; F:electron transporter activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR006662; ThioRed.
 DR InterPro: IPR006663; ThioRedox_dom2.
 DR InterPro: IPR005746; ThioRedoxin.
 DR InterPro: IPR012336; ThioRedoxin-like.
 DR InterPro: IPR012335; ThioRedoxin_fold.
 DR Pfam: PF00085; ThioRedoxin_1.
 DR PRINTS: PR00421; THIOREDOXIN.
 DR TIGRFAMs: TIGR01068; thioRedoxin; 1.
 DR PROSITE: PS00194; THIOREDOXIN; 1.
 SQ SEQUENCE 103 AA; 11487 MW; 4B78100038A53620 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6

DB 29 WCGPCK 34
 |||||

RESULT 32
 O7P4W8 FUSNV PRELIMINARY; PRT; 103 AA.
 ID O7P4W8_1
 AC O7P4W8_1
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE ThioRedoxin.
 GN Name=FNW0931;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 CC Fusobacterium
 OX NCBI_Taxid=209882;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 49256;
 RA Karpatal V., Ivanova N., Anderson I., Reznik G., Bhattacharya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haseikorn R., Overbeek R., Kyrides N.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL: AABP01000093; EAA23714.1; -; Genomic_DNA.
 DR HSBP: P00274; IKXB.
 DR GO: GO:0005489; F:electron transporter activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR006662; ThioRed.
 DR InterPro: IPR005746; ThioRedoxin.
 DR InterPro: IPR006663; ThioRedox_dom2.
 DR Pfam: PF00085; ThioRedoxin_1.
 DR PRINTS: PR00421; THIOREDOXIN.
 DR TIGRFAMs: TIGR01068; thioRedoxin; 1.
 SQ SEQUENCE 103 AA; 11369 MW; 4437B8AAD056D7C0 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 30 WCGPCK 35

RESULT 33
 OSFLM1 LACAC PRELIMINARY; PRT; 103 AA.
 ID OSFLM1_1
 AC OSFLM1_1
 DT 10-MAY-2005 (TRENBLrel. 30, Created)
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
 DE ThioRedoxin reductase.
 GN OrderedCusNames=LBX0422;
 OS Lactobacillus acidophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_Taxid=1579;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCFM;
 RX PubMed=15671160; DOI=10.1073/pnas.0409189102;
 RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
 RA Buck B.L., McAlliffe O., Souther N., Dobson A., Duong T., Callanan M.,
 RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
 RT "Complete genome sequence of the probiotic lactic acid bacterium
 Lactobacillus acidophilus NCFM";
 RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
 DR EMBL: CP000033; AAV42313.1; -; Genomic_DNA.

DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-1ike.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; ThioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Complete proteome.
 KW COMPLETE
 SQ SEQUENCE 103 AA; 11754 MW; F888C9923C13B9BC CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 27 WCGPCK 32

RESULT 34
 O8RH23 FUSNN PRELIMINARY; PRT; 103 AA.

AC O8RH23_1
 DT 01-UN-2002 (TRENBLrel. 21, Created)
 DT 01-UN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE ThioRedoxin.
 GN Ordered locus names=FNO093;
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 NCBI_Taxid=76856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=2186394; PubMed=11889109;
 RX DOI=10.1128/JB.184.7.2005-2018.2002;
 RA Kaptehal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Gotsman E., Bernal A.,
 RA Larsen N., D'Souza M., Malunas T., Puech G., Haselkorn R.,
 RA Fomstein M., Kytrides N.C., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 nucleatum strain ATCC 25586."
 RT J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AR009951; AAL94306.1; -; Genomic_DNA.
 DR HSSP; P00274; 1T7P.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-1ike.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; ThioRedoxin; 1.
 DR Complete proteome.
 KW COMPLETE
 SQ SEQUENCE 103 AA; 11342 MW; 27E003A221A4C780 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 35
 O7AKU7 LACJO PRELIMINARY; PRT; 103 AA.

AC O7AKU7_1
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE ThioRedoxin.
 GN Ordered locus names=LJ0480;
 OS Lactobacillus johnsonii.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 NCBI_Taxid=33959;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=NC 533;
 RX PubMed=14963040; DOI=10.1073/pnas.0307327101;
 RA Pidmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
 RA Pitter A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,
 RA Mollet B., Mercadier A., Klaenhammer T., Arigoni F., Scheil M.A.;
 RT "The genome sequence of the probiotic intestinal bacterium
 Lactobacillus johnsonii NC 533."
 RT Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
 DR EMBL; AE017201; AAS08472.1; -; Genomic_DNA.
 DR HSSP; P10599; 1AUC.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-1ike.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PR00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; ThioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Complete proteome.
 KW COMPLETE
 SQ SEQUENCE 103 AA; 11762 MW; B1FC16C916B944C3 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 27 WCGPCK 32

RESULT 36
 THIO BOVIN STANDARD; PRT; 104 AA.
 AC O97680;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE ThioRedoxin.
 GN Name=TXN;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 NCBI_Taxid=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=20189621; PubMed=10727087;
 RA Terashima H., Gotoh S., Yagi K., Mizoguchi T.;
 RT "cDNA sequence of bovine thioRedoxin.";
 RT DNA Seq. 10:331-333(1999).

-I- FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide
 and catalyzes dithiol-disulfide exchange reactions (By
 similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC

```
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF104105; AAC83380.1; -; mRNA.
CC HSSP; P10599; 1ERT.
CC SMR; O97680; 1-104.
CC InterPro; IPR006662; Thiored.
CC InterPro; IPR006663; Thioredox dom2.
CC InterPro; IPR005746; Thioredoxin.
CC InterPro; IPR012336; Thioredoxin-like.
CC InterPro; IPR012335; Thioredoxin-fold.
CC Pfam; PF00085; Thioredoxin_1.
CC PRINTS; PR00421; THIOREDOXIN.
CC TIGRFA; TIGR01068; thioredoxin; 1.
CC PROSITE; PS00194; THIOREDOXIN; 1.
CC Electron transport; Redox-active center; Transport.
CC INIT MET 0 0
CC ACT SITE 31 31 Nucleophile (By similarity).
CC ACT SITE 34 34 Nucleophile (By similarity).
CC SITE 25 25 Deprotonates C-terminal active site Cys
CC SITE 32 32 (By similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC DISULFID 31 34 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11681 MW; 506CFP696A208D CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 37
THIO_CALJA STANDARD; PRT; 104 AA.
ID THIO_CALJA
AC O9BDJ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thioredoxin.
GN Name=TXN; Synonyms=TRX;
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
OC Callitrichidae; Callitrichi.
OX NCBI_TaxID=9483;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA MEDLINE=21576430; PubMed=11719593; DOI=10.1093/molenv/7.12.1159;
RA Lopata A., Sibson M.C., Anders A.C., Bloomfield K.L., Gregory M.S.,
RA Trapani G.D., Perkins A.V., Tonsissen K.F., Clarke F.M.;
RA "Expression and localization of thioredoxin during early implantation
RT in the marmoset monkey.";
RL Mol. Hum. Reprod. 7:1159-1165(2001).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF353204; AKJ0295.1; -; mRNA.
CC HSSP; P10599; 1ERT.
CC SMR; O9BDJ3; 1-104.
CC InterPro; IPR006662; Thiored.
CC InterPro; IPR006663; Thioredox dom2.
CC InterPro; IPR005746; Thioredoxin.
CC InterPro; IPR012336; Thioredoxin-like.
CC InterPro; IPR012335; Thioredoxin-fold.
CC Pfam; PF00085; Thioredoxin_1.
CC PRINTS; PR00421; THIOREDOXIN.
CC TIGRFA; TIGR01068; thioredoxin; 1.
CC PROSITE; PS00194; THIOREDOXIN; 1.
CC Electron transport; Redox-active center; Transport.
CC INIT MET 0 0
CC ACT SITE 31 31 Nucleophile (By similarity).
CC ACT SITE 34 34 Nucleophile (By similarity).
CC SITE 25 25 Deprotonates C-terminal active site Cys
CC SITE 32 32 (By similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC DISULFID 31 34 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11626 MW; 3E0F5243A04BBE81 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 38
THIO_CHICK STANDARD; PRT; 104 AA.
ID THIO_CHICK
AC P08629;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thioredoxin.
GN Name=TXN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA MEDLINE=88257080; PubMed=2838473;
RA Jones S.W., Lusk K.-C.;
RA "Isolation of a chicken thioredoxin cDNA clone. Thioredoxin mRNA is
RT differentially expressed in normal and Rous sarcoma virus-transformed
RT chicken embryo fibroblasts.";
RL J. Biol. Chem. 263:9607-9611(1988).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
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CC removed.
CC -----
CC EMBL, J03882; AAA49092.1; -, mRNA.
CC PIR, A30006; A30006.
CC HSSP, P10599; 1ERT.
CC SMR, P08629; 1-104.
CC Ensemble; ENSGALG00000015704; Gallus gallus.
CC InterPro; IPR006662; Thiores.
CC InterPro; IPR006663; Thiores dom2.
CC InterPro; IPR012336; Thioresoxin-like.
CC InterPro; IPR012335; Thioresoxin-fold.
CC Pfam; PF00085; Thioresoxin_1.
CC PRINTS; PR00421; THIOREDOXIN.
CC PROSITE; PS00194; THIOREDOXIN; 1.
CC Electron transport; Redox-active center; Transport.
CC INT_MET 0 0
CC ACT_SITE 31 31 Nucleophile (By similarity).
CC ACT_SITE 34 34 Nucleophile (By similarity).
CC SITE 25 25 Deprotonates C-terminal active site Cys
CC SITE 25 25 (By similarity).
CC SITE 32 32 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC DISULFID 31 34 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11569 MW; 6086687590105B12 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 39
THIO HORSE STANDARD; PRT; 104 AA.
AC 097508;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thioresoxin.
GN Name=TXN;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Thoroughbred;
RA Tajima Y., Ishida N.;
RT "Molecular cloning of equine thioresoxin."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the thioresoxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AB022431; BAA37154.1; -, mRNA.
CC HSSP, P10599; 3TRX.
CC SMR, O97508; 1-104.
CC InterPro; IPR006662; Thiores.
CC InterPro; IPR006663; Thioresox_2.

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DR InterPro; IPR005746; Thioresoxin.
DR InterPro; IPR012336; Thioresoxin-like.
DR InterPro; IPR012335; Thioresoxin-fold.
DR Pfam; PF00085; Thioresoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; Thioresoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
CC Electron transport; Redox-active center; Transport.
CC INT_MET 0 0
CC ACT_SITE 31 31 Nucleophile (By similarity).
CC ACT_SITE 34 34 Nucleophile (By similarity).
CC SITE 25 25 Deprotonates C-terminal active site Cys
CC SITE 25 25 (By similarity).
CC SITE 32 32 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC DISULFID 31 34 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11605 MW; 586C1092964C206D CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 40
THIO HUMAN STANDARD; PRT; 104 AA.
AC P10599; Q96K13;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thioresoxin (ATL-derived factor) (ADF) (Surface associated sulphhydryl
DE protein) (SASP).
GN Name=TXN; Synonyms=PRDX, TRX, TRX1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89008454; PubMed=1874447; DOI=10.1016/0378-1119(91)90081-L;
RA Tomassen K.F., Wells J.R.E.;
RT "Isolation and characterization of human thioresoxin-encoding genes."
RL Gene 102:221-226(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89008454; PubMed=3170595;
RA Wollman E.E., D'Aurilio L., Rinsky L., Shaw A., Jacquot J.-P.,
RA Wingfield P., Graber P., Desarses F.;
RT "Cloning and expression of a cDNA for human thioresoxin."
RL J. Biol. Chem. 263:15506-15512(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89251607; PubMed=2785919;
RA Tagaya Y., Meda Y., Mitsui A., Kudo N., Matsui H., Hamuro J.,
RA Brown N., Arai K.-I., Yokota T., Makasugi H., Yodoi J.;
RT "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to
RT thioresoxin; possible involvement of dithiol-reduction in the IL-2
RT receptor induction."
RL EMBO J. 8:757-764(1989).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Reddy P.G., Bhuyan D.K., Bhuyan K.C.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.

```

RC TISSUE=Lens;
 RA Liu A., Lou M.F.;
 RT "Cloning, purification and characterization of human lens
 RT thioredoxin.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RC NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=Brain;
 RA Xu J.Y., Xu L., Li K.S., Dai R.;
 RT "Cloning and sequencing of thioredoxin cDNA from human brain.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RT "NIHES-SNPE, environmental genome project. NIHES ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Cervix;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins C.P., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millaly S.J.,
 RA Bosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP PROTEIN SEQUENCE OF 1-14.
 RX MEDLINE=91151337; PubMed=1998498;
 RA Martin H., Dean M.;
 RT "Identification of a thioredoxin-related protein associated with
 RT plasma membranes.";
 RL Biochem. Biophys. Res. Commun. 175:123-128(1991).
 RN [10]
 RP STRUCTURE BY NMR.
 RX MEDLINE=90057393; PubMed=2684271;
 RA Forman-Kay J.D., Clore G.M., Dyrce P.C., Wingfield P.,
 RA Richards P.M., Gronenborn A.M.;
 RT "A proton nuclear magnetic resonance assignment and secondary
 RT structure determination of recombinant human thioredoxin.";
 RL Biochemistry 28:7088-7097(1989).
 RN [11]
 RP STRUCTURE BY NMR.
 RX MEDLINE=91159399; PubMed=2001356;
 RA Forman-Kay J.D., Clore G.M., Wingfield P., Gronenborn A.M.;
 RT "High-resolution three-dimensional structure of reduced recombinant
 RT human thioredoxin in solution.";
 RL Biochemistry 30:2685-2698(1991).
 RN [12]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95006318; PubMed=7922028;
 RA Qin J., Clore G.M., Gronenborn A.M.;
 RT "The high-resolution three-dimensional solution structures of the
 RT oxidized and reduced states of human thioredoxin.";
 RL Structure 2:503-522(1994).
 RN [13]

RP STRUCTURE BY NMR.
 RX MEDLINE=96347359; PubMed=8736558; DOI=10.1016/S0969-2126(96)00065-2;
 RA Qin J., Clore G.M., Kennedy W.P., Kuszewski J., Gronenborn A.M.;
 RT "The solution structure of human thioredoxin complexed with its target
 RT from Ref-1 reveals peptide chain reversal.";
 RL Structure 4:613-620(1996).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
 RX MEDLINE=96399719; PubMed=8805557; DOI=10.1016/S0969-2126(96)00079-2;
 RA Weltsch A., Gasdaske J.R., Powis G., Montfort W.R.;
 RT "Crystal structures of reduced, oxidized, and mutated human
 RT thioredoxins: evidence for a regulatory homodimer.";
 RL Structure 4:735-751(1996).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF MUTANT ASN-60.
 RX MEDLINE=98039128; PubMed=9369469; DOI=10.1021/1971004s;
 RA Andersen J.F., Sanders D.A., Gasdaske J.R., Weltsch A., Powis G.,
 RA Montfort W.R.;
 RT "Human thioredoxin homodimers: regulation by pH, role of aspartate 60,
 RT and crystal structure of the aspartate 60 --> asparagine mutant.";
 RL Biochemistry 36:13979-13988(1997).
 RN [16]
 RP ACTIVITY.
 RX MEDLINE=91097576; PubMed=2176490;
 RA Jacquot J.-P., de Lamotte F., Fontecay M., Schnermann P.,
 RA Decottignies P., Migoniac-Maslow M., Wollman E.;
 RT "Human thioredoxin reactivity-structure/function relationship.";
 RL Biochem. Biophys. Res. Commun. 173:1375-1381(1990).
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC -1- FUNCTION: ADP augments the expression of the Interleukin-2
 CC receptor TAC (IL2R/P55).
 CC -1- SUBUNIT: Homodimer.
 CC -1- INTERACTION:
 CC Q92805:CORP5; Nbxp-5; InAct-EBI-594644, EBI-594661;
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL: X7584; CAA54687.1; -; mRNA.
 CC EMBL: X54539; CAA38410.1; -; Genomic_DNA.
 CC EMBL: X54540; CAA38410.1; JOINED; Genomic_DNA.
 CC EMBL: X54541; CAA38410.1; JOINED; Genomic_DNA.
 CC EMBL: J04026; AAA74596.1; -; mRNA.
 CC EMBL: AF276919; AAF86466.1; -; mRNA.
 CC EMBL: AY004872; AAF87085.1; -; mRNA.
 CC EMBL: AF313911; AAG34699.1; -; mRNA.
 CC EMBL: AF548001; AAN03187.1; -; Genomic_DNA.
 CC EMBL: BC000337; AAN03377.1; -; mRNA.
 CC EMBL: BC054866; AAH54866.1; -; mRNA.
 CC PIR: JH0568; JH0568.
 CC PDB: 1ATU; X-ray; @=1-104.
 CC PDB: 1AUC; X-ray; @=1-104.
 CC PDB: 1COG; NMR; A=1-104.
 CC PDB: 1COH; NMR; A=1-104.
 CC PDB: 1ERT; X-ray; @=1-104.
 CC PDB: 1ERV; X-ray; @=1-104.
 CC PDB: 1ERW; X-ray; @=1-104.
 CC PDB: 1W7T; NMR; A=-.
 CC PDB: 1MDI; NMR; A=1-104.
 CC PDB: 1MDJ; NMR; A=1-104.
 CC PDB: 1MDK; NMR; A=1-104.
 CC PDB: 1TRS; NMR; @=1-104.
 CC PDB: 1TRU; NMR; @=1-104.
 CC PDB: 1TRV; NMR; @=1-104.

DR PDB; 1TRW; NMR; @=1-104.
 DR PDB; 3TRX; NMR; @=1-104.
 DR PDB; 4TRX; NMR; @=1-104.
 DR IntAct; P10599; -.
 DR SWISS-2DPAGE; P10599; HUMAN.
 DR Aairus/Ghent-2DPAGE; 8006; IEF.
 DR PHCI-2DPAGE; P10599; -.
 DR Siema-2DPAGE; P10599; -.
 DR Ensembl; ENSG00000136810; Homo sapiens.
 DR HGNC; HGNC:12435; TXN.
 DR H-InvDB; HIX0008275; -.
 DR Reactome; P10599; -.

Query Match Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 30 WCGPCK 35

RESULT 41
 ID THIO_MACMU STANDARD; PRT; 104 AA.
 AC P29451;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioedoxin.
 GN Name=TXN;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_TaxID=9544;
 [1]
 RX NUCLEOTIDE SEQUENCE [MRNA].
 MEDLINE=92181438; PubMed=1543487;
 RA An G., Wu R.;
 RT "thioedoxin gene expression is transcriptionally up-regulated by
 retinol in monkey conducting airway epithelial cells."
 RL Biochem. Biophys. Res. Commun. 183:170-175(1992).
 CC -1- FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide
 and catalyzes dithiol-disulfide exchange reactions.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioedoxin family.
 CC -1- SIMILARITY: Contains 1 thioedoxin domain.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 CC EMBL; M84643; AAA36921.1; -. mRNA.
 DR PIR; J50667; J50667.
 DR HSSP; P10599; IERT.
 DR SMR; P29451; 1-104.
 DR InterPro; IPR006663; Thioedox.
 DR InterPro; IPR006663; Thioedox dom.
 DR InterPro; IPR005746; Thioedoxin.
 DR InterPro; IPR012336; Thioedoxin-like.
 DR InterPro; IPR012335; Thioedoxin_fold.
 DR Pfam; PF00085; Thioedoxin_1.
 DR PRINTS; PR00421; THIOEDOXIN.
 DR TIGRFAMs; TIGR01068; thioedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KM Electron transport; Redox-active center; Transport.
 FT INIT MET 0 By similarity.
 FT ACT SITE 31 Nucleophile (By similarity).
 FT ACT_SITE 34 Nucleophile (By similarity).

FT SITE 25 25 Deprotonates C-terminal active site Cys
 FT SITE 32 32 (By similarity).
 FT SITE 33 33 Contributes to redox potential value (By
 FT SITE 33 33 similarity).
 FT DISULFID 31 34 Contributes to redox potential value (By
 FT DISULFID 31 34 similarity).
 SQ SEQUENCE 104 AA; 11606 MW; C804D5152F8870EB CRC64;

Query Match Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 30 WCGPCK 35

RESULT 42
 ID THIO_MOUSE STANDARD; PRT; 104 AA.
 AC P10639; Q9P8R0;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioedoxin (ATL-derived factor) (ADF).
 GN Name=Txn; Synonyms=Txnl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RX NUCLEOTIDE SEQUENCE [MRNA].
 MEDLINE=89251607; PubMed=2785919;
 RA Tagaya Y., Maeda Y., Mitsui A., Kudo N., Matsui H., Hamuro J.,
 RA Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
 RT "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to
 thioedoxin; possible involvement of dithiol-reduction in the IL-2
 RT receptor induction."
 RL EMBO J. 8:757-764(1989).
 [2]
 RP ERRATUM, AND SEQUENCE REVISION.
 RX MEDLINE=94244626; PubMed=8187776;
 RA Tagaya Y., Maeda Y., Mitsui A., Kudo N., Matsui H., Hamuro J.,
 RA Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
 RL EMBO J. 13:2244-2244(1994).
 [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=129/Sv; TISSUE=Liver;
 RX MEDLINE=95137382; PubMed=7835695; DOI=10.1016/0378-1119(94)00707-Y;
 RA Matsui M., Taniguchi Y., Hirota K., Taketo M., Yodoi J.;
 RT "Structure of the mouse thioedoxin-encoding gene and its processed
 RT pseudogene."
 RL Gene 152:165-171(1995).
 [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamanaoka H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbett L.E., Cousins S.,
 RA Dalia E., Dregan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Gilmard S., Guevinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongsaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunnata K., Okido T., Pavan W.J., Perle G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

KM	Electron transport; Redox-active center; Transport.
FT	INT MET 0 0
FT	ACT_SITE 31 31 Nucleophile (By similarity).
FT	ACT_SITE 34 34 Nucleophile (By similarity).
FT	ACT_SITE 34 34 Deprotonates C-terminal active site Cys
FT	SITE 25 25 (By similarity).
FT	SITE 32 32 Contributes to redox potential value (By similarity).
FT	SITE 33 33 Contributes to redox potential value (By similarity).
FT	DISULFID 31 34 Redox-active (By similarity).
FT	CONFLICT 99 99 S -> C (in Ref. 4; BAB25256).
SO	SEQUENCE 104 AA; 11544 MW; 60BE6196090ACT73 CRC64;
Qy	Query Match 100.0%; Score 47; DB 1; Length 104;
Db	Best Local Similarity 100.0%; Pred. No. 2.5; Indels 0; Gaps 0;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 WCGPCK 6
	30 WCGPCK 35
RESULT 43	
ID	THIO_OPHNA STANDARD; PRT; 104 AA.
AC	Q96TX1;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Thioredoxin.
GN	Name:TXN;
OS	Ophiophagus hannah (King cobra) (Naja hannah).
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC	Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC	Elapidae; Elapinae; Ophiophagus.
OX	NCBI_TaxID=8665;
RP	[1]
RP	NUCLEOTIDE SEQUENCE [mRNA].
RA	Lee W., Liu H., Zhang Y.;
RC	TISSUE=Venom gland;
RT	"cDNA sequence of Ophiophagus hannah venom gland thioredoxin protein".
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC	-1- FUNCTION: Participates in various redox reactions through the reversible oxidation of its active center dithiol to a disulfide and catalyzes dithiol-disulfide exchange reactions (By similarity).
CC	-1- SIMILARITY: Belongs to the thioredoxin family.
CC	-1- SIMILARITY: Contains 1 thioredoxin domain.
CC	-----
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC	-----
DR	EMBL; AF321769; AAK09384.1; -; mRNA.
DR	HSSP; P10599; TRX.
DR	InterPro; IPR006662; ThioRed.
DR	InterPro; IPR006663; ThioRedox dom2.
DR	InterPro; IPR012336; ThioRedoxin-like.
DR	InterPro; IPR012335; ThioRedoxin_1.
DR	Pfam; PF00085; ThioRedoxin_1.
DR	PRINTS; PS00421; THIOREDOXIN.
DR	PROSITE; PS00194; THIOREDOXIN; 1.
KM	Electron transport; Redox-active center; Transport.
FT	INT MET 0 0
FT	ACT_SITE 31 31 Nucleophile (By similarity).
FT	ACT_SITE 34 34 Nucleophile (By similarity).
FT	ACT_SITE 34 34 Deprotonates C-terminal active site Cys
FT	SITE 25 25 (By similarity).
FT	SITE 32 32 Contributes to redox potential value (By similarity).

```

FT SITE 33 33 similarity).
FT SITE 33 33 contributes to redox potential value (By
FT DISULFID 31 34 similarity). (By similarity).
SQ SEQUENCE 104 AA; 11872 MW; 852896C8EF850AFB CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 44
THIO_PIG
ID THIO_PIG STANDARD; PRT; 104 AA.
AC P82460; Q95JF9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thioredoxin.
GN Name=TXN;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxID=9823;
RN (1)
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Liver;
RA Yu G.W., Xu J.Y., Xu L., Cheung P.Y., Lee K.S.;
RT "The cloning and expression of porcine thioredoxin in E. coli.";
RT Submitted (May-2001) to the EMBL/GenBank/DBD databases.
[2]
RP PROTEIN SEQUENCE OF 1-33.
RC TISSUE=Erythrocyte;
RA Lee K.S., Tang W.K., Cheung P.Y., Siu Y.L., Wong N.S.;
RL Submitted (May-2000) to Swiss-Prot.
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: Erythrocytes.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF382821; AAK60272.1; -; mRNA.
CC DR HSSP; P10599; 1ERF.
CC DR SMR; P82460; 1-104.
CC DR InterPro; IPR006662; ThioRed.
CC DR InterPro; IPR006663; ThioRedox_dom2.
CC DR InterPro; IPR005746; ThioRedoxin.
CC DR InterPro; IPR012336; Thioredoxin-like.
CC DR Pfam; PF00085; Thioredoxin_fold.
CC DR InterPro; IPR012335; Thioredoxin_fold.
CC DR Pfam; PF00085; Thioredoxin; 1.
CC DR PRINTS; PR00421; THIOREDOXIN.
CC DR TIGRFS; TIGR01068; thioredoxin; 1.
CC DR PROSITE; PS00194; THIOREDOXIN; 1.
CC KW Direct protein sequencing; Electron transport; Redox-active center;
CC Transport.
CC FT INIT MET 0
CC FT ACT_SITE 31 31 Nucleophile (By similarity).
CC FT ACT_SITE 34 34 Nucleophile (By similarity).
CC FT SITE 25 25 Deprotonates C-terminal active site Cys
CC (By similarity).

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FT SITE 32 32 similarity).
FT SITE 33 33 contributes to redox potential value (By
FT DISULFID 31 34 similarity). (By similarity).
SQ SEQUENCE 104 AA; 11697 MW; 9816FP9696A2396A CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 45
THIO_RABIT
ID THIO_RABIT STANDARD; PRT; 104 AA.
AC P08628;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioredoxin.
GN Name=TXN;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
NCBI_TaxID=9986;
RN (1)
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Bone marrow;
RA MEDLINE=88257078; PubMed=3164311;
RA Johnson R.S., Mathews W.R., Blemann K., Hopper S.;
RT "Amino acid sequence of thioredoxin isolated from rabbit bone marrow
RT determined by tandem mass spectrometry.";
RL J. Biol. Chem. 263:9589-9597(1988).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A28086; A28086.
CC DR HSSP; P10599; 1ERF.
CC DR SMR; P08628; 1-104.
CC DR InterPro; IPR006662; ThioRed.
CC DR InterPro; IPR006663; Thioredox.
CC DR InterPro; IPR005746; Thioredoxin.
CC DR InterPro; IPR012336; Thioredoxin.
CC DR InterPro; IPR012335; Thioredoxin-like.
CC DR Pfam; PF00085; Thioredoxin_fold.
CC DR PRINTS; PR00421; THIOREDOXIN.
CC DR TIGRFS; TIGR01068; thioredoxin; 1.
CC DR PROSITE; PS00194; THIOREDOXIN; 1.
CC KW Direct protein sequencing; Electron transport; Redox-active center;
CC Transport.
CC FT ACT_SITE 31 31 Nucleophile (By similarity).
CC FT ACT_SITE 34 34 Nucleophile (By similarity).
CC FT SITE 25 25 Deprotonates C-terminal active site Cys
CC (By similarity).
CC FT SITE 32 32 contributes to redox potential value (By
CC FT SITE 33 33 similarity).
CC FT SITE 33 33 contributes to redox potential value (By
CC similarity).

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FT DISULFID 31 34 Redox-active (By similarity).
 SQ SEQUENCE 104 AA; 11629 MW; C4B6E5EBEC231F CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 46
 THIO_RAT STANDARD; PRT; 104 AA.
 AC P1132;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioedoxin.
 OS Name=Txn;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Liver;
 RX MEDLINE=9282399; PubMed=2734107;
 RA Tonissen K.F., Robins A.J., Wells J.R.E.;
 RT "Nucleotide sequence of a cDNA encoding rat thioedoxin.";
 RL Nucleic Acids Res. 17:3973-3973(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Xie Z.H., Liu C.Z., He Y.H., Wang A.M., Ma C.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioedoxin family.
 CC -1- SIMILARITY: Contains 1 thioedoxin domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; X14878; CAJ3019.1; -, mRNA.
 DR EMBL; AF311055; AAG49923.1; -, mRNA.
 DR EMBL; BC058454; AA58454.1; -, mRNA.
 DR PIR; S04352; S04352.
 DR HSSP; P10599; 1ERT.
 DR SMR; P1132; 1-103.
 DR Ensemble; ENSMNOG0000012081; Rattus norvegicus.
 DR RGD; 621157; Txn.
 DR GO; GO:0004791; P:thioedoxin-disulfide reductase activity; TAS.
 DR GO; GO:0006118; P:electron transport; TAS.
 DR InterPro; IPR006662; Thioedox.
 DR InterPro; IPR006663; Thioedox_dom2.
 DR InterPro; IPR012336; Thioedoxin-like.
 DR InterPro; IPR012335; Thioedoxin_fold.
 DR Pfam; PF00085; Thioedoxin_1.
 DR PRINTS; PR00421; THIOEDOXIN.
 DR PROSITE; PS00194; THIOEDOXIN; 1.

KW Electron transport; Redox-active center; Transport.
 FT INIT MET 0 0 By similarity.
 FT ACT SITE 31 31 Nucleophile (By similarity).
 FT ACT_SITE 34 34 Nucleophile (By similarity).
 FT SITE 25 25 Deprotonates C-terminal active site Cys
 FT SITE 25 25 (By similarity).
 FT SITE 32 32 Contributes to redox potential value (By
 FT SITE 33 33 similarity).
 FT SITE 33 33 Contributes to redox potential value (By
 FT SITE 34 34 similarity).
 FT DISULFID 31 34 Redox-active (By similarity).
 SQ SEQUENCE 104 AA; 11542 MW; 60ACF19609ED773 CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 47
 THIO_SHEEP STANDARD; PRT; 104 AA.
 ID THIO_SHEEP
 AC P50413;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioedoxin.
 OS Name=Txn;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=95078463; PubMed=7987015;
 RA Droogmans L., Cleuter Y., Mollman E.E., Kettmann R., Burny A.;
 RT "Nucleotide sequence of ovine thioedoxin cDNA.";
 RL DNA Seq. 4:277-279(1994).
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioedoxin family.
 CC -1- SIMILARITY: Contains 1 thioedoxin domain.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Z25864; CAAB1083.1; -, mRNA.
 DR HSSP; P10599; 1ERT.
 DR SMR; P50413; 1-104.
 DR InterPro; IPR006662; Thioedox.
 DR InterPro; IPR006663; Thioedox_dom2.
 DR InterPro; IPR012336; Thioedoxin-like.
 DR InterPro; IPR012335; Thioedoxin_fold.
 DR Pfam; PF00085; Thioedoxin_1.
 DR PRINTS; PR00421; THIOEDOXIN.
 DR PROSITE; PS00194; THIOEDOXIN; 1.
 DR EPROSITE; PS00194; THIOEDOXIN; 1.
 KW ELECTRON TRANSPORT; Redox-active center; Transport.
 FT INIT MET 0 0 By similarity.
 FT ACT SITE 31 31 Nucleophile (By similarity).
 FT ACT_SITE 34 34 Nucleophile (By similarity).
 FT SITE 25 25 Deprotonates C-terminal active site Cys
 FT SITE 25 25 (By similarity).
 FT SITE 32 32 Contributes to redox potential value (By
 FT SITE 33 33 similarity).
 FT SITE 33 33 Contributes to redox potential value (By
 FT SITE 34 34 similarity).
 FT DISULFID 31 34 Redox-active (By similarity).
 SQ SEQUENCE 104 AA; 11542 MW; 60ACF19609ED773 CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FT SITE 33 33 similarity).
FT SITE 31 34 contributes to redox potential value (By
FT DISULFID 31 34 similarity).
SQ SEQUENCE 104 AA; 11711 MW; 506CE54C5642208D CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 48
THIO_STAA
ID THIO_STAA STANDARD; PRT; 104 AA.
AC POAOK4; Q9ZEH4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioedoxin (TRX).
GN Name=trxA; Ordered locus names=SAV1145;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- FUNCTION: Component of the thioredoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -!- SIMILARITY: Belongs to the thioredoxin family.
CC -!- SIMILARITY: Contains 1 thioredoxin domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC DR EMBL; BA000017; BAB57307.1; -; Genomic_DNA.
CC DR HSSP; P00274; ITPP.
CC DR InterPro; IPR006662; ThioRed.
CC DR InterPro; IPR006663; ThioRedox_dom2.
CC DR InterPro; IPR005746; ThioRedoxin.
CC DR InterPro; IPR012336; ThioRedoxin-like.
CC DR InterPro; IPR012335; ThioRedoxin_fold.
CC DR Pfam; PF00085; ThioRedoxin_1.
CC DR PRINTS; PR00421; THIOREDOXIN.
CC DR TIGRfam; TIGR01068; ThioRedoxin; 1.
CC DR PROSITE; PS00194; THIOREDOXIN; 1.
CC DR Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 29 32 Redox-active (By similarity).
SQ SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 WCGPCK 6
DB 28 WCGPCK 33

RESULT 49
THIO_STAA
ID THIO_STAA STANDARD; PRT; 104 AA.
AC P99132; Q9ZEH4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioedoxin (TRX).
GN Name=trxA; Ordered locus names=SA0992;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- FUNCTION: Component of the thioredoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -!- SIMILARITY: Belongs to the thioredoxin family.
CC -!- SIMILARITY: Contains 1 thioredoxin domain.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC DR EMBL; BA000018; BAB4241.1; -; Genomic_DNA.
CC DR PIR; E89885; E89885.
CC DR HSSP; P00274; ITPP.
CC DR SWISS-2DPAGE; P99132; STAA.
CC DR InterPro; IPR006662; ThioRed.
CC DR InterPro; IPR006663; ThioRedox_dom2.
CC DR InterPro; IPR005746; ThioRedoxin.
CC DR InterPro; IPR012336; ThioRedoxin-like.
CC DR InterPro; IPR012335; ThioRedoxin_fold.
CC DR Pfam; PF00085; ThioRedoxin_1.
CC DR PRINTS; PR00421; THIOREDOXIN.
CC DR TIGRfam; TIGR01068; ThioRedoxin; 1.
CC DR PROSITE; PS00194; THIOREDOXIN; 1.
CC DR Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 29 32 Redox-active (By similarity).
SQ SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 28 WCGPCK 33

RESULT 50
THIO_STAA
ID THIO_STAA STANDARD; PRT; 104 AA.

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AC O6GHU0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE ThioRedoxin (TRX).
GN Name=trxA; OrderedLocNames=SAR1118;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
(1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Errington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- FUNCTION: Component of the thioRedoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioRedoxin family.
CC -1- SIMILARITY: Contains 1 thioRedoxin domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; BX571856; CAG40121.1; -; Genomic_DNA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KM Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 29 32 Redox-active (By similarity).
SQ SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RN
RX PubMed=15213324; DOI=10.1073/pnas.0402521101.
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Errington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- FUNCTION: Component of the thioRedoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioRedoxin family.
CC -1- SIMILARITY: Contains 1 thioRedoxin domain.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; BX571857; CAG42854.1; -; Genomic_DNA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KM Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 29 32 Redox-active (By similarity).
SQ SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 52
THIO_STNAU
ID THIO_STNAU STANDARD; PRT; 104 AA.
AC POA0K6; Q9ZE4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE ThioRedoxin (TRX).
GN Name=trxA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
(1)
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Oxiford;
RA Uziel O., Borovok I., Schreiber R., Cohen G., Aharonowitz Y.;
RT "Transcriptional analysis of the thioRedoxin (trxA) and thioRedoxin
RT reductase (trxB) genes in Staphylococcus aureus.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Component of the thioRedoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the

```

```
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
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CC removed.
CC -----
CC EMBL; AJ223480; CA11404.1; -; Genomic_DNA.
CC HSSP; P00274; 1T7P.
CC InterPro; IPR006662; Thiored.
CC InterPro; IPR006663; Thioredox_dom2.
CC InterPro; IPR005746; Thioredoxin.
CC InterPro; IPR012336; Thioredoxin-like.
CC InterPro; IPR012335; Thioredoxin_fold.
CC Pfam; PF00085; Thioredoxin_1.
CC PRINTS; PR00421; THIOREDOXIN.
CC TIGRfam; TIGR01068; thioredoxin; 1.
CC PROSITE; PS00194; THIOREDOXIN; 1.
CC Electron transport; Redox-active center; Transport.
CC DISULFID 29 32 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 28 WCGPCK 33

RESULT 53
THIO_STAAM STANDARD; PRT; 104 AA.
AC P0A0F5; Q9ZE84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioredoxin (TRX).
GN Name:trxA; OrderedLocustNames=MM1028;
OS Staphylococcus aureus (strain MM02).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=196620;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamamoto K., Hiratake K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- FUNCTION: Component of the thioredoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000033; BAB94893.1; -; Genomic_DNA.
CC HSSP; P00274; 1T7P.
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DR InterPro; IPR006662; Thiored.
DR InterPro; IPR006663; Thioredox_dom2.
DR InterPro; IPR005746; Thioredoxin.
DR InterPro; IPR012336; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF00085; Thioredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfam; TIGR01068; thioredoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 29 32 Redox-active (By similarity).
SQ SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 28 WCGPCK 33

RESULT 54
THIO_STAAM STANDARD; PRT; 104 AA.
AC O8CPF5;
DT 29-MAR-2004 (Rel. 43, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE Thioredoxin (TRX).
GN Name:trxA; OrderedLocustNames=SE0838;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1282;
RX MEDLINE=22832016; PubMed=12950922;
DOI=10.1046/j.1365-2958.2003.03671.x;
RA Zhang Y.-Q., Ren S.-X., Li H.-U., Wang Y.-X., Fu G., Yang J.,
RA Qian Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yin Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
CC -1- FUNCTION: Component of the thioredoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE016746; AA004435.1; -; Genomic_DNA.
CC HSSP; P00274; 1T7P.
CC InterPro; IPR006662; Thiored.
CC InterPro; IPR006663; Thioredox_dom2.
CC InterPro; IPR005746; Thioredoxin.
CC InterPro; IPR012336; Thioredoxin-like.
CC InterPro; IPR012335; Thioredoxin_fold.
CC Pfam; PF00085; Thioredoxin_1.
CC PRINTS; PR00421; THIOREDOXIN.
CC TIGRfam; TIGR01068; thioredoxin; 1.
CC PROSITE; PS00194; THIOREDOXIN; 1.
CC Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 29 32 Redox-active (By similarity).
SQ SEQUENCE 104 AA; 11443 MW; DBBC61D2DA7E770 CRC64;
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Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 28 WCGPCK 33

RESULT 55
 Q6CN03_KLULA PRELIMINARY; PRT; 104 AA.
 AC Q6CN03;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Similar to sp|P22217 Saccharomyces cerevisiae YLR043c TRX1 thioredoxin
 DE 1.
 GN OrderedLocustNames=KLULA0B16401g;
 OS Kluyveromyces lactic (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxId=28985;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 Lafontaine I., de Montigny J., Marck C., Neuvéglise S., Talla E.,
 Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 Boistrame A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,
 Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
 Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 Nicard J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 Swennen D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
 Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissendach J.,
 Wincker P., Souciet J.-L.;
 RA "Genome evolution in yeasts."
 RT Nature 430:35-44(2004).
 DR EMBL: CR382125; CAG9773.1; -; Genomic DNA.
 DR GO: GO:0005489; P:electron transporter activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR006662; ThioRed.
 DR InterPro: IPR006663; ThioRedox_dom2.
 DR InterPro: IPR005746; ThioRedoxin.
 DR InterPro: IPR012336; ThioRedoxin-like.
 DR InterPro: IPR012335; ThioRedoxin_fold.
 DR Pfam: PF00085; ThioRedoxin_1.
 DR PRINTS: PR00421; THIOREDOXIN.
 DR TIGRFS: TIGR01068; thioredoxin; 1.
 DR PROSITE: PS00194; THIOREDOXIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 104 AA; 11332 MW; D2EACE1R82EDFE5 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 29 WCGPCK 34

RESULT 56
 Q6C399_YARLI PRELIMINARY; PRT; 104 AA.
 AC Q6C399;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)

DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Similar to sp|P22803 Saccharomyces cerevisiae YCR209c TRX2 thioredoxin
 DE 1.
 GN OrderedLocustNames=YALIOF01496g;
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxId=4952;
 [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CLIB 122 / E 150;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 Lafontaine I., de Montigny J., Marck C., Neuvéglise S., Talla E.,
 Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 Boistrame A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,
 Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
 Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 Nicard J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 Swennen D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
 Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissendach J.,
 Wincker P., Souciet J.-L.;
 RA "Genome evolution in yeasts."
 RT Nature 430:35-44(2004).
 DR EMBL: CR382132; CAG77665.1; -; Genomic DNA.
 DR GO: GO:0005489; P:electron transporter activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR006662; ThioRed.
 DR InterPro: IPR006663; ThioRedox_dom2.
 DR InterPro: IPR005746; ThioRedoxin.
 DR InterPro: IPR012336; ThioRedoxin-like.
 DR InterPro: IPR012335; ThioRedoxin_fold.
 DR Pfam: PF00085; ThioRedoxin_1.
 DR PRINTS: PR00421; THIOREDOXIN.
 DR TIGRFS: TIGR01068; thioredoxin; 1.
 DR PROSITE: PS00194; THIOREDOXIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 104 AA; 11336 MW; 9A92D40C2B494CFB CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 30 WCGPCK 35

RESULT 57
 Q5K555_CRYNE PRELIMINARY; PRT; 104 AA.
 AC Q5K555;
 DT 10-MAY-2005 (T-EMBLrel. 30, Created)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
 DE Thioredoxin (Allergen cop c 2), putative.
 GN ORFNames=CNC04200;
 OS Crypsococcus neoformans var. neoformans JEC21.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxId=214684;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JEC21;
 RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
 Van Aken S., Fraser C.;
 RN Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JEC21;
 RX PubMed=15653466; DOI=10.1126/science.1103773;
 RA Loftus B.J., Fung B., Roncaglia P., Rowley D., Amadio P., Bruno D.,
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grimbey V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janson G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Perera M., Riggs F.R., Salzberg S.L.,
 RA Schein J.E., Schwartzbeyn A., Shin H., Shimway M., Specht C.A.,
 RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.;
 RT "The genome of the basidiomycetous yeast and human pathogen
 RT *Cryptococcus neoformans*."
 RL Science 307:1321-1324(2005).
 DR EMBL; AB017343; AA042360.1; -, Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006663; Thiorod. domain2.
 DR InterPro; IPR005746; Thiorodoxin.
 DR InterPro; IPR012336; Thiorodoxin-like.
 DR InterPro; IPR012335; Thiorodoxin_fold.
 DR Pfam; PF00085; Thiorodoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; thiorodoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 104 AA; 11451 MW; 1594CFPF30868BA CRC64;

Query Match
 Best Local Similarity 100.0%; Score 47; DB 2; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 58
 OS5W38 CRYNE PRELIMINARY; PRT; 104 AA.
 ID 05W38 CRYNE PRELIMINARY; PRT; 104 AA.
 AC 05W38;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=CNBC2990;
 OS *Cryptococcus neoformans* var. *neoformans* B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellales; Tremellaceae; Filobasidiella.
 OC NCBI_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung B., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wickes B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing."
 RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AA01000013; EAL22161.1; -, Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006663; Thiorod.
 DR InterPro; IPR005746; Thiorodox.
 DR InterPro; IPR012336; Thiorodoxin-like.
 DR InterPro; IPR012335; Thiorodoxin_fold.
 DR Pfam; PF00085; Thiorodoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; thiorodoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 SQ SEQUENCE 104 AA; 11717 MW; 2F507E17F276171F CRC64;

DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; thiorodoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 104 AA; 11451 MW; 1594CFPF30868BA CRC64;

Query Match
 Best Local Similarity 100.0%; Score 47; DB 2; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 59
 OS9NIR2 PLAFa PRELIMINARY; PRT; 104 AA.
 ID 09NIR2 PLAFa PRELIMINARY; PRT; 104 AA.
 AC 09NIR2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Thiorodoxin 1.
 GN Name=TXR1;
 OS *Plasmodium falciparum*.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5833;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20568274; PubMed=11013257; DOI=10.1074/jbc.M007633200;
 RA Kanok S.M., Schimer R.H., Turbachova I., Iozef R., Becker K.;
 RT "The thiorodoxin system of the malaria parasite *Plasmodium falciparum*.
 RT Glutathione reduction revisited".
 RL J. Biol. Chem. 275:40180-40186(2000).
 DR EMBL; AF202664; AAF34541.1; -, mRNA.
 DR HSSP; P80028; 1EP7.
 DR SMR; 09NIR2; 1-103.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006663; Thiorod.
 DR InterPro; IPR005746; Thiorodox.
 DR InterPro; IPR012336; Thiorodoxin-like.
 DR InterPro; IPR012335; Thiorodoxin_fold.
 DR Pfam; PF00085; Thiorodoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; thiorodoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 SQ SEQUENCE 104 AA; 11717 MW; 2F507E17F276171F CRC64;

Query Match
 Best Local Similarity 100.0%; Score 47; DB 2; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 60
 OS9NFK9 PLAFa PRELIMINARY; PRT; 104 AA.
 ID 09NFK9 PLAFa PRELIMINARY; PRT; 104 AA.
 AC 09NFK9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Thiorodoxin.
 GN Name=txr;
 OS *Plasmodium falciparum*.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5833;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=3D7;
RL Krnajtski Z., Gilberger T.W., Walter R.D., Mueller S.;
  Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A2277839; CAB90828.1; -, mRNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR012336; ThioRedoxin.
DR InterPro; IPR012335; ThioRedoxin-like.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAM; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match          100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
DB 29 WCGSPCK 34

RESULT 61
ID Q7RH10.PLAYO PRELIMINARY; PRT; 104 AA.
AC Q7RH10;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ThioRedoxin.
GN Name=pf04185;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=73239;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1XNU;
  MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
  Carlson J.M., Angluoli S.V., Suh B.B., Kooij T.W., Perrea M.,
  Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.P., Koo H.L.,
  Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
  Shallow S.J., van Aken S.E., Riedmiller S.B., Feldbylun T.V.,
  Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
  Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
  Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
  van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
  Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
  Carucci D.J.;
  "Genome sequence and comparative analysis of the model rodent malaria
  parasite Plasmodium yoelii yoelii."
  Nature 419:512-519(2002).
-1- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
CC EMBL; AABL01001248; EAA16007.1; -, Genomic DNA.
CC HSSP; P80028; 1EP7.
DR SMR; Q7RH10; 1-103.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAM; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN 1.
SQ SEQUENCE 104 AA; 11622 MW; A29D2915116F2B83 CRC64;

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Query Match          100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
DB 29 WCGSPCK 34

RESULT 62
ID Q7KOL8.PLAF7 PRELIMINARY; PRT; 104 AA.
AC Q7KOL8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE ThioRedoxin.
GN ORFNames=PF14_0545;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=36329;
[1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
  Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
  Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
  Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
  Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angluoli S.,
  Perrea M., Allen J., Selengut J., Hatt D., Mather M.W., Valdivia A.B.,
  Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
  McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
  Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
  Fraser C.M., Barrell B.G.;
  "Genome sequence of the human malaria parasite Plasmodium
  falciparum."
  Nature 419:498-511(2002).
DR EMBL; AE014825; AAN37158.1; -, Genomic DNA.
DR PDB; 1SYR; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-104.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAM; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match          100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
DB 29 WCGSPCK 34

RESULT 63
ID O6B963.SCHMA PRELIMINARY; PRT; 104 AA.
AC O6B963;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ThioRedoxin 2.
GN Name=Trx-2;
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
  Schistosomatidae; Schistosomatidae; Schistosoma.

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OX NCBI_TaxID=6183;
 RN [1]
 AC NUCLEOTIDE SEQUENCE.
 RC STRAIN=Puerto Rican;
 RA Beers L.F., Williams D.L.;
 DT "Thioredoxin-2 in Schistosoma mansoni";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY673828; AAT76629.1; -; mRNA.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRPFAMs; TIGR01068; ThioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 SQ SEQUENCE 104 AA; 11995 MW; 8D36E829BF4A4A2 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGSPCK 6
 |||||
 DB 30 WCGSPCK 35

RESULT 64
 ID OSDAX8 SCHUA PRELIMINARY; PRT; 104 AA.
 AC OSDAX8;
 DT 10-MAY-2005 (TReMBLrel. 30, Created)
 DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Han Z.;
 RT "The full-length cDNA sequences of Schistosoma japonicum genes";
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY815296; AAW27028.1; -; mRNA.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRPFAMs; TIGR01068; ThioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 104 AA; 11921 MW; 8D36E83058742262 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGSPCK 6
 |||||
 DB 30 WCGSPCK 35

RESULT 65
 Q48985_MYCCA

ID Q48985 MYCCA PRELIMINARY; PRT; 104 AA.
 AC Q48985;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Thioredoxin (Fragment).
 OS Mycoplasma capricolum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2095;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 27343;
 RX MEDLINE=96059641; PubMed=7476192;
 RA Bork P., Ouzounis C., Casari G., Schneider R., Sander C., Dolan M.,
 RA Gilbert W., Gillevet P.M.;
 RT "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
 its physiology";
 RL Mol. Microbiol. 16:955-967(1995).
 DR EMBL; Z33053; CAA83726.1; -; Genomic_DNA.
 DR PIR; S77780; S77780.
 DR HSSP; PR0028; 1BP7.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR005746; ThioRedoxin.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRPFAMs; TIGR01068; ThioRedoxin; 1.
 FT NON TER 1
 SQ SEQUENCE 104 AA; 11825 MW; C133AFBFB027A001 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGSPCK 6
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 DB 32 WCGSPCK 37

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 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Thioredoxin.
 GN Name:trx; ORFNames=CUP1008;
 OS Campylobacter upsaliensis RM3195.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteriaceae; Campylobacter.
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 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=RM3195;
 RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasco D.A.,
 RA Jacques R.J., Birkack L.M., Deboy R.T., Parker C.T., Daugherty S.C.,
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
 RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
 RA Nelson K.E.;
 RT "Major structural and novel potential virulence mechanisms from the
 genomes of multiple Campylobacter species";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AA01000012; EAL52411.1; -; Genomic DNA.
 SQ SEQUENCE 104 AA; 11271 MW; 3056CAA6930B8F74 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
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 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candellon B.,
 RA Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Gotsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pasch G., Haselkorn R., Fomstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;
 RT "Genome sequence of *Bacillus cereus* and comparative analysis with
 RT *Bacillus anthracis*."
 RL Nature 423:87-91(2003).
 DR EMBL: AE017012; AAP11431.1; -; Genomic_DNA.
 DR HSSP: P80579; INSW.
 DR GO: GO:0005489; F:electron transporter activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR006662; ThioRed.
 DR InterPro: IPR005746; ThioRedox_dom2.
 DR InterPro: IPR006663; ThioRedoxin.
 DR Pfam: PF00085; ThioRedoxin; 1.
 DR PRINTS: PR00421; THIOREDOXIN.
 DR TIGRFAMs: TIGR01068; thioRedoxin; 1.
 DR PROSITE: PS00134; THIOREDOXIN; 1.
 KM Complete proteome.
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Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
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 Db 28 WCGPCK 33

Search completed: February 23, 2006, 00:42:00
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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:42:19 ; Search time 34.5 Seconds
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Title: US-10-660-118A-3
Perfect score: 47
Sequence: 1 WCGPCK 6

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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2	47	100.0	6	2	US-08-627-907A-6 Sequence 6, Appl1
3	47	100.0	6	2	US-07-901-713A-3 Sequence 3, Appl1
4	47	100.0	12	2	US-08-750-142B-54 Sequence 54, Appl1
5	47	100.0	104	6	5210073-1 Patent No. 5210073
6	47	100.0	105	1	US-08-826-910-3 Sequence 3, Appl1
7	47	100.0	105	1	US-08-826-910-4 Sequence 4, Appl1
8	47	100.0	105	2	US-09-601-144-68 Sequence 68, Appl1
9	47	100.0	105	2	US-09-513-999C-8037 Sequence 8037, Ap
10	47	100.0	106	1	US-08-386-729A-10 Sequence 10, Appl
11	47	100.0	109	1	US-07-745-382-22 Sequence 22, Appl
12	47	100.0	109	1	US-07-921-848-22 Sequence 22, Appl
13	47	100.0	109	1	US-08-165-301A-22 Sequence 22, Appl
14	47	100.0	109	1	US-08-165-301A-26 Sequence 26, Appl
15	47	100.0	109	1	US-08-165-301A-28 Sequence 28, Appl
16	47	100.0	109	2	US-08-810-436-22 Sequence 22, Appl
17	47	100.0	109	2	US-08-810-436-26 Sequence 26, Appl
18	47	100.0	109	2	US-08-810-436-28 Sequence 28, Appl
19	47	100.0	109	2	US-09-485-885-17 Sequence 17, Appl
20	47	100.0	109	2	US-09-166-966E-10 Sequence 10, Appl
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22	47	100.0	109	4	PCT-US94-14179-22 Sequence 22, Appl
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76	47	93.6	114	2	US-09-107-433-2930 Sequence 2930, Ap
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93	47	93.6	130	2	US-10-091-841A-6 Sequence 6, Appl1
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143	38	80.9	139	2	US-08-874-102-36	Sequence 36, Appl	216	38	80.9	505	1	US-08-068-395A-3	Sequence 3, Appl1
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156	38	80.9	179	2	US-08-874-102-44	Sequence 44, Appl	229	38	80.9	510	1	US-08-557-122A-28	Sequence 28, Appl
157	38	80.9	179	2	US-08-984-919A-41	Sequence 41, Appl	230	38	80.9	510	1	US-08-557-122A-30	Sequence 30, Appl
158	38	80.9	179	2	US-08-984-919A-44	Sequence 44, Appl	231	38	80.9	510	1	US-08-557-122A-36	Sequence 36, Appl
159	38	80.9	179	2	US-09-248-796A-18386	Sequence 18386, A	232	38	80.9	510	2	US-09-262-666-28	Sequence 28, Appl
160	38	80.9	200	1	US-08-557-122A-12	Sequence 12, Appl	233	38	80.9	510	2	US-09-262-666-30	Sequence 30, Appl
161	38	80.9	200	2	US-09-262-666-12	Sequence 12, Appl	234	38	80.9	510	2	US-09-262-666-36	Sequence 36, Appl
162	38	80.9	201	2	US-09-252-991A-29895	Sequence 29895, A	235	38	80.9	511	1	US-08-557-122A-4	Sequence 4, Appl1
163	38	80.9	207	2	US-09-603-208A-68	Sequence 68, Appl	236	38	80.9	511	2	US-09-262-666-4	Sequence 4, Appl1
164	38	80.9	207	2	US-09-605-703B-1726	Sequence 1726, Ap	237	38	80.9	512	2	US-08-557-122A-33	Sequence 33, Appl
165	38	80.9	235	2	US-08-781-420-6	Sequence 6, Appl1	238	38	80.9	512	2	US-09-262-666-33	Sequence 33, Appl
166	38	80.9	235	2	US-08-874-102-6	Sequence 6, Appl1	239	38	80.9	515	1	US-08-557-122A-3	Sequence 3, Appl1
167	38	80.9	235	2	US-08-984-919A-6	Sequence 6, Appl1	240	38	80.9	515	1	US-08-557-122A-34	Sequence 34, Appl
168	38	80.9	244	2	US-09-006-595A-6	Sequence 6, Appl1	241	38	80.9	515	2	US-09-262-666-3	Sequence 3, Appl1
169	38	80.9	244	2	US-09-807-258-20	Sequence 20, Appl	242	38	80.9	515	2	US-09-262-666-34	Sequence 34, Appl
170	38	80.9	266	2	US-09-248-796A-19900	Sequence 19900, A	243	38	80.9	515	2	US-09-807-258-38	Sequence 38, Appl
171	38	80.9	281	1	US-08-557-122A-5	Sequence 5, Appl1	244	38	80.9	521	1	US-08-557-122A-32	Sequence 32, Appl
172	38	80.9	281	2	US-09-262-666-5	Sequence 5, Appl1	245	38	80.9	521	2	US-09-262-666-32	Sequence 32, Appl
173	38	80.9	289	2	US-09-807-258-22	Sequence 22, Appl	246	38	80.9	522	2	US-09-368-588-2	Sequence 2, Appl1

247	38	80.9	530	1	US-08-557-122A-35	Sequence 35, Appl	320	34	72.3	362	2	US-09-296-840A-2	Sequence 2, Appl
248	38	80.9	531	1	US-09-262-666-35	Sequence 35, Appl	321	34	72.3	367	2	US-09-296-840A-3	Sequence 3, Appl
249	38	80.9	531	1	US-08-923-538A-12	Sequence 12, Appl	322	34	72.3	322	2	US-10-315-432-6	Sequence 6, Appl
250	38	80.9	566	1	US-08-419-078-2	Sequence 2, Appl	323	34	72.3	494	2	US-09-949-016-7790	Sequence 7790, Ap
251	38	80.9	566	1	US-08-726-883-2	Sequence 2, Appl	324	34	72.3	541	2	US-09-417-251A-8	Sequence 8, Appl
252	38	80.9	638	1	US-08-557-122A-38	Sequence 38, Appl	325	34	72.3	541	2	US-09-417-251A-8	Sequence 8, Appl
253	38	80.9	638	2	US-09-262-666-38	Sequence 38, Appl	326	34	72.3	549	2	US-09-902-5540-11972	Sequence 11972, A
254	38	80.9	645	2	US-09-538-092-920	Sequence 920, App	327	34	72.3	551	2	US-09-417-251A-16	Sequence 16, Appl
255	38	80.9	3052	1	US-08-557-122A-26	Sequence 26, Appl	328	34	72.3	551	2	US-09-417-251A-16	Sequence 16, Appl
256	38	80.9	3052	1	US-09-262-666-26	Sequence 26, Appl	329	34	72.3	570	2	US-09-417-251A-10	Sequence 10, Appl
257	37	78.7	183	2	US-09-543-681A-5268	Sequence 5268, Ap	330	34	72.3	591	2	US-09-252-991A-31286	Sequence 3186, A
258	37	78.7	255	2	US-09-248-796A-18387	Sequence 18387, A	331	34	72.3	591	2	US-09-252-991A-31286	Sequence 3186, A
259	37	78.7	312	2	US-09-270-767-46652	Sequence 46652, A	332	34	72.3	675	2	US-10-104-047-3810	Sequence 3810, Ap
260	37	78.7	581	2	US-09-649-747A-13	Sequence 13, Appl	333	33	70.2	8	2	US-08-882-046-105	Sequence 105, App
261	37	78.7	581	2	US-09-649-747A-21	Sequence 21, Appl	334	33	70.2	8	2	US-09-566-047-105	Sequence 105, App
262	36	76.6	37	2	US-09-330-914A-10	Sequence 10, Appl	335	33	70.2	38	2	US-08-504-358A-17	Sequence 17, Appl
263	36	76.6	40	2	US-09-270-767-61997	Sequence 61997, A	336	33	70.2	38	2	US-08-630-052-17	Sequence 17, Appl
264	36	76.6	63	2	US-09-252-991A-22358	Sequence 22358, A	337	33	70.2	38	4	PCT-US95-09307-17	Sequence 17, Appl
265	36	76.6	80	2	US-09-330-914A-4	Sequence 4, Appl	338	33	70.2	53	2	US-09-513-999C-5904	Sequence 5904, Ap
266	36	76.6	104	2	US-09-134-000C-5853	Sequence 5853, Ap	339	33	70.2	65	2	US-09-248-796A-22500	Sequence 22500, A
267	36	76.6	105	2	US-09-583-110-3678	Sequence 3678, Ap	340	33	70.2	67	2	US-09-513-999C-5905	Sequence 5905, Ap
268	36	76.6	109	2	US-09-107-532A-6799	Sequence 6799, Ap	341	33	70.2	78	2	US-09-513-999C-5905	Sequence 5905, Ap
269	36	76.6	109	2	US-09-107-433-3306	Sequence 3306, Ap	342	33	70.2	91	2	US-09-621-976-6454	Sequence 6454, Ap
270	36	76.6	109	2	US-09-902-540-13327	Sequence 13327, A	343	33	70.2	97	2	US-09-621-976-6454	Sequence 6454, Ap
271	36	76.6	126	2	US-09-902-540-15842	Sequence 15842, A	344	33	70.2	109	2	US-09-252-991A-28451	Sequence 28451, A
272	36	76.6	127	2	US-09-489-039A-13310	Sequence 13310, A	345	33	70.2	114	2	US-08-918-288-71	Sequence 71, Appl
273	36	76.6	127	2	US-09-621-976-6292	Sequence 6292, Ap	346	33	70.2	114	2	US-09-282-357-71	Sequence 71, Appl
274	36	76.6	129	2	US-10-104-047-2145	Sequence 2145, Ap	347	33	70.2	121	2	US-10-360-101-251	Sequence 251, App
275	36	76.6	140	2	US-09-330-914A-9	Sequence 9, Appl	348	33	70.2	122	2	US-09-630-273-1	Sequence 273, Appl
276	36	76.6	150	2	US-09-330-914A-6	Sequence 6, Appl	349	33	70.2	125	2	US-09-199-637A-317	Sequence 317, App
277	36	76.6	168	2	US-09-252-991A-30752	Sequence 30752, A	350	33	70.2	130	2	US-09-621-976-6905	Sequence 6905, Ap
278	36	76.6	173	2	US-09-270-767-47576	Sequence 47576, A	351	33	70.2	134	2	US-08-543-246B-20	Sequence 20, Appl
279	36	76.6	173	2	US-09-270-767-47576	Sequence 47576, A	352	33	70.2	145	2	US-09-489-039A-13200	Sequence 13200, A
280	36	76.6	225	2	US-09-252-991A-29348	Sequence 29348, A	353	33	70.2	145	2	US-09-489-039A-13200	Sequence 13200, A
281	36	76.6	368	2	US-09-252-991A-32498	Sequence 32498, A	354	33	70.2	151	2	US-09-252-991A-17203	Sequence 17203, A
282	36	76.6	380	2	US-08-468-846-2	Sequence 2, Appl	355	33	70.2	163	2	US-09-252-991A-22083	Sequence 22083, A
283	36	76.6	380	2	US-08-915-096A-2	Sequence 2, Appl	356	33	70.2	171	2	US-09-902-540-13819	Sequence 13819, A
284	36	76.6	384	2	US-09-949-016-9661	Sequence 9661, Ap	357	33	70.2	178	2	US-08-748-506-17	Sequence 17, Appl
285	36	76.6	404	2	US-09-248-796A-15586	Sequence 15586, A	358	33	70.2	182	2	US-09-252-991A-17152	Sequence 17152, A
286	36	76.6	445	2	US-09-252-991A-20277	Sequence 20277, A	359	33	70.2	196	2	US-09-252-991A-26388	Sequence 26388, A
287	36	76.6	451	2	US-09-489-039A-12526	Sequence 12526, A	360	33	70.2	199	2	US-09-252-991A-26388	Sequence 26388, A
288	36	76.6	461	2	US-09-543-681A-4286	Sequence 4286, Ap	361	33	70.2	216	2	US-08-543-246B-9	Sequence 9, Appl
289	36	76.6	462	2	US-09-328-352-4742	Sequence 4742, Ap	362	33	70.2	216	2	US-08-543-246B-24	Sequence 24, Appl
290	36	76.6	491	2	US-09-540-236-2383	Sequence 2383, Ap	363	33	70.2	223	2	US-09-543-681A-8063	Sequence 8063, Ap
291	36	76.6	537	2	US-09-252-991A-31581	Sequence 31581, A	364	33	70.2	223	2	US-09-949-002-508	Sequence 508, App
292	36	76.6	572	2	US-09-949-016-11207	Sequence 11207, A	365	33	70.2	228	2	US-09-252-991A-32898	Sequence 32898, A
293	36	76.6	609	2	US-09-270-767-46418	Sequence 46418, A	366	33	70.2	234	2	US-08-918-288-9	Sequence 9, Appl
294	36	76.6	627	2	US-09-902-540-15743	Sequence 15743, A	367	33	70.2	234	2	US-09-282-357-9	Sequence 9, Appl
295	36	76.6	671	2	US-09-248-796A-15763	Sequence 15763, A	368	33	70.2	256	2	US-09-270-767-45809	Sequence 45809, A
296	36	76.6	961	2	US-09-657-472-4	Sequence 4, Appl	369	33	70.2	258	2	US-08-303-861-18	Sequence 18, Appl
297	36	76.6	961	4	PCT-US93-11725-4	Sequence 4, Appl	370	33	70.2	258	2	US-08-303-861-19	Sequence 19, Appl
298	36	76.6	970	2	US-09-949-016-10131	Sequence 10131, A	371	33	70.2	258	2	US-09-213-343-2	Sequence 2, Appl
299	35	74.5	105	2	US-09-598-747-5	Sequence 5, Appl	372	33	70.2	287	1	US-08-424-641B-10	Sequence 10, Appl
300	35	74.5	174	2	US-09-489-039A-11944	Sequence 11944, A	373	33	70.2	287	1	US-08-820-980-10	Sequence 10, Appl
301	35	74.5	261	1	US-07-971-096-2	Sequence 2, Appl	374	33	70.2	287	1	US-08-820-980-10	Sequence 10, Appl
302	35	74.5	261	1	US-08-175-096-2	Sequence 2, Appl	375	33	70.2	287	1	US-08-820-980-10	Sequence 10, Appl
303	35	74.5	663	2	US-09-270-767-45897	Sequence 45897, A	376	33	70.2	291	2	US-09-438-165A-359	Sequence 359, App
304	35	74.5	111	2	US-10-315-432-2	Sequence 2, Appl	377	33	70.2	302	2	US-08-303-861-20	Sequence 20, Appl
305	34	72.3	138	2	US-09-898-659-30	Sequence 30, Appl	378	33	70.2	305	2	US-09-248-796A-19800	Sequence 19800, A
306	34	72.3	148	2	US-09-270-767-46808	Sequence 46808, A	379	33	70.2	311	2	US-09-248-796A-20384	Sequence 20384, A
307	34	72.3	150	2	US-09-252-991A-29049	Sequence 29049, A	380	33	70.2	321	2	US-08-748-506-10	Sequence 10, Appl
308	34	72.3	163	2	US-09-252-991A-25077	Sequence 25077, A	381	33	70.2	321	2	US-08-748-506-11	Sequence 11, Appl
309	34	72.3	193	2	US-09-270-767-61072	Sequence 61072, A	382	33	70.2	321	2	US-08-748-506-12	Sequence 12, Appl
310	34	72.3	220	2	US-09-417-251A-12	Sequence 12, Appl	383	33	70.2	321	2	US-08-748-506-13	Sequence 13, Appl
311	34	72.3	220	2	US-09-417-251A-12	Sequence 12, Appl	384	33	70.2	321	2	US-08-748-506-18	Sequence 18, Appl
312	34	72.3	251	2	US-08-811-682-17	Sequence 17, Appl	385	33	70.2	321	2	US-08-748-506-19	Sequence 19, Appl
313	34	72.3	287	2	US-09-489-039A-7596	Sequence 7596, Ap	386	33	70.2	321	2	US-08-748-506-19	Sequence 19, Appl
314	34	72.3	294	2	US-09-417-251A-20	Sequence 20, Appl	387	33	70.2	358	2	US-10-104-047-3307	Sequence 3307, Ap
315	34	72.3	294	2	US-09-417-251A-20	Sequence 20, Appl	388	33	70.2	393	2	US-09-252-991A-28045	Sequence 28045, A
316	34	72.3	302	2	US-09-270-767-32413	Sequence 32413, A	389	33	70.2	433	2	US-09-252-991A-20376	Sequence 20376, A
317	34	72.3	302	2	US-09-270-767-47630	Sequence 47630, A	390	33	70.2	472	2	US-09-902-540-15926	Sequence 15926, A
318	34	72.3	330	2	US-09-252-991A-27803	Sequence 27803, A	391	33	70.2	477	2	US-09-876-221-2	Sequence 2, Appl
319	34	72.3	331	2	US-09-252-991A-21022	Sequence 21022, A	392	33	70.2	482	2	US-09-902-540-14708	Sequence 14708, A

393	33	70.2	524	2	US-09-252-991A-19294	Sequence 19294, A	466	32	68.1	149	1	US-08-425-673-5	Sequence 5, Appl1
394	33	70.2	559	2	US-09-512-260A-3	Sequence 3, Appl1	467	32	68.1	152	2	US-09-270-767-62449	Sequence 62449, A
395	33	70.2	566	2	US-09-252-991A-18531	Sequence 18531, A	468	32	68.1	163	1	US-08-463-262A-10	Sequence 10, Appl1
396	33	70.2	580	2	US-09-252-991A-29484	Sequence 29484, A	469	32	68.1	163	1	US-08-463-989-10	Sequence 10, Appl1
397	33	70.2	585	2	US-09-248-796A-20439	Sequence 20439, A	470	32	68.1	163	2	US-09-003-579-10	Sequence 10, Appl1
398	33	70.2	604	1	US-08-735-041A-4	Sequence 4, Appl1	471	32	68.1	163	2	US-09-003-579-10	Sequence 10, Appl1
399	33	70.2	604	2	US-09-190-476B-4	Sequence 4, Appl1	472	32	68.1	163	2	US-09-864-541A-10	Sequence 10, Appl1
400	33	70.2	604	2	US-09-190-889A-4	Sequence 4, Appl1	473	32	68.1	207	2	US-08-811-519-16	Sequence 16, Appl1
401	33	70.2	604	2	US-09-190-938B-4	Sequence 4, Appl1	474	32	68.1	207	2	US-08-811-519-16	Sequence 16, Appl1
402	33	70.2	610	2	US-09-902-540-13312	Sequence 13312, A	475	32	68.1	259	2	US-09-270-767-48758	Sequence 48758, A
403	33	70.2	615	2	US-09-345-473E-49	Sequence 49, Appl1	476	32	68.1	282	2	US-09-461-913A-38	Sequence 38, Appl1
404	33	70.2	615	2	US-09-862-027-49	Sequence 49, Appl1	477	32	68.1	304	2	US-09-397-550-16	Sequence 16, Appl1
405	33	70.2	659	2	US-09-270-767-44991	Sequence 44991, A	478	32	68.1	305	2	US-09-270-767-44149	Sequence 41419, A
406	33	70.2	701	1	US-08-735-041A-6	Sequence 6, Appl1	479	32	68.1	323	2	US-09-397-550-17	Sequence 17, Appl1
407	33	70.2	701	2	US-09-190-476B-6	Sequence 6, Appl1	480	32	68.1	326	2	US-09-252-991A-10870	Sequence 10870, A
408	33	70.2	701	2	US-09-190-889A-6	Sequence 6, Appl1	481	32	68.1	333	2	US-09-252-991A-13345	Sequence 13345, A
409	33	70.2	701	2	US-09-190-938B-6	Sequence 6, Appl1	482	32	68.1	335	2	US-09-252-991A-24494	Sequence 24494, A
410	33	70.2	717	2	US-09-949-016-6273	Sequence 6273, Ap	483	32	68.1	350	2	US-09-397-550-18	Sequence 18, Appl1
411	33	70.2	772	2	US-09-949-016-7655	Sequence 7655, Ap	484	32	68.1	370	2	US-09-902-540-10486	Sequence 10486, A
412	33	70.2	850	2	US-10-029-180-96	Sequence 96, Appl1	485	32	68.1	373	2	US-09-149-476-374	Sequence 374, Ap
413	33	70.2	859	2	US-10-029-180-108	Sequence 108, App	486	32	68.1	382	2	US-09-328-352-7738	Sequence 7738, Ap
414	33	70.2	956	2	US-09-949-016-11332	Sequence 11332, A	487	32	68.1	388	2	US-09-605-703B-2250	Sequence 2250, Ap
415	33	70.2	1010	2	US-08-882-046-7	Sequence 7, Appl1	488	32	68.1	405	2	US-09-799-978-38	Sequence 38, Appl1
416	33	70.2	1010	2	US-09-586-047-7	Sequence 7, Appl1	489	32	68.1	411	1	US-08-381-433A-4	Sequence 4, Appl1
417	33	70.2	1036	2	US-09-068-740A-6	Sequence 6, Appl1	490	32	68.1	411	2	US-08-981-189B-12	Sequence 12, Appl1
418	33	70.2	1067	2	US-09-579-536C-18	Sequence 18, Appl1	491	32	68.1	411	2	US-09-799-978-18	Sequence 18, Appl1
419	33	70.2	1187	2	US-09-068-740A-7	Sequence 7, Appl1	492	32	68.1	411	2	US-09-881-401-4	Sequence 4, Appl1
420	33	70.2	1193	1	US-08-400-159-10	Sequence 10, Appl1	493	32	68.1	430	2	US-09-799-978-26	Sequence 26, Appl1
421	33	70.2	1193	2	US-08-611-729A-10	Sequence 10, Appl1	494	32	68.1	431	1	US-08-381-433A-2	Sequence 2, Appl1
422	33	70.2	1193	2	US-09-195-524-10	Sequence 10, Appl1	495	32	68.1	431	2	US-08-981-189B-11	Sequence 11, Appl1
423	33	70.2	1193	2	US-09-310-685-8	Sequence 8, Appl1	496	32	68.1	431	2	US-08-981-189B-13	Sequence 13, Appl1
424	33	70.2	1208	2	US-09-199-865-1	Sequence 1, Appl1	497	32	68.1	431	2	US-08-482-746-10	Sequence 10, Appl1
425	33	70.2	1208	2	US-10-213-329-1	Sequence 1, Appl1	498	32	68.1	431	2	US-09-580-734-10	Sequence 10, Appl1
426	33	70.2	1218	1	US-08-400-159-6	Sequence 6, Appl1	499	32	68.1	431	2	US-08-374-009-10	Sequence 10, Appl1
427	33	70.2	1218	2	US-08-611-729A-6	Sequence 6, Appl1	500	32	68.1	431	2	US-09-191-724-10	Sequence 10, Appl1
428	33	70.2	1218	2	US-08-882-046-2	Sequence 2, Appl1	501	32	68.1	431	2	US-09-799-978-20	Sequence 20, Appl1
429	33	70.2	1218	2	US-09-214-278-7	Sequence 7, Appl1	502	32	68.1	431	2	US-09-799-978-24	Sequence 24, Appl1
430	33	70.2	1218	2	US-09-068-740A-11	Sequence 11, Appl1	503	32	68.1	431	2	US-09-881-401-2	Sequence 2, Appl1
431	33	70.2	1218	2	US-09-855-722-7	Sequence 7, Appl1	504	32	68.1	461	2	US-09-252-991A-19438	Sequence 19438, A
432	33	70.2	1218	2	US-09-566-047-2	Sequence 2, Appl1	505	32	68.1	483	2	US-09-252-991A-32383	Sequence 32383, A
433	33	70.2	1218	2	US-09-917-254-85	Sequence 85, Appl1	506	32	68.1	484	2	US-09-554-726A-2	Sequence 2, Appl1
434	33	70.2	1218	2	US-09-195-524-6	Sequence 6, Appl1	507	32	68.1	484	2	US-09-554-726A-12	Sequence 12, Appl1
435	33	70.2	1218	2	US-09-579-536C-1	Sequence 1, Appl1	508	32	68.1	522	2	US-10-070-634-11	Sequence 11, Appl1
436	33	70.2	1218	2	US-09-949-016-5902	Sequence 5902, Ap	509	32	68.1	625	2	US-09-252-991A-19871	Sequence 19871, A
437	33	70.2	1218	2	US-09-310-685-4	Sequence 4, Appl1	510	32	68.1	638	1	US-08-463-989-11	Sequence 11, Appl1
438	33	70.2	1219	2	US-08-882-046-5	Sequence 5, Appl1	511	32	68.1	638	1	US-08-463-989-11	Sequence 11, Appl1
439	33	70.2	1219	2	US-09-566-047-5	Sequence 5, Appl1	512	32	68.1	638	2	US-09-003-574-11	Sequence 11, Appl1
440	33	70.2	1254	2	US-09-949-016-10297	Sequence 10297, A	513	32	68.1	638	2	US-09-003-574-11	Sequence 11, Appl1
441	33	70.2	1551	2	US-09-231-899-73	Sequence 73, Appl1	514	32	68.1	638	2	US-09-864-541A-11	Sequence 11, Appl1
442	33	70.2	1622	2	US-09-211-899-72	Sequence 72, Appl1	515	32	68.1	676	2	US-09-003-574-34	Sequence 34, Appl1
443	33	70.2	2146	2	US-09-949-016-6947	Sequence 6947, Ap	516	32	68.1	676	2	US-09-003-574-34	Sequence 34, Appl1
444	33	70.2	29	2	US-09-149-476-627	Sequence 627, App	517	32	68.1	676	2	US-09-864-541A-34	Sequence 34, Appl1
445	32	68.1	50	2	US-10-178-449A-26	Sequence 26, Appl1	518	32	68.1	692	2	US-09-003-574-31	Sequence 31, Appl1
446	32	68.1	64	2	US-09-149-476-504	Sequence 504, App	519	32	68.1	692	2	US-09-003-570-31	Sequence 31, Appl1
447	32	68.1	68	2	US-09-248-796A-24682	Sequence 24682, A	520	32	68.1	762	2	US-09-864-541A-31	Sequence 31, Appl1
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449	32	68.1	70	2	US-09-580-734-8	Sequence 8, Appl1	522	32	68.1	976	1	US-08-449-645A-18	Sequence 18, Appl1
450	32	68.1	70	2	US-08-374-009-8	Sequence 8, Appl1	523	32	68.1	976	1	US-08-702-367A-18	Sequence 18, Appl1
451	32	68.1	70	2	US-09-191-724-8	Sequence 8, Appl1	524	32	68.1	976	4	US-09-949-016-6499	Sequence 6499, Ap
452	32	68.1	76	2	US-10-178-449A-28	Sequence 28, Appl1	525	32	68.1	976	4	PCT-US85-04681-18	Sequence 18, Appl1
453	32	68.1	82	2	US-09-902-540-15132	Sequence 15132, A	526	32	68.1	977	1	US-08-673-789-8	Sequence 8, Appl1
454	32	68.1	103	1	US-08-241-853-27	Sequence 27, Appl1	527	32	68.1	1013	2	US-09-949-016-7991	Sequence 7991, Ap
455	32	68.1	103	1	US-08-850-917-27	Sequence 27, Appl1	528	32	68.1	1214	2	US-10-164-595-24	Sequence 24, Appl1
456	32	68.1	110	2	US-09-621-976-4028	Sequence 4028, Ap	529	32	68.1	2703	1	US-08-185-433-19	Sequence 19, Appl1
457	32	68.1	122	2	US-09-513-999C-7856	Sequence 7856, Ap	530	32	68.1	2703	2	US-08-899-923-4	Sequence 4, Appl1
458	32	68.1	143	2	US-10-012-231A-302	Sequence 302, App	531	32	68.1	2703	2	US-09-121-457-4	Sequence 4, Appl1
459	32	68.1	143	2	US-10-015-389A-302	Sequence 302, App	532	32	68.1	2813	2	US-08-896-449A-2	Sequence 2, Appl1
460	32	68.1	143	2	US-10-006-768A-302	Sequence 302, App	533	32	68.1	2813	2	US-09-132-652-2	Sequence 2, Appl1
461	32	68.1	143	2	US-10-015-671A-302	Sequence 302, App	534	32	68.1	2813	2	US-09-886-900A-2	Sequence 2, Appl1
462	32	68.1	143	2	US-10-015-393A-302	Sequence 302, App	535	32	68.1	2813	2	US-09-662-478C-2	Sequence 2, Appl1
463	32	68.1	143	2	US-10-011-833A-302	Sequence 302, App	536	32	68.1	4302	2	US-08-658-136-5	Sequence 5, Appl1
464	32	68.1	143	2	US-10-006-041A-302	Sequence 302, App	537	32	68.1	4302	2	US-09-052-465-8	Sequence 8, Appl1
465	32	68.1	143	2	US-10-012-064A-302	Sequence 302, App	538	32	68.1	4302	2	US-08-422-582-8	Sequence 8, Appl1

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540	32	68.1	4303	1	US-08-460-751-2	Sequence 2, Appl	613	31	66.0	191	2	US-08-882-816-2	Sequence 2, Appl
541	32	68.1	4303	2	US-09-479-467A-2	Sequence 2, Appl	614	31	66.0	191	2	US-09-574-708A-6	Sequence 6, Appl
542	32	68.1	4303	2	US-09-655-160-2	Sequence 2, Appl	615	31	66.0	191	2	US-08-802-052B-2	Sequence 2, Appl
543	31	66.0	4	1	US-07-820-688A-5	Sequence 5, Appl	616	31	66.0	191	2	US-09-431-888-4	Sequence 4, Appl
544	31	66.0	4	1	US-08-274-043B-5	Sequence 5, Appl	617	31	66.0	191	2	US-09-532-310B-2	Sequence 2, Appl
545	31	66.0	4	1	US-08-386-729A-5	Sequence 5, Appl	618	31	66.0	191	2	US-08-671-573B-55	Sequence 55, Appl
546	31	66.0	4	1	US-08-687-276-3	Sequence 5, Appl	619	31	66.0	191	2	US-09-392-931-6	Sequence 6, Appl
547	31	66.0	4	1	US-08-883-804-2	Sequence 2, Appl	620	31	66.0	191	2	US-09-631-092B-55	Sequence 55, Appl
548	31	66.0	4	2	US-08-504-538A-21	Sequence 21, Appl	621	31	66.0	191	2	US-08-734-443-14	Sequence 14, Appl
549	31	66.0	4	2	US-09-579-883A-1	Sequence 1, Appl	622	31	66.0	191	2	US-09-534-376A-56	Sequence 56, Appl
550	31	66.0	4	2	US-09-679-705-2	Sequence 1, Appl	623	31	66.0	191	2	US-10-268-447-6	Sequence 6, Appl
551	31	66.0	6	1	US-08-883-804-4	Sequence 4, Appl	624	31	66.0	191	6	5332671-4	Patent No. 5332671
552	31	66.0	8	1	US-08-571-985-27	Sequence 27, Appl	625	31	66.0	192	2	US-09-438-046-10	Sequence 10, Appl
553	31	66.0	8	1	US-09-116-766-27	Sequence 27, Appl	626	31	66.0	192	2	US-09-902-540-1548	Sequence 1548, A
554	31	66.0	8	2	US-08-836-480-34	Sequence 34, Appl	627	31	66.0	196	2	US-09-949-016-7039	Sequence 7039, Ap
555	31	66.0	16	2	US-09-562-897-34	Sequence 34, Appl	628	31	66.0	208	2	US-09-244-583-26	Sequence 26, Appl
556	31	66.0	28	2	US-09-160-513-217	Sequence 17, App	629	31	66.0	211	2	US-09-286-529-20	Sequence 20, Appl
557	31	66.0	28	2	US-09-230-041-31	Sequence 31, Appl	630	31	66.0	214	2	US-09-963-156A-1	Sequence 1, Appl
558	31	66.0	29	2	US-09-881-572A-25	Sequence 25, Appl	631	31	66.0	214	6	5240848-11	Patent No. 5240848
559	31	66.0	30	2	US-09-881-572A-5	Sequence 5, Appl	632	31	66.0	215	2	US-08-807-992B-3	Sequence 3, Appl
560	31	66.0	35	2	US-10-044-359-26	Sequence 26, Appl	633	31	66.0	215	2	US-08-586-039B-49	Sequence 49, Appl
561	31	66.0	38	1	US-08-239-256-16	Sequence 16, Appl	634	31	66.0	215	2	US-09-699-769-49	Sequence 49, Appl
562	31	66.0	43	2	US-09-244-583-20	Sequence 20, Appl	635	31	66.0	215	2	US-09-532-310B-3	Sequence 3, Appl
563	31	66.0	44	2	US-09-583-638-11	Sequence 11, Appl	636	31	66.0	215	2	US-09-392-931-8	Sequence 8, Appl
564	31	66.0	45	2	US-09-579-420B-19	Sequence 1, Appl	637	31	66.0	215	2	US-09-468-647A-105	Sequence 105, App
565	31	66.0	50	2	US-09-579-420B-19	Sequence 19, Appl	638	31	66.0	215	6	5219739-32	Patent No. 5219739
566	31	66.0	51	2	US-09-513-999C-7252	Sequence 7252, Ap	639	31	66.0	215	6	5240848-7	Patent No. 5240848
567	31	66.0	58	1	US-08-676-125A-36	Sequence 36, Appl	640	31	66.0	217	2	US-09-252-991A-24627	Sequence 24627, A
568	31	66.0	58	1	US-09-136-012A-36	Sequence 36, Appl	641	31	66.0	224	2	US-10-104-047-3343	Sequence 3343, Ap
569	31	66.0	58	2	US-08-676-124-67	Sequence 67, Appl	642	31	66.0	231	4	PCR-US96-09001-10	Sequence 10, Appl
570	31	66.0	58	2	US-09-414-878-67	Sequence 67, Appl	643	31	66.0	232	1	US-08-999-811-7	Sequence 7, Appl
571	31	66.0	58	2	US-09-240-136-67	Sequence 67, Appl	644	31	66.0	232	1	US-08-824-996-9	Sequence 9, Appl
572	31	66.0	58	2	US-09-638-770A-67	Sequence 67, Appl	645	31	66.0	232	2	US-08-807-992B-4	Sequence 4, Appl
573	31	66.0	58	2	US-10-167-351-67	Sequence 67, Appl	646	31	66.0	232	2	US-09-042-105-7	Sequence 7, Appl
574	31	66.0	77	2	US-09-502-540-11828	Sequence 11828, A	647	31	66.0	232	2	US-09-574-708A-10	Sequence 10, Appl
575	31	66.0	80	2	US-09-630-273-2	Sequence 2, Appl	648	31	66.0	232	2	US-09-532-310B-4	Sequence 4, Appl
576	31	66.0	88	2	US-09-902-540-10178	Sequence 10178, A	649	31	66.0	232	2	US-08-465-968-5	Sequence 5, Appl
577	31	66.0	102	2	US-09-621-976-5629	Sequence 5629, Ap	650	31	66.0	232	2	US-10-084-488-7	Sequence 7, Appl
578	31	66.0	106	2	US-09-383-586-13	Sequence 13, Appl	651	31	66.0	232	2	US-09-214-982-33	Sequence 33, Appl
579	31	66.0	106	2	US-09-823-038A-13	Sequence 13, Appl	652	31	66.0	232	2	US-10-268-447-10	Sequence 10, Appl
580	31	66.0	109	2	US-09-134-001C-5529	Sequence 5529, Ap	653	31	66.0	244	2	US-09-538-092-259	Sequence 259, App
581	31	66.0	113	2	US-10-104-047-3199	Sequence 3199, Ap	654	31	66.0	261	2	US-09-461-325-413	Sequence 413, App
582	31	66.0	126	2	US-09-107-532A-5571	Sequence 5571, Ap	655	31	66.0	261	2	US-10-012-542-413	Sequence 413, App
583	31	66.0	130	1	US-08-826-910-1	Sequence 1, Appl	656	31	66.0	261	2	US-10-115-123-413	Sequence 413, App
584	31	66.0	136	2	US-09-134-001C-5147	Sequence 5147, Ap	657	31	66.0	264	2	US-09-949-016-11555	Sequence 11555, A
585	31	66.0	136	2	US-09-252-991A-17421	Sequence 17421, A	658	31	66.0	268	2	US-09-270-767-42351	Sequence 42351, A
586	31	66.0	139	2	US-09-248-796A-28003	Sequence 28003, A	659	31	66.0	271	2	US-09-936-019-1	Sequence 1, Appl
587	31	66.0	146	2	US-09-690-454-47	Sequence 47, Appl	660	31	66.0	299	2	US-09-286-529-17	Sequence 17, Appl
588	31	66.0	146	2	US-09-523-323-59	Sequence 59, Appl	661	31	66.0	300	1	US-08-794-796-2	Sequence 2, Appl
589	31	66.0	147	2	US-08-469-260A-520	Sequence 520, App	662	31	66.0	300	2	US-09-632-227A-2	Sequence 2, Appl
590	31	66.0	147	2	US-08-488-446-520	Sequence 520, App	663	31	66.0	300	2	US-09-523-323-52	Sequence 52, Appl
591	31	66.0	147	2	US-08-467-344A-520	Sequence 520, App	664	31	66.0	300	2	US-09-896-096A-1	Sequence 1, Appl
592	31	66.0	147	2	US-08-424-550B-520	Sequence 520, App	665	31	66.0	300	2	US-09-936-019-3	Sequence 3, Appl
593	31	66.0	163	2	US-09-949-016-10680	Sequence 10680, A	666	31	66.0	308	2	US-09-252-991A-26483	Sequence 26483, A
594	31	66.0	163	6	5194596-17	Patent No. 5194596	667	31	66.0	308	2	US-09-252-991A-31991	Sequence 31991, A
595	31	66.0	164	6	5219739-17	Patent No. 5219739	668	31	66.0	310	2	US-09-949-016-7763	Sequence 7763, Ap
596	31	66.0	164	6	5219739-18	Patent No. 5219739	669	31	66.0	325	2	US-09-599-360B-74	Sequence 74, Appl
597	31	66.0	165	2	US-08-882-816-3	Sequence 3, Appl	670	31	66.0	329	2	US-09-252-991A-25774	Sequence 25774, A
598	31	66.0	165	2	US-08-802-052B-3	Sequence 3, Appl	671	31	66.0	330	2	US-09-252-991A-24637	Sequence 24637, A
599	31	66.0	165	2	US-09-706-722A-3	Sequence 3, Appl	672	31	66.0	333	2	US-09-949-016-7678	Sequence 7678, Ap
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603	31	66.0	180	2	US-09-270-767-50509	Sequence 50909, A	676	31	66.0	388	2	US-09-248-796A-17265	Sequence 17265, A
604	31	66.0	188	2	US-09-252-991A-32934	Sequence 32934, A	677	31	66.0	392	2	US-09-764-325A-23	Sequence 23, Appl
605	31	66.0	188	2	US-09-893-737-16	Sequence 16, Appl	678	31	66.0	392	2	US-09-764-325A-25	Sequence 25, Appl
606	31	66.0	190	6	5332671-3	Patent No. 5332671	679	31	66.0	392	2	US-09-912-935-23	Sequence 23, Appl
607	31	66.0	191	2	US-08-567-200A-2	Sequence 2, Appl	680	31	66.0	392	2	US-09-912-935-25	Sequence 25, Appl
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609	31	66.0	191	2	US-08-691-794-2	Sequence 2, Appl	682	31	66.0	406	2	US-09-543-681A-5458	Sequence 5458, Ap
610	31	66.0	191	2	US-08-795-430-56	Sequence 56, Appl	683	31	66.0	416	2	US-09-949-016-6201	Sequence 6201, Ap
611	31	66.0	191	2	US-09-392-932-3	Sequence 3, Appl	684	31	66.0	425	2	US-09-252-991A-29556	Sequence 29556, A

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686	31	66.0	426	2	US-08-675-499A-6	Sequence 6, App1	759	31	66.0	1003	2	US-09-402-181B-336	Sequence 336, App
687	31	66.0	426	2	US-08-812-008-6	Sequence 6, App1	760	31	66.0	1003	2	US-09-721-456-336	Sequence 336, App
688	31	66.0	428	2	US-09-423-340-2	Sequence 2, App1	761	31	66.0	1003	2	US-10-054-295-217	Sequence 217, App
689	31	66.0	428	2	US-09-423-340-4	Sequence 4, App1	762	31	66.0	1003	2	US-09-438-486A-217	Sequence 217, App
690	31	66.0	428	2	US-09-820-155-2	Sequence 4, App1	763	31	66.0	1004	2	US-09-949-016-9925	Sequence 9925, App
691	31	66.0	428	2	US-09-820-155-4	Sequence 4, App1	764	31	66.0	1055	2	US-09-214-278-2	Sequence 2, App1
692	31	66.0	430	2	US-10-104-047-2204	Sequence 2204, App	765	31	66.0	1055	2	US-09-855-722-3	Sequence 3, App1
693	31	66.0	433	2	US-09-949-016-10900	Sequence 10900, App	766	31	66.0	1060	2	US-09-248-796A-18062	Sequence 18062, App
694	31	66.0	436	2	US-09-949-016-6983	Sequence 6983, App	767	31	66.0	1065	1	US-08-400-159-8	Sequence 8, App1
695	31	66.0	448	2	US-09-342-681C-17	Sequence 17, App1	768	31	66.0	1073	2	US-09-949-016-9771	Sequence 9771, App
696	31	66.0	448	2	US-09-342-681C-19	Sequence 19, App1	769	31	66.0	1148	2	US-08-882-046-4	Sequence 4, App1
697	31	66.0	449	2	US-09-912-935-34	Sequence 34, App1	770	31	66.0	1148	2	US-09-566-047-4	Sequence 4, App1
698	31	66.0	454	1	US-08-166-316-2	Sequence 2, App1	771	31	66.0	1196	2	US-10-237-551-200	Sequence 200, App
699	31	66.0	457	2	US-09-949-016-7165	Sequence 7165, App	772	31	66.0	1196	2	US-10-237-551-232	Sequence 232, App
700	31	66.0	473	2	US-09-902-540-13895	Sequence 13895, App	773	31	66.0	1208	2	US-09-463-703A-2	Sequence 2, App1
701	31	66.0	476	2	US-09-949-016-11726	Sequence 11726, App	774	31	66.0	1208	2	US-09-699-135-2	Sequence 2, App1
702	31	66.0	479	2	US-09-248-796A-15907	Sequence 15907, App	775	31	66.0	1112	2	US-09-214-278-3	Sequence 3, App1
703	31	66.0	484	2	US-09-248-796A-18223	Sequence 18223, App	776	31	66.0	1212	2	US-09-855-722-3	Sequence 3, App1
704	31	66.0	484	2	US-09-949-016-9440	Sequence 9440, App	777	31	66.0	1238	2	US-09-214-278-5	Sequence 5, App1
705	31	66.0	499	2	US-09-912-935-31	Sequence 31, App1	778	31	66.0	1238	2	US-09-855-722-5	Sequence 5, App1
706	31	66.0	529	2	US-09-912-935-28	Sequence 28, App1	779	31	66.0	1248	2	US-08-882-046-6	Sequence 6, App1
707	31	66.0	529	2	US-09-912-935-40	Sequence 40, App1	780	31	66.0	1248	2	US-09-566-047-6	Sequence 6, App1
708	31	66.0	530	2	US-09-912-935-38	Sequence 38, App1	781	31	66.0	1257	2	US-08-611-729A-8	Sequence 8, App1
709	31	66.0	584	1	US-08-313-288B-17	Sequence 17, App1	782	31	66.0	1257	2	US-09-195-524-8	Sequence 8, App1
710	31	66.0	585	2	US-09-370-807-4	Sequence 4, App1	783	31	66.0	1441	2	US-09-310-685-6	Sequence 6, App1
711	31	66.0	585	2	US-09-921-259-4	Sequence 4, App1	784	31	66.0	1452	2	US-09-949-016-10397	Sequence 2, App1
712	31	66.0	585	2	US-09-370-767-59685	Sequence 59685, App	785	31	66.0	1452	2	US-09-127-227-2	Sequence 2, App1
713	31	66.0	622	2	US-09-352-991A-30739	Sequence 30739, App	786	31	66.0	1564	2	US-09-976-559-309	Sequence 309, App
714	31	66.0	643	2	US-09-352-991A-23842	Sequence 23842, App	787	31	66.0	1125	2	US-09-562-702A-20	Sequence 20, App1
715	31	66.0	645	2	US-09-315-127-8	Sequence 8, App1	788	31	66.0	1125	2	US-09-561-818A-20	Sequence 20, App1
716	31	66.0	645	2	US-09-315-127-9	Sequence 9, App1	789	31	66.0	1257	2	US-10-037-182-12	Sequence 12, App1
717	31	66.0	654	2	US-09-315-127-11	Sequence 11, App1	790	31	66.0	1186	2	US-09-562-702A-18	Sequence 18, App1
718	31	66.0	654	2	US-09-315-127-12	Sequence 12, App1	791	31	66.0	1186	2	US-09-561-818A-18	Sequence 18, App1
719	31	66.0	658	2	US-09-248-796A-17674	Sequence 17674, App	792	31	66.0	1186	2	US-10-037-182-10	Sequence 10, App1
720	31	66.0	667	2	US-09-315-127-5	Sequence 5, App1	793	30.5	64.9	44	2	US-09-443-780C-30	Sequence 30, App1
721	31	66.0	667	2	US-09-315-127-6	Sequence 6, App1	794	30.5	64.9	44	2	US-09-079-723-14	Sequence 14, App1
722	31	66.0	667	2	US-09-070-630-13	Sequence 13, App1	795	30.5	64.9	145	2	US-09-471-276-1156	Sequence 1156, App
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724	31	66.0	687	1	US-08-164-839-33	Sequence 33, App1	797	30	63.8	13	1	US-08-335-832-39	Sequence 39, App1
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981 28 59.6 45 2 US-08-834-130A-65 Sequence 65, Appl
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983 28 59.6 49 2 US-08-905-223-463 Sequence 463, App
984 28 59.6 52 2 US-09-621-976-7037 Sequence 7037, App
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ALIGNMENTS

RESULT 1
US-08-883-804-5
; Sequence 5, Application US/08883804
; Patent No. 5985261
; GENERAL INFORMATION:
; APPLICANT: white, Carl W.
; APPLICANT: Das, Kumuda C.
; TITLE OF INVENTION: USE OF THIOREDOXIN-LIKE MOLECULES FOR
; TITLE OF INVENTION: INDUCTION OF MMSOD TO TREAT OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,804
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-883-804-5

Query Match 100.0%; Score 47; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
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Db 1 WCGPCK 6

RESULT 2
US-08-627-907A-6
; Sequence 6, Application US/08627907A
; Patent No. 6060302
; GENERAL INFORMATION:
; APPLICANT: HIRANO, Naoto
; APPLICANT: HIRAI, Hisamaru
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND DNA
; TITLE OF INVENTION: SEQUENCE ENCODING THE SAME
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
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; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,907A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-238402
; FILING DATE: 24-SEP-1993
; APPLICATION DATA: PCT/JP94/01572
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-627-907A-6

Query Match 100.0%; Score 47; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 WCGPCK 6

RESULT 3
US-07-901-713A-3
; Sequence 3, Application US/07901713A
; Patent No. 6291205
; GENERAL INFORMATION:
; APPLICANT: Tuille, Michael F.
; APPLICANT: Freedman, Robert B.
; APPLICANT: Markus, Henry Z.
; APPLICANT: Schultz, Loren D.
; APPLICANT: Montgomery, Donna L.

APPLICANT: Ellis, Ronald W.
TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF
TITLE OF INVENTION: DISULFIDE BONDED RECOMBINANT PROTEINS BY SACCAROMYCES
TITLE OF INVENTION: CEREVISIAE
FILE REFERENCE: 18469
CURRENT APPLICATION NUMBER: US/07/901,713A
CURRENT FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: S. cerevisiae PDI thioredoxin active site
US-07-901-713A-3

Query Match 100.0%; Score 47; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 1 WCGPCK 6

RESULT 4
US-08-750-142B-54
Sequence 54, Application US/08750142B
Patent No. 6228373
GENERAL INFORMATION:
APPLICANT: Bergerstrand, Hakan
APPLICANT: Eriksson, Tomas
APPLICANT: Lindvall, Magnus
APPLICANT: Samstrand, Bengt
TITLE OF INVENTION: NEW PEPTIDES WITH
TITLE OF INVENTION: IMMUNOMODULATORY EFFECTS
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,142B
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00365
FILING DATE: 23-MAR-1996
APPLICATION NUMBER: SE9501067-4
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06275/062001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-750-142B-54

Query Match 100.0%; Score 47; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 1 WCGPCK 6

RESULT 5
5210073-1
Patent No. 5210073
APPLICANT: YODOI, JUNJI,UCHIDA, ATSUSHI,TAGAWA, YUTAKA
MITSUI, AKIRA,HIRAKAWA, TADASHI
TITLE OF INVENTION: METHOD FOR TREATING CANCER THERAPY
RADIATION DAMAGE OR ARTERIOSCLEROSIS USING HUMAN ADF
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/589,616
FILING DATE: 28-SEP-1990
SEQ ID NO:1
LENGTH: 104
5210073-1

Query Match 100.0%; Score 47; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 6
US-08-826-910-3
Sequence 3, Application US/08826910
Patent No. 5919657
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: THIOREDOXIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,910
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0268 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 339649
US-08-826-910-3

Query Match 100.0%; Score 47; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 7
US-08-826-910-4
; Sequence 4, Application US/08826910
; Patent No. 5919657
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: THIOREDUXIN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,910
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0268 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 453972
; US-08-826-910-4

Query Match 100.0%; Score 47; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 8

US-09-601-144-68
; Sequence 68, Application US/09601144
; Patent No. 6566514
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Young, Aiping H.
; APPLICANT: Lee, Yoon S.
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDUXIN
; TITLE OF INVENTION: AND THIOREDUXIN REDUCTASE GENES AND METHODS OF USING
; FILE REFERENCE: 683-112US-A
; CURRENT APPLICATION NUMBER: US/09/601,144
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/073,196
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 68
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
US-09-601-144-68

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 9
US-09-513-999C-8037
; Sequence 8037, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8037
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-8037

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 10
US-08-386-729A-10
; Sequence 10, Application US/08386729A
; Patent No. 5753435
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.

APPLICANT: Schreiber, Rachel
APPLICANT: Argaman, Anat
APPLICANT: Av-Gay, Yosef
APPLICANT: Nan, Helena M.
APPLICANT: Kattewilder, Alfred
APPLICANT: Paliassa, Harriet
TITLE OF INVENTION: An oxido reductase enzyme system
TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
TITLE OF INVENTION: production
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Well, Gotel & Manges
STREET: 2882 Sand Hill Road, Ste. 280
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,729A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/274,043
FILING DATE: 12-JULY-1994
APPLICATION NUMBER: US 07/820,688
FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/IL91/000101
FILING DATE: 18-JUNE-1991
APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-024/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-386-729A-10

Query Match 100.0%; Score 47; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 11
US-07-745-382-22
Sequence 22, Application US/07/45382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Caerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-382-22

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 32 WCGPCK 37

RESULT 12
US-07-921-848-22
Sequence 22, Application US/07/921848
Patent No. 5282646
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: Gaert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-921-848-22

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 13
US-08-165-301A-22
Sequence 22, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: G1 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-22

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

Db 32 WCGPCK 37
|||||
RESULT 14
US-08-165-301A-26
Sequence 26, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: G1 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-26

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 15
US-08-165-301A-28
Sequence 28, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-28

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 32 WCGPCK 37

RESULT 16
US-08-810-436-22
Sequence 22, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-22

Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 32 WCGPCK 37

RESULT 17
US-08-810-436-26
Sequence 26, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-26

Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 32 WCGPCK 37

Db 32 WCGPCK 37

```
RESULT 18
US-08-810-436-28
; Sequence 28, Application US/08810436
; Patent No. 6143524
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBiase-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,436
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/165,301
; FILING DATE: 10-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinerl, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-436-28

Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 19
US-09-485-885-17
; Sequence 17, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Gislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
```

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; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-17
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Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WCGPCK 6
Db 32 WCGPCK 37
```

```
RESULT 20
US-09-166-966E-10
; Sequence 10, Application US/09166966E
; Patent No. 6407208
; GENERAL INFORMATION:
; APPLICANT: CHEN, DAVID CHANHAN
; APPLICANT: HU, NIEN-TAI
; APPLICANT: CHEN, YUN-JU
; APPLICANT: HSEU, TZONG-HSIUNG
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
; FILE REFERENCE: 32350-150960
; CURRENT APPLICATION NUMBER: US/09/166,966E
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: TW 86114750
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: thioredoxin
; LOCATION: 1..109
; OTHER INFORMATION: amino acid of thioredoxin
US-09-166-966E-10
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```
Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 WCGPCK 6
Db 32 WCGPCK 37
```

```
RESULT 21
US-09-248-796A-19911
; Sequence 19911, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19911
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LENGTH: 109
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19911

Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 35 WCGPCK 40

RESULT 22
PCT-US94-14179-22
Sequence 22, Application PC/TUS9414179
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION/DOCKET NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14179-22
Query Match 100.0%; Score 47; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WCGPCK 6
Db 32 WCGPCK 37
RESULT 23
PCT-US94-14179-26
Sequence 26, Application PC/TUS9414179
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen

APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION/DOCKET NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14179-26
Query Match 100.0%; Score 47; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 32 WCGPCK 37
RESULT 24
PCT-US94-14179-28
Sequence 28, Application PC/TUS9414179
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:

```
/
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Mehnert, M. C.
/   REGISTRATION NUMBER: 33,544
/   REFERENCE/DOCKET NUMBER: CI 5188D
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (617) 876-1170
/   TELEFAX: (617) 876-5851
/   INFORMATION FOR SEQ ID NO: 28:
/   SEQUENCE CHARACTERISTICS:
/       LENGTH: 109 amino acids
/       TYPE: amino acid
/       TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   PCT-US94-14179-28

Query Match      100.0%; Score 47; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      32 WCGPCK 37

RESULT 25
US-09-264-419C-6
/   Sequence 6; Application US/09264419C
/   Patent No. 6174682
/   GENERAL INFORMATION:
/   APPLICANT: Khodadoust, Mehran
/   TITLE OF INVENTION: No. 6174682el Thioresdoxin Family Active Site Molecules and Uses
/   TITLE OF INVENTION: Therefor
/   FILE REFERENCE: MNI-076
/   CURRENT APPLICATION NUMBER: US/09/264,419C
/   CURRENT FILING DATE: 1999-03-08
/   NUMBER OF SEQ ID NOS: 6
/   SOFTWARE: PatentIn Ver. 2.0
/   SEQ ID NO 6
/   LENGTH: 111
/   TYPE: PRT
/   ORGANISM: Artificial Sequence
/   FEATURE:
/   OTHER INFORMATION: Description of Artificial Sequence: consensus
/   OTHER INFORMATION: sequence
US-09-264-419C-6

Query Match      100.0%; Score 47; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      33 WCGPCK 38

RESULT 26
US-09-134-001C-3859
/   Sequence 3859; Application US/09134001C
/   Patent No. 6380370
/   GENERAL INFORMATION:
/   APPLICANT: Lynn Doucette-Stamm et al
/   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/   TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
/   FILE REFERENCE: GTC-007
/   CURRENT APPLICATION NUMBER: US/09/134,001C
/   CURRENT FILING DATE: 1998-08-13
/   PRIOR APPLICATION NUMBER: US 60/064,964
/   PRIOR FILING DATE: 1997-11-08
/   PRIOR APPLICATION NUMBER: US 60/055,779
/   PRIOR FILING DATE: 1997-08-14
/   NUMBER OF SEQ ID NOS: 5674
/   SEQ ID NO 3859
/   LENGTH: 111
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/   TYPE: PRT
/   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3859

Query Match      100.0%; Score 47; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      35 WCGPCK 40

RESULT 27
US-09-882-835-5
/   Sequence 5; Application US/09882835
/   Patent No. 6462187
/   GENERAL INFORMATION:
/   APPLICANT: Bandaru, Rajasekhar
/   TITLE OF INVENTION: 22109, A NOVEL HUMAN THIOREDOXIN FAMILY
/   TITLE OF INVENTION: MEMBER AND USES THEREOF
/   FILE REFERENCE: 10448-063001
/   CURRENT APPLICATION NUMBER: US/09/882,835
/   CURRENT FILING DATE: 2001-06-15
/   PRIOR APPLICATION NUMBER: 60/211,673
/   PRIOR FILING DATE: 2000-06-15
/   NUMBER OF SEQ ID NOS: 5
/   SOFTWARE: PasteSeq for Windows Version 4.0
/   SEQ ID NO 5
/   LENGTH: 116
/   TYPE: PRT
/   ORGANISM: Artificial Sequence
/   FEATURE:
/   OTHER INFORMATION: consensus sequence
US-09-882-835-5

Query Match      100.0%; Score 47; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      33 WCGPCK 38

RESULT 28
US-09-543-681A-4397
/   Sequence 4397; Application US/09543681A
/   Patent No. 6605709
/   GENERAL INFORMATION:
/   APPLICANT: GARY BRETON
/   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
/   TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
/   FILE REFERENCE: 2709.1002-001
/   CURRENT APPLICATION NUMBER: US/09/543,681A
/   CURRENT FILING DATE: 2000-04-05
/   PRIOR APPLICATION NUMBER: US 60/128,706
/   PRIOR FILING DATE: 1999-04-09
/   NUMBER OF SEQ ID NOS: 8344
/   SEQ ID NO 4397
/   LENGTH: 122
/   TYPE: PRT
/   ORGANISM: Proteus mirabilis
US-09-543-681A-4397

Query Match      100.0%; Score 47; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      46 WCGPCK 51
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```
RESULT 29
US-09-489-039A-8017
; Sequence 8017, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8017
; LENGTH: 124
; TYPE: PR1
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8017

Query Match          100.0%; Score 47; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db       47 WCGPCK 52

RESULT 30
US-09-949-016-9663
; Sequence 9663, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9663
; LENGTH: 125
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-9663

Query Match          100.0%; Score 47; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db       51 WCGPCK 56

RESULT 31
US-09-272-342B-5
; Sequence 5, Application US/09272342B
; Patent No. 6294341
; GENERAL INFORMATION:
; APPLICANT: YU, YEON-GYU
; APPLICANT: KIM, SONG-HOU
; APPLICANT: RYU, JAE-RYEON
; TITLE OF INVENTION: METHOD FOR DETECTING A SUBSTANCE HAVING AN ACTIVITY TO
```

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; TITLE OF INVENTION: INHIBIT HIV INFECTION USING IMMUNOSSAY AND VARIANT
; FILE REFERENCE: 2901-0125-0
; CURRENT APPLICATION NUMBER: US/09/272,342B
; CURRENT FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 134
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-272-342B-5

Query Match          100.0%; Score 47; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db       32 WCGPCK 37

RESULT 32
US-08-961-083-40
; Sequence 40, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8512
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-40

Query Match          100.0%; Score 47; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db       61 WCGPCK 66
```

RESULT 33
US-09-536-784-40
; Sequence 40, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-536-784-40
Query Match 100.0%; Score 47; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 61 WCGPCK 66
RESULT 34
US-09-765-271-40
; Sequence 40, Application US/09765271
; Patent No. 6887663
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,271
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/536,784
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-765-271-40
Query Match 100.0%; Score 47; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 61 WCGPCK 66
RESULT 35
US-09-765-272A-40
; Sequence 40, Application US/09765272A
; Patent No. 6929930
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 454
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Dell Latitude C610
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272A
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin J. Hymel
; REGISTRATION NUMBER: 45,414
; REFERENCE/DOCKET NUMBER: PB340P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-765-272A-40

Query Match 100.0%; Score 47; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 61 WCGPCK 66

RESULT 36
US-09-328-352-5360
; Sequence 5360, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5360
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5360

Query Match 100.0%; Score 47; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 64 WCGPCK 69

RESULT 37
US-09-166-966E-8
; Sequence 8, Application US/09166966E
; Patent No. 6407208
; GENERAL INFORMATION:
; APPLICANT: CHEN, DAVID CHANHAN
; APPLICANT: HU, NIEN-TAI
; APPLICANT: CHEN, YUN-JU
; APPLICANT: HSEU, TIONG-HSIUNG
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
; FILE REFERENCE: 32350-150960
; CURRENT APPLICATION NUMBER: US/09/166,966E
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: TW 86114750
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 8
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: thioredoxin
; LOCATION: 1..109
; OTHER INFORMATION: Combined amino acid of thioredoxin and an artificial sequence
US-09-166-966E-8

Query Match 100.0%; Score 47; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 38
US-08-775-978-1
; Sequence 1, Application US/08775978
; Patent No. 5831049
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: GOLI, SURYA K.
; TITLE OF INVENTION: NOVEL HUMAN THIOREDOXIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,978
; FILING DATE: To be assigned
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0176 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 1430906
US-08-775-978-1

Query Match 100.0%; Score 47; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 89 WCGPCK 94

RESULT 39
US-08-775-978-3
; Sequence 3, Application US/08775978
; Patent No. 5831049
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: GOLI, SURYA K.
; TITLE OF INVENTION: NOVEL HUMAN THIOREDOXIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,978
FILING DATE: To Be Assigned
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0176 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1545817
US-08-775-978-3

Query Match 100.0%; Score 47; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 89 WCGPCK 94

RESULT 40
US-09-741-243C-4
Sequence 4, Application US/09741243C
Patent No. 6399352
GENERAL INFORMATION:
APPLICANT: Crawford Jr., John Milton
APPLICANT: Rice, John
APPLICANT: Sevala, Veeresh
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: NOVEL PLANT PORPHOBILINOGEN AND FUSION
FILE REFERENCE: 2022US
CURRENT APPLICATION NUMBER: US/09/741,243C
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/171,785
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 167
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Thioredoxin functional fragment
US-09-741-243C-4

Query Match 100.0%; Score 47; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 41
US-09-270-767-32473
Sequence 32473, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 32473
LENGTH: 170
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-32473

Query Match 100.0%; Score 47; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 44 WCGPCK 49

RESULT 42
US-09-270-767-47690
Sequence 47690, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 47690
LENGTH: 170
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-47690

Query Match 100.0%; Score 47; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 44 WCGPCK 49

RESULT 43
US-09-272-342B-6
Sequence 6, Application US/09272342B
Patent No. 6294341
GENERAL INFORMATION:
APPLICANT: YU, YEON-GYU
APPLICANT: KIM, SUNG-HOU
APPLICANT: RYU, JAE-REON
TITLE OF INVENTION: METHOD FOR DETECTING A SUBSTANCE HAVING AN ACTIVITY TO
INHIBIT HIV INFECTION USING IMMUNOSSAY AND VARIANT
TITLE OF INVENTION: PROTEIN USED FOR SAID METHOD
FILE REFERENCE: 2901-0125-0
CURRENT APPLICATION NUMBER: US/09/272,342B

;; CURRENT FILING DATE: 1999-03-19
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 177
;; TYPE: PRT
;; ORGANISM: homo sapiens and HIV hybrid
US-09-272-342B-6

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 177;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 44
US-09-583-110-5222
; Sequence 5222, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PTH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5222
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5222

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 185;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 80 WCGPCK 85

RESULT 45
US-09-107-433-5104
; Sequence 5104, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/107,433
;; FILING DATE: 30-Jun-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/ 085131
;; FILING DATE: May 12, 1998
;; APPLICATION NUMBER: 60/051553
;; FILING DATE: July 2, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ariniello, Pamela Deneke
;; REGISTRATION NUMBER: 40,489
;; REFERENCE/DOCKET NUMBER: GTC-011
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (781)893-5007
;; TELEFAX: (781)893-8277
;; INFORMATION FOR SEQ ID NO: 5104:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 194 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Streptococcus pneumoniae
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (B) LOCATION 1...194
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5104:
US-09-107-433-5104

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 194;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 89 WCGPCK 94

RESULT 46
US-09-166-966E-11
; Sequence 11, Application US/09166966E
; Patent No. 6407208
; GENERAL INFORMATION:
; APPLICANT: CHEN, DAVID CHANHAN
; APPLICANT: HU, NIEN-TAI
; APPLICANT: CHEN, YUN-JU
; APPLICANT: HSEU, TZONG-HSIUNG
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
; FILE REFERENCE: 32350-150960
; CURRENT APPLICATION NUMBER: US/09/166,966E
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: TW 86114750
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 11
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: Chloredoxin
; LOCATION: 1..109
; NAME/KEY: Cellulose-binding domain
; LOCATION: 162..197
; NAME/KEY: RGD
; LOCATION: 204..206
; OTHER INFORMATION: Combined amino acid sequence of chloredoxin,
; OTHER INFORMATION: artificial sequence, cellulose-binding domain, and
; OTHER INFORMATION: artificial sequence; the two artificial sequences
; OTHER INFORMATION: flanking the cellulose-binding domain contain restriction sites
US-09-166-966E-11

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 209;

Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 47
US-08-180-371-6
; Sequence 6, Application US/08180371
; Patent No. 6254861
; GENERAL INFORMATION:
; APPLICANT: Choudhury, Chandra
; TITLE OF INVENTION: Hematopoietic Growth Factor Derived
; TITLE OF INVENTION: From T Lymphocytes and Methods of Use Therefor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,371
; FILING DATE: 12-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 906866
; FILING DATE: 01 July 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gruber, Lewis S.
; REGISTRATION NUMBER: 30,060
; REFERENCE/DOCKET NUMBER: 27620/31668
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-180-371-6
Query Match 100.0%; Score 47; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
|||||
Db 106 WCGPCK 111
RESULT 48
PCT-US92-05707-6
; Sequence 6, Application PC/TUS9205707
; GENERAL INFORMATION:
; APPLICANT: Choudhury, Chandra
; TITLE OF INVENTION: Hematopoietic Growth Factor Derived from
; TITLE OF INVENTION: T Lymphocytes and Methods of Use Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell

STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05707
; FILING DATE: 19920707
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gruber, Lewis S.
; REGISTRATION NUMBER: 30,060
; REFERENCE/DOCKET NUMBER: 27620/30933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-05707-6

Query Match 100.0%; Score 47; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 106 WCGPCK 111

RESULT 49
US-08-778-717-17
; Sequence 17, Application US/08778717
; Patent No. 6602689
; GENERAL INFORMATION:
; APPLICANT: UENO, EIICHI
; APPLICANT: NOBUYUKI, FUJII
; APPLICANT: OKADA, MASAHISA
; TITLE OF INVENTION: FUSED DNA SEQUENCE, FUSED PROTEIN
; TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
; TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,717
; FILING DATE: 12-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 352225/1995
; FILING DATE: 28-DEC-1995
; ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2084-031-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: RECOMBINANT
PUBLICATION INFORMATION:
AUTHORS: NOBUYUKI FUJII ET AL,
TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF
TITLE: EXPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1 TO 265
US-08-778-717-17

Query Match 100.0%; Score 47; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 50 WCGPCK 55

RESULT 50

US-07-745-382-14
Sequence 14, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-745-382-14

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 51

US-07-921-848-14
Sequence 14, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-921-848-14

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 52

US-08-115-660-4
Sequence 4, Application US/08115660
Patent No. 5437863
GENERAL INFORMATION:

APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIAUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-115-680-4

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No.10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 53
US-07-941-372-4
Sequence 4, Application US/07941372
Patent No. 5460810
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,372
FILING DATE: 19920902

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDUS1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-941-372-4

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No.10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 54
US-08-165-301A-14
Sequence 14, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meiner, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-14

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No.10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 55

US-08-810-436-14
; Sequence 14, Application US/08810436
; Patent No. 6143524
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: LaVallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,436
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/165,301
; FILING DATE: 10-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinerdt, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-810-436-14

Query Match 100.0%; Score 47; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 56
PCT-US93-08247-4
; Sequence 4, Application PC/TUS9308247
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.,
; APPLICANT: 87 Cambridgepark Drive,
; APPLICANT: Cambridge, MA 02140, USA
; TITLE OF INVENTION: Method of Treating Cell Damage or
; TITLE OF INVENTION: Depletion
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08247
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IND1Apct
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08247-4

Query Match 100.0%; Score 47; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 57
PCT-US94-14179-14
; Sequence 14, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: LaVallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14179
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinerdt, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14179-14

Query Match 100.0%; Score 47; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 58
US-10-012-896-1011
; Sequence 1011, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Roy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1011
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-1011

Query Match 100.0%; Score 47; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 59
US-08-683-007A-2

; Sequence 2, Application US/08683007A
; Patent No. 5858724
; GENERAL INFORMATION:
; APPLICANT: No. 5858724Y, Robert E
; APPLICANT: Domancio, Michael
; APPLICANT: Jaeger, Keith
; APPLICANT: Kroeker, Warren
; TITLE OF INVENTION: Recombinant Rabbit Tissue Factor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,007A
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 740380.90040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-683-007A-2

Query Match 100.0%; Score 47; DB 1; Length 408;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 60
US-09-513-442-2
; Sequence 2, Application US/09513442
; Patent No. 6387664
; GENERAL INFORMATION:
; APPLICANT: Ikemoto, Mitsunshi
; TITLE OF INVENTION: SPARC Fusion Protein and a Process for Producing the
; TITLE OF INVENTION: Same
; FILE REFERENCE: HIRAKI-04218
; CURRENT APPLICATION NUMBER: US/09/513,442
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-513-442-2

Query Match 100.0%; Score 47; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

|||||
Db 32 WCGPCK 37

RESULT 61
US-08-260-582-77
; Sequence 77, Application US/08260582
; Patent No. 5635182

GENERAL INFORMATION:

APPLICANT: McCoy, John M.

APPLICANT: Lu, Zhijian

TITLE OF INVENTION: METHOD OF DETECTING LIGAND

TITLE OF INVENTION: INTERACTIONS

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/260,582

FILING DATE: 16-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meinert, M. C.

REGISTRATION NUMBER: 31,544

REFERENCE/DOCKET NUMBER: GI 5236

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-260-582-77

Query Match 100.0%; Score 47; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 275 WCGPCK 280

RESULT 62
PCT-US95-05471-77
; Sequence 77, Application PC/TUS9505471
; GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: METHOD OF DETECTING LIGAND

TITLE OF INVENTION: INTERACTIONS

NUMBER OF SEQUENCES: 76

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05471

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US95-05471-77

Query Match 100.0%; Score 47; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 275 WCGPCK 280

RESULT 63
US-10-057-531A-1
; Sequence 1, Application US/10057531A
; Patent No. 685332

GENERAL INFORMATION:

APPLICANT: Lyon, Jeffrey A.

APPLICANT: Angov, Evelina

TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite

TITLE OF INVENTION: Protein-142 Vaccine

FILE REFERENCE: 003/241/SAP

CURRENT APPLICATION NUMBER: US/10/057,531A

CURRENT FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: US 60/264,535

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: US 60/347,564

PRIOR FILING DATE: 2001-10-26

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Apple Macintosh Microsoft Word 6.0

SEQ ID NO 1

LENGTH: 546

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein

OTHER INFORMATION: Sequence in pET-Trx42

Patent No. 6853322

US-10-057-531A-1

Query Match 100.0%; Score 47; DB 2; Length 546;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 64
US-09-741-243C-2
; Sequence 2, Application US/09741243C
; Patent No. 6399352

GENERAL INFORMATION:

APPLICANT: Crawford Jr., John Milton

APPLICANT: Rice, John

APPLICANT: Sevala, Veeresh

APPLICANT: Stewart, Sandy

TITLE OF INVENTION: NOVEL PLANT PORPHOBILINOGEN AND FUSION

TITLE OF INVENTION: PROTEIN THEREOF

FILE REFERENCE: 2022US

CURRENT APPLICATION NUMBER: US/09/741,243C

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/171,785

PRIOR FILING DATE: 1999-12-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 551

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: A plant thioedoxin-porphobilinogen

OTHER INFORMATION: synthase fusion protein
US-09-741-243C-2

Query Match 100.0%; Score 47; DB 2; Length 551;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
| | | | |
Db 32 WCGPCK 37

RESULT 65
US-09-252-991A-22943
Sequence 22943, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22943
LENGTH: 580
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22943

Query Match 100.0%; Score 47; DB 2; Length 580;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
| | | | |
Db 504 WCGPCK 509

RESULT 66
US-09-626-589-3
Sequence 3, Application US/09626589
Patent No. 6326164
GENERAL INFORMATION:
APPLICANT: Rice, John
APPLICANT: Klotz, Andreas
APPLICANT: Crawford, John
APPLICANT: Lanning, Beth
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: IDENTIFICATION OF MODULATORS OF DEOXYXYLULOSE 5-PHOSPHATE
FILE REFERENCE: 2037 US
CURRENT APPLICATION NUMBER: US/09/626,589
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 824
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Residues 1-165 are from the thioredoxin sequence
OTHER INFORMATION: found in the vector pET32 supplied by No. 6326164agen.
OTHER INFORMATION: Residues 166-824 represent the tdxps sequence from
OTHER INFORMATION: Arabidopsis shown in SEQ ID NO.2.
US-09-626-589-3

Query Match 100.0%; Score 47; DB 2; Length 824;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
| | | | |
Db 32 WCGPCK 37

RESULT 67
US-10-237-551-92
Sequence 92, Application US/10237551
Patent No. 6821519
GENERAL INFORMATION:
APPLICANT: Day, Craig H.
APPLICANT: Hosken, Nancy A.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538C3
CURRENT APPLICATION NUMBER: US/10/237,551
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 92
LENGTH: 858
TYPE: PRT
ORGANISM: Homo sapiens
US-10-237-551-92

Query Match 100.0%; Score 47; DB 2; Length 858;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
| | | | |
Db 40 WCGPCK 45

RESULT 68
US-08-974-549A-600
Sequence 600, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION: /note="fusion protein composed of
OTHER INFORMATION: enterokinase cleavable, His tagged
OTHER INFORMATION: thiorodoxin moiety and full length htrr"
US-08-974-549A-600

Query Match 100.0%; Score 47; DB 2; Length 1285;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 69
US-08-912-951-314
Sequence 314, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 314:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-314

Query Match 100.0%; Score 47; DB 2; Length 1285;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 70
US-09-402-181B-600
Sequence 600, Application US/09402181B
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633

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COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

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REFERENCE/DOCKET NUMBER: 01389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

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OTHER INFORMATION: /note="fusion protein composed of
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db 32 WCGPCK 37

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Search completed: February 23, 2006, 00:43:50
Job time : 39.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-10-660-118A-3

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Sequence: 1 WGPCPK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	47	100.0	52	US-10-145-586-43	Sequence 43, Appl1
6	47	100.0	82	US-10-425-115-351019	Sequence 351019,
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169	47	100.0	219	4	US-10-425-000-52	Sequence 52, Appl	242	47	100.0	458	4	US-10-032-201B-51	Sequence 51, Appl
170	47	100.0	219	4	US-10-425-000-60	Sequence 60, Appl	243	47	100.0	458	4	US-10-032-201B-127	Sequence 127, App
171	47	100.0	219	4	US-10-425-000-72	Sequence 72, Appl	244	47	100.0	458	4	US-10-032-201B-214	Sequence 214, App
172	47	100.0	219	4	US-10-424-999-40	Sequence 40, Appl	245	47	100.0	458	4	US-10-290-072-67	Sequence 67, Appl
173	47	100.0	221	4	US-10-424-999-34	Sequence 34, Appl	246	47	100.0	458	4	US-10-290-072-84	Sequence 84, Appl

247	47	100.0	458	4	US-10-290-072-93	Sequence 93, Appl	320	44	93.6	105	4	US-10-032-201B-94	Sequence 94, Appl
248	47	100.0	458	4	US-10-290-072-102	Sequence 102, App	321	44	93.6	105	4	US-10-032-201B-114	Sequence 114, App
249	47	100.0	458	4	US-10-290-072-111	Sequence 111, App	322	44	93.6	105	4	US-10-032-201B-135	Sequence 135, App
250	47	100.0	458	4	US-10-290-072-120	Sequence 120, App	323	44	93.6	106	4	US-10-032-201B-58	Sequence 58, Appl
251	47	100.0	458	4	US-10-290-072-129	Sequence 129, App	324	44	93.6	106	4	US-10-032-201B-70	Sequence 70, Appl
252	47	100.0	458	4	US-10-290-072-138	Sequence 138, App	325	44	93.6	106	4	US-10-032-201B-113	Sequence 113, App
253	47	100.0	458	4	US-10-290-072-147	Sequence 147, App	326	44	93.6	106	4	US-10-032-201B-140	Sequence 140, App
254	47	100.0	458	4	US-10-290-072-156	Sequence 156, App	327	44	93.6	107	4	US-10-032-201B-171	Sequence 171, App
255	47	100.0	458	4	US-10-290-072-165	Sequence 165, App	328	44	93.6	107	4	US-10-032-201B-75	Sequence 75, Appl
256	47	100.0	458	4	US-10-290-072-183	Sequence 183, App	329	44	93.6	107	4	US-10-032-201B-139	Sequence 139, App
257	47	100.0	458	4	US-10-290-072-192	Sequence 192, App	330	44	93.6	107	4	US-10-032-201B-139	Sequence 139, App
258	47	100.0	458	4	US-10-290-072-201	Sequence 201, App	331	44	93.6	107	4	US-10-032-201B-139	Sequence 139, App
259	47	100.0	458	4	US-10-290-072-201	Sequence 201, App	332	44	93.6	109	4	US-10-032-201B-73	Sequence 73, Appl
260	47	100.0	513	4	US-10-032-201B-32	Sequence 32, Appl	333	44	93.6	109	4	US-10-032-201B-141	Sequence 141, App
261	47	100.0	516	3	US-09-804-626-4	Sequence 4, Appl	334	44	93.6	109	4	US-10-032-201B-185	Sequence 185, App
262	47	100.0	518	3	US-09-804-626-2	Sequence 2, Appl	335	44	93.6	110	4	US-10-156-761-11840	Sequence 11840, A
263	47	100.0	522	4	US-10-296-770-2	Sequence 2, Appl	336	44	93.6	110	4	US-10-032-201B-138	Sequence 138, App
264	47	100.0	530	4	US-10-296-770-5	Sequence 5, Appl	337	44	93.6	110	4	US-10-032-201B-138	Sequence 138, App
265	47	100.0	546	4	US-10-057-531A-1	Sequence 1, Appl	338	44	93.6	112	3	US-09-954-342-32	Sequence 32, Appl
266	47	100.0	546	4	US-10-057-531A-1	Sequence 1, Appl	339	44	93.6	112	4	US-10-425-115-106849	Sequence 306849, A
267	47	100.0	591	3	US-09-938-864-334	Sequence 334, App	340	44	93.6	114	3	US-09-897-898-6	Sequence 6, Appl
268	47	100.0	591	3	US-09-785-019-334	Sequence 334, App	341	44	93.6	114	3	US-09-897-898-6	Sequence 6, Appl
269	47	100.0	591	4	US-10-125-635A-334	Sequence 334, App	342	44	93.6	114	4	US-10-194-885-23	Sequence 23, Appl
270	47	100.0	591	4	US-10-002-603-334	Sequence 334, App	343	44	93.6	114	4	US-10-032-201B-15	Sequence 15, Appl
271	47	100.0	591	4	US-10-195-835-334	Sequence 334, App	344	44	93.6	114	4	US-10-032-201B-39	Sequence 39, Appl
272	47	100.0	591	4	US-10-286-333-334	Sequence 334, App	345	44	93.6	114	4	US-10-032-201B-76	Sequence 76, Appl
273	47	100.0	591	4	US-10-244-830-334	Sequence 334, App	346	44	93.6	114	5	US-10-617-330-2930	Sequence 2930, Ap
274	47	100.0	591	4	US-10-427-717-334	Sequence 334, App	347	44	93.6	114	5	US-10-978-538-11	Sequence 11, Appl
275	47	100.0	591	4	US-10-648-780-334	Sequence 334, App	348	44	93.6	116	4	US-10-032-201B-88	Sequence 88, Appl
276	47	100.0	602	4	US-10-290-072-226	Sequence 226, App	349	44	93.6	117	4	US-10-424-599-26151	Sequence 26151, A
277	47	100.0	602	4	US-10-290-072-226	Sequence 226, App	350	44	93.6	117	4	US-10-424-599-28383	Sequence 28383, A
278	47	100.0	602	4	US-10-290-072-230	Sequence 230, App	351	44	93.6	118	4	US-10-032-201B-91	Sequence 91, Appl
279	47	100.0	602	4	US-10-290-072-232	Sequence 232, App	352	44	93.6	118	4	US-10-767-701-16089	Sequence 16089, A
280	47	100.0	710	4	US-10-296-770-4	Sequence 4, Appl	353	44	93.6	118	4	US-10-425-115-200792	Sequence 200792, A
281	47	100.0	824	4	US-10-046-583A-3	Sequence 3, Appl	354	44	93.6	118	4	US-10-425-115-316523	Sequence 316523, A
282	47	100.0	858	4	US-10-121-988-92	Sequence 92, Appl	355	44	93.6	118	5	US-10-978-538-4	Sequence 4, Appl
283	47	100.0	858	4	US-10-200-562-92	Sequence 92, Appl	356	44	93.6	118	5	US-10-978-538-10	Sequence 10, Appl
284	47	100.0	858	4	US-10-237-551-92	Sequence 92, Appl	357	44	93.6	118	5	US-10-978-538-13	Sequence 13, Appl
285	47	100.0	858	5	US-10-945-050-92	Sequence 92, Appl	358	44	93.6	119	4	US-10-032-201B-175	Sequence 175, App
286	47	100.0	1285	4	US-10-044-697-314	Sequence 314, App	359	44	93.6	119	4	US-10-424-599-227977	Sequence 227977, A
287	47	100.0	1285	4	US-10-044-539-314	Sequence 314, App	360	44	93.6	120	4	US-10-424-599-190543	Sequence 190543, A
288	47	100.0	1285	4	US-10-325-810-600	Sequence 600, App	361	44	93.6	120	4	US-10-425-115-283633	Sequence 283633, A
289	47	100.0	1285	5	US-10-877-124-600	Sequence 600, App	362	44	93.6	120	5	US-10-978-538-6	Sequence 6, Appl
290	47	100.0	1285	5	US-10-877-124-600	Sequence 600, App	363	44	93.6	121	4	US-10-437-963-117121	Sequence 117121, A
291	47	100.0	1285	5	US-10-877-146-600	Sequence 600, App	364	44	93.6	121	4	US-10-425-115-283697	Sequence 283697, A
292	47	93.6	19	3	US-09-963-339-10	Sequence 10, Appl	365	44	93.6	122	4	US-10-194-885-9	Sequence 9, Appl
293	47	93.6	19	4	US-10-145-386-59	Sequence 59, Appl	366	44	93.6	122	4	US-10-194-885-19	Sequence 19, Appl
294	47	93.6	32	4	US-10-424-599-160512	Sequence 160512, A	367	44	93.6	122	4	US-10-194-885-21	Sequence 21, Appl
295	47	93.6	49	4	US-10-425-115-34172	Sequence 34172, A	368	44	93.6	122	4	US-10-091-841-2	Sequence 2, Appl
296	47	93.6	55	4	US-10-425-115-307743	Sequence 307743, A	369	44	93.6	122	4	US-10-032-201B-89	Sequence 89, Appl
297	47	93.6	56	4	US-10-425-115-219153	Sequence 219153, A	370	44	93.6	122	4	US-10-425-115-280376	Sequence 280376, A
298	47	93.6	59	4	US-10-424-599-176362	Sequence 176362, A	371	44	93.6	122	4	US-10-425-115-280388	Sequence 280388, A
299	47	93.6	61	4	US-10-425-115-336734	Sequence 336734, A	372	44	93.6	122	4	US-10-425-115-280382	Sequence 280382, A
300	47	93.6	71	3	US-09-764-875-1015	Sequence 1015, App	373	44	93.6	122	5	US-10-810-160-25	Sequence 25, Appl
301	47	93.6	79	4	US-10-437-963-147189	Sequence 147189, A	374	44	93.6	122	5	US-10-978-538-2	Sequence 2, Appl
302	47	93.6	81	4	US-10-425-115-311489	Sequence 311489, A	375	44	93.6	123	4	US-10-425-115-283692	Sequence 283692, A
303	47	93.6	83	4	US-10-425-115-243739	Sequence 243739, A	376	44	93.6	123	4	US-10-425-115-283655	Sequence 283655, A
304	47	93.6	88	4	US-10-032-201B-115	Sequence 115, App	377	44	93.6	123	5	US-10-978-538-8	Sequence 8, Appl
305	47	93.6	88	4	US-10-032-201B-116	Sequence 116, App	378	44	93.6	124	4	US-10-425-115-312480	Sequence 312480, A
306	47	93.6	96	4	US-10-425-115-286533	Sequence 286533, A	379	44	93.6	125	4	US-10-194-885-20	Sequence 20, Appl
307	47	93.6	96	4	US-10-425-115-334150	Sequence 334150, A	380	44	93.6	125	4	US-10-032-201B-90	Sequence 90, Appl
308	47	93.6	102	4	US-10-032-201B-72	Sequence 72, Appl	381	44	93.6	125	4	US-10-437-963-135318	Sequence 135318, A
309	47	93.6	102	4	US-10-032-201B-103	Sequence 103, App	382	44	93.6	126	4	US-10-194-885-32	Sequence 32, Appl
310	47	93.6	102	4	US-10-289-762-697	Sequence 697, App	383	44	93.6	126	4	US-10-032-201B-79	Sequence 79, Appl
311	47	93.6	102	5	US-10-275-652-20	Sequence 20, Appl	384	44	93.6	126	4	US-10-032-201B-92	Sequence 92, Appl
312	47	93.6	103	4	US-10-032-201B-124	Sequence 124, App	385	44	93.6	126	5	US-10-978-538-12	Sequence 12, Appl
313	47	93.6	103	4	US-10-660-118A-6	Sequence 6, Appl	386	44	93.6	127	4	US-10-091-841-4	Sequence 4, Appl
314	47	93.6	103	4	US-10-425-115-243742	Sequence 243742, A	387	44	93.6	127	4	US-10-425-114-60505	Sequence 60505, A
315	47	93.6	103	4	US-10-425-115-280404	Sequence 280404, A	388	44	93.6	128	4	US-10-425-115-200323	Sequence 200323, A
316	47	93.6	104	4	US-10-032-201B-134	Sequence 134, App	389	44	93.6	128	4	US-10-156-761-14876	Sequence 14876, A
317	47	93.6	104	4	US-10-474-776-712	Sequence 712, App	390	44	93.6	130	4	US-10-091-841-6	Sequence 6, Appl
318	47	93.6	104	4	US-10-660-118A-5	Sequence 5, Appl	391	44	93.6	130	4	US-10-425-115-344247	Sequence 344247, A
319	47	93.6	104	5	US-10-472-928-3670	Sequence 3670, App	392	44	93.6	131	4	US-10-032-201B-170	Sequence 170, App

393	44	93.6	131	4	US-10-032-201B-171	Sequence 171, App	466	44	93.6	180	4	US-10-425-114-66813	Sequence 66813, A
394	44	93.6	131	4	US-10-032-201B-172	Sequence 172, App	467	44	93.6	180	4	US-10-437-963-17191	Sequence 147191, A
395	44	93.6	131	4	US-10-032-201B-174	Sequence 174, App	468	44	93.6	181	4	US-10-424-599-178291	Sequence 178291, A
396	44	93.6	131	4	US-10-032-201B-193	Sequence 193, App	469	44	93.6	181	4	US-10-424-599-27345	Sequence 27345, A
397	44	93.6	131	4	US-10-424-599-231070	Sequence 231070, A	470	44	93.6	181	4	US-10-437-963-20466	Sequence 20466, A
398	44	93.6	131	4	US-10-425-115-320098	Sequence 320098, A	471	44	93.6	182	4	US-10-424-599-250227	Sequence 250227, A
399	44	93.6	132	4	US-10-425-115-317382	Sequence 317382, A	472	44	93.6	182	4	US-10-425-114-67114	Sequence 67114, A
400	44	93.6	133	4	US-10-032-201B-80	Sequence 80, App1	473	44	93.6	182	4	US-10-767-701-46296	Sequence 46296, A
401	44	93.6	133	4	US-10-425-114-61965	Sequence 61965, A	474	44	93.6	183	4	US-10-767-701-46296	Sequence 46296, A
402	44	93.6	133	4	US-10-767-701-43666	Sequence 43666, A	475	44	93.6	188	4	US-10-425-115-360038	Sequence 360038, A
403	44	93.6	134	4	US-10-660-118A-13	Sequence 13, App1	476	44	93.6	189	4	US-10-437-963-204668	Sequence 204668, A
404	44	93.6	134	4	US-10-425-115-247611	Sequence 247611, A	477	44	93.6	191	4	US-10-424-599-275952	Sequence 275952, A
405	44	93.6	135	4	US-10-425-115-237035	Sequence 237035, A	478	44	93.6	193	4	US-10-032-201B-62	Sequence 62, App1
406	44	93.6	136	4	US-10-425-114-62450	Sequence 62450, A	479	44	93.6	194	4	US-10-437-963-204634	Sequence 204634, A
407	44	93.6	137	4	US-10-425-114-48233	Sequence 48233, A	480	44	93.6	204	4	US-10-425-114-47113	Sequence 47113, A
408	44	93.6	137	4	US-10-425-114-53102	Sequence 53102, A	481	44	93.6	216	4	US-10-425-114-66365	Sequence 66365, A
409	44	93.6	137	4	US-10-425-114-60594	Sequence 60594, A	482	44	93.6	229	4	US-10-425-115-207582	Sequence 207582, A
410	44	93.6	137	4	US-10-425-114-64437	Sequence 64437, A	483	44	93.6	232	3	US-09-897-898-11	Sequence 11, App1
411	44	93.6	137	4	US-10-425-114-65475	Sequence 65475, A	484	44	93.6	232	3	US-10-425-115-207582	Sequence 207582, A
412	44	93.6	137	4	US-10-425-115-272549	Sequence 272549, A	485	44	93.6	232	3	US-10-032-201B-20	Sequence 20, App1
413	44	93.6	137	4	US-10-425-115-272551	Sequence 272551, A	486	44	93.6	264	4	US-10-767-701-47316	Sequence 47316, A
414	44	93.6	139	4	US-10-032-201B-119	Sequence 119, App	487	44	93.6	318	5	US-10-732-923-9556	Sequence 9556, App
415	44	93.6	139	4	US-10-425-114-66598	Sequence 66598, A	488	44	93.6	329	5	US-10-732-923-9551	Sequence 9551, App
416	44	93.6	140	4	US-10-032-201B-64	Sequence 64, App1	489	44	93.6	330	4	US-10-437-963-15436	Sequence 15436, A
417	44	93.6	140	4	US-10-425-114-60597	Sequence 60597, A	490	44	93.6	345	5	US-10-732-923-9550	Sequence 9550, App
418	44	93.6	140	4	US-10-425-114-48043	Sequence 48043, A	491	44	93.6	375	5	US-10-732-923-9537	Sequence 9537, App
419	44	93.6	141	4	US-10-425-114-48133	Sequence 48133, A	492	44	93.6	375	5	US-10-732-923-9538	Sequence 9538, App
420	44	93.6	141	4	US-10-425-114-60598	Sequence 60598, A	493	44	93.6	379	4	US-10-424-599-160099	Sequence 160099, A
421	44	93.6	141	4	US-10-425-114-61985	Sequence 61985, A	494	44	93.6	380	5	US-10-732-923-9531	Sequence 9531, App
422	44	93.6	142	4	US-10-378-029-75	Sequence 75, App1	495	44	93.6	380	5	US-10-732-923-9532	Sequence 9532, App
423	44	93.6	143	4	US-10-425-115-247344	Sequence 247344, A	496	44	93.6	385	5	US-10-732-923-9524	Sequence 9524, App
424	44	93.6	144	4	US-10-425-115-247348	Sequence 247348, A	497	44	93.6	386	5	US-10-732-923-9542	Sequence 9542, App
425	44	93.6	144	4	US-10-425-114-49225	Sequence 49225, A	498	44	93.6	446	4	US-10-290-072-212	Sequence 212, App
426	44	93.6	149	3	US-09-738-626-67923	Sequence 67923, App	499	44	93.6	446	4	US-10-290-072-214	Sequence 214, App
427	44	93.6	150	4	US-10-425-114-65385	Sequence 65385, A	500	44	93.6	447	4	US-10-290-072-216	Sequence 216, App
428	44	93.6	150	4	US-10-767-701-41404	Sequence 41404, A	501	44	93.6	447	4	US-10-290-072-210	Sequence 210, App
429	44	93.6	151	4	US-10-156-761-14771	Sequence 14771, A	502	44	93.6	447	4	US-10-290-072-229	Sequence 239, App
430	44	93.6	152	4	US-10-425-114-62447	Sequence 62447, A	503	44	93.6	469	5	US-10-511-699-18	Sequence 18, App1
431	44	93.6	153	4	US-10-424-599-178292	Sequence 178292, A	504	44	93.6	471	4	US-10-032-201B-17	Sequence 37, App1
432	44	93.6	153	4	US-10-425-114-50523	Sequence 50523, A	505	44	93.6	483	5	US-10-511-699-17	Sequence 17, App1
433	44	93.6	155	4	US-10-425-115-196289	Sequence 196289, A	506	44	93.6	486	3	US-09-963-339-5	Sequence 5, App1
434	44	93.6	160	4	US-10-032-201B-181	Sequence 181, App	507	44	93.6	486	4	US-10-145-586-54	Sequence 54, App1
435	44	93.6	163	4	US-10-425-114-41500	Sequence 41500, A	508	44	93.6	518	4	US-10-032-201B-35	Sequence 35, App1
436	44	93.6	163	4	US-10-425-114-52657	Sequence 52657, A	509	44	93.6	549	4	US-10-424-599-250228	Sequence 250228, A
437	44	93.6	165	4	US-10-437-963-131521	Sequence 131521, A	510	44	93.6	553	4	US-10-108-260A-4505	Sequence 4505, App
438	44	93.6	167	4	US-10-032-201B-65	Sequence 65, App1	511	44	93.6	569	4	US-10-437-963-132372	Sequence 132372, A
439	44	93.6	167	4	US-10-437-963-137652	Sequence 137652, A	512	44	93.6	588	4	US-10-408-765A-907	Sequence 907, App
440	44	93.6	167	4	US-10-660-118A-14	Sequence 14, App1	513	44	93.6	588	4	US-10-732-923-13420	Sequence 13420, A
441	44	93.6	167	4	US-10-425-115-196292	Sequence 196292, A	514	44	93.6	588	5	US-10-732-923-13422	Sequence 13422, A
442	44	93.6	168	4	US-10-425-115-196290	Sequence 196290, A	515	44	93.6	596	4	US-10-114-087-17	Sequence 17, App1
443	44	93.6	169	3	US-09-897-898-9	Sequence 9, App1	516	44	93.6	596	4	US-10-712-124-44	Sequence 44, App1
444	44	93.6	169	3	US-09-897-898-9	Sequence 9, App1	517	44	93.6	596	4	US-10-511-698-16	Sequence 16, App1
445	44	93.6	169	4	US-10-032-201B-18	Sequence 18, App1	518	44	93.6	629	5	US-10-723-860-19	Sequence 19, App1
446	44	93.6	169	4	US-10-424-599-176516	Sequence 176516, A	519	44	93.6	629	4	US-10-437-963-119462	Sequence 119462, A
447	44	93.6	172	4	US-10-032-201B-66	Sequence 66, App1	520	44	93.6	981	4	US-10-437-963-127070	Sequence 127070, A
448	44	93.6	172	4	US-10-032-201B-67	Sequence 67, App1	521	44	93.6	105	4	US-10-032-201B-118	Sequence 118, App
449	44	93.6	172	4	US-10-437-963-137025	Sequence 137025, A	522	44	93.6	105	4	US-10-032-201B-184	Sequence 184, App1
450	44	93.6	172	4	US-10-660-118A-15	Sequence 15, App1	523	44	93.6	110	4	US-10-032-201B-77	Sequence 77, App1
451	44	93.6	173	4	US-10-032-201B-61	Sequence 61, App1	524	44	93.6	111	4	US-10-437-963-182983	Sequence 182983, A
452	44	93.6	174	4	US-10-767-701-32096	Sequence 32096, A	525	44	93.6	126	4	US-10-741-601-389	Sequence 389, App
453	44	93.6	174	4	US-10-425-115-317875	Sequence 317875, A	526	44	93.6	126	5	US-10-741-601-389	Sequence 1162, App
454	44	93.6	175	4	US-10-032-201B-69	Sequence 69, App1	527	44	93.6	151	4	US-10-032-201B-168	Sequence 168, App
455	44	93.6	175	4	US-10-032-201B-156	Sequence 156, App	528	44	93.6	167	4	US-10-425-115-249338	Sequence 249338, A
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457	44	93.6	175	4	US-10-424-599-282487	Sequence 282487, A	530	44	93.6	183	4	US-10-424-599-225032	Sequence 225032, A
458	44	93.6	175	4	US-10-425-114-50857	Sequence 50857, A	531	44	93.6	327	4	US-10-032-585-7827	Sequence 7827, App
459	44	93.6	175	4	US-10-767-701-40803	Sequence 40803, A	532	44	93.6	459	5	US-10-450-766-48425	Sequence 48425, A
460	44	93.6	177	4	US-10-425-115-349412	Sequence 349412, A	533	44	93.6	570	4	US-10-424-599-218210	Sequence 218210, A
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462	44	93.6	179	4	US-10-425-114-66811	Sequence 66811, A	535	44	93.6	747	3	US-09-978-295A-459	Sequence 459, App
463	44	93.6	179	4	US-10-425-115-280370	Sequence 280370, A	536	44	93.6	747	3	US-09-938-418-9	Sequence 9, App1
464	44	93.6	180	4	US-10-425-114-48070	Sequence 48070, A	537	44	93.6	747	3	US-09-978-697-459	Sequence 459, App
465	44	93.6	180	4	US-10-425-114-52471	Sequence 52471, A	538	44	93.6	747	3	US-09-978-192A-459	Sequence 459, App

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554	-43	91.5	747	3	US-09-978-757A-459	Sequence 459, App	627	43	91.5	747	4	US-10-123-215-426	Sequence 426, App
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596	-43	91.5	747	4	US-10-016-177A-459	Sequence 459, App	669	43	91.5	747	4	US-10-121-061-426	Sequence 426, App
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687	43	91.5	747	4	US-10-127-832A-426	Sequence 426, App	760	43	91.5	747	4	US-10-153-386-426	Sequence 426, App
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689	43	91.5	747	4	US-10-127-834A-426	Sequence 426, App	762	43	91.5	747	4	US-10-158-786A-459	Sequence 426, App
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708	43	91.5	747	4	US-10-158-785-426	Sequence 426, App	781	43	91.5	747	4	US-10-141-705-426	Sequence 426, App
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726	43	91.5	747	4	US-10-146-788-426	Sequence 426, App	799	43	91.5	747	4	US-10-143-116-426	Sequence 426, App
727	43	91.5	747	4	US-10-152-380-426	Sequence 426, App	800	43	91.5	747	4	US-10-144-957-426	Sequence 426, App
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729	43	91.5	747	4	US-10-140-807-426	Sequence 426, App	802	43	91.5	747	4	US-10-145-015-426	Sequence 426, App
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736	43	91.5	747	4	US-10-142-432-426	Sequence 426, App	809	43	91.5	747	4	US-10-145-752-426	Sequence 426, App
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ALIGNMENTS

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; Sequence 4, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; APPLICANT: Kwon, MiJung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: mammalian
US-10-304-287-4
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Db      1 WCGPCK 6
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; Sequence 3, Application US/10660118A
; Publication No. US20040131606A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; FILE REFERENCE: 2879-98
; CURRENT APPLICATION NUMBER: US/10/660,118A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-10-660-118A-3
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; Sequence 4, Application US/10735577
; Publication No. US20040142897A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metastasis
; FILE REFERENCE: ME03-009
; CURRENT APPLICATION NUMBER: US/10/735,577
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/433,140
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word
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; TYPE: PRT
; ORGANISM: mammalian
US-10-735-577-4
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US-09-801-260-4
; Sequence 4, Application US/09801260
; Patent No. US20020034801A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 22105, A NOVEL HUMAN THIOREDOXIN FAMILY
; FILE REFERENCE: 10448-022001
; CURRENT APPLICATION NUMBER: US/09/801,260
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,447
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 52
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; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-801-260-4
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Db 20 WCGPCK 25

RESULT 5
US-10-145-586-43
; Sequence 43, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Gluckemann, Maria
; APPLICANT: Silos-Santiago, Imaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-145-586-43

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Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
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Db 20 WCGPCK 25

RESULT 6
US-10-425-115-351019
; Sequence 351019, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351019
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83299C.1.pep
US-10-425-115-351019

Query Match 100.0%; Score 47; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

Db 5 WCGPCK 10
|||||

RESULT 7
US-10-408-765A-312
; Sequence 312, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boi D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-312

Query Match 100.0%; Score 47; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 8
US-10-424-599-280571
; Sequence 280571, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 280571
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .. (90)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95379C.1.pep
US-10-424-599-280571

Query Match 100.0%; Score 47; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 13 WCGPCK 18

```
RESULT 9
US-10-032-201B-143
; Sequence 143, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Thiocapsa roseopersicina
US-10-032-201B-143
```

```
Query Match          100.0%; Score 47; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       32 WCGPCK 37
```

```
RESULT 10
US-10-032-201B-102
; Sequence 102, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Chlamydia muridarum
US-10-032-201B-102
```

```
Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       27 WCGPCK 32
```

```
RESULT 11
US-10-032-201B-104
```

```
; Sequence 104, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Paiticaci
US-10-032-201B-104
```

```
Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       27 WCGPCK 32
```

```
RESULT 12
US-10-032-201B-105
; Sequence 105, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-10-032-201B-105
```

```
Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       27 WCGPCK 32
```

```
RESULT 13
US-10-032-201B-126
; Sequence 126, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mycoplasma genitalium
US-10-032-201B-126
```

```

Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       29 WCGPCK 34
```

```

RESULT 14
US-10-032-201B-128
; Sequence 128, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mycoplasma pneumoniae
US-10-032-201B-128
```

```

Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       29 WCGPCK 34
```

```

RESULT 15
US-10-501-282-3126
; Sequence 3126, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCWITCHAEL, JOHN CALHOUN
; APPLICANT: ZAGORSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
```

```

; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOTOCOCUS OTTIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT FILING DATE: 2004-07-09
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3126
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Allostococcus ottidis
US-10-501-282-3126
```

```

Query Match          100.0%; Score 47; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       27 WCGPCK 32
```

```

RESULT 16
US-10-032-201B-96
; Sequence 96, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-032-201B-96
```

```

Query Match          100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       27 WCGPCK 32
```

```

RESULT 17
US-10-032-585-7785
; Sequence 7785, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jlang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
```

/ TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
/ FILE REFERENCE: 10182-005-999
/ CURRENT APPLICATION NUMBER: US/10/032,585
/ NUMBER OF SEQ ID NOS: 8000
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7785
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-10-032-585-7785

Query Match 100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 29 WCGPCK 34

RESULT 18
US-10-660-118a-7
/ Sequence 7, Application US/10660118A
/ Publication No. US20040131606A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
/ FILE REFERENCE: 2879-98
/ CURRENT APPLICATION NUMBER: US/10/660,118A
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
US-10-660-118a-7

Query Match 100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 29 WCGPCK 34

RESULT 19
US-10-451-467A-270
/ Sequence 270, Application US/10451467A
/ Publication No. US20040161840A1
/ GENERAL INFORMATION:
/ APPLICANT: CONTRERAS, ROLAND HENRI
/ APPLICANT: EBERHARDT, INES
/ APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
/ APPLICANT: REEKMAN, RIEKA JOSEPHINA
/ TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
/ FILE REFERENCE: JAB-1667
/ CURRENT APPLICATION NUMBER: US/10/451,467A
/ PRIOR FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: EP 00870318.3
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: EP 01870002.1
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: EP 01870003.9
/ PRIOR FILING DATE: 2001-01-09
/ NUMBER OF SEQ ID NOS: 732

/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 270
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-270

Query Match 100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 29 WCGPCK 34

RESULT 20
US-10-451-467A-450
/ Sequence 450, Application US/10451467A
/ Publication No. US20040161840A1
/ GENERAL INFORMATION:
/ APPLICANT: CONTRERAS, ROLAND HENRI
/ APPLICANT: EBERHARDT, INES
/ APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
/ APPLICANT: REEKMAN, RIEKA JOSEPHINA
/ TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
/ FILE REFERENCE: JAB-1667
/ CURRENT APPLICATION NUMBER: US/10/451,467A
/ PRIOR FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: EP 00870318.3
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: EP 01870002.1
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: EP 01870003.9
/ PRIOR FILING DATE: 2001-01-09
/ NUMBER OF SEQ ID NOS: 732
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 450
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-10-451-467A-450

Query Match 100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 29 WCGPCK 34

RESULT 21
US-10-451-467A-614
/ Sequence 614, Application US/10451467A
/ Publication No. US20040161840A1
/ GENERAL INFORMATION:
/ APPLICANT: CONTRERAS, ROLAND HENRI
/ APPLICANT: EBERHARDT, INES
/ APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
/ APPLICANT: REEKMAN, RIEKA JOSEPHINA
/ TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
/ FILE REFERENCE: JAB-1667
/ CURRENT APPLICATION NUMBER: US/10/451,467A
/ PRIOR FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: EP 00870318.3
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: EP 01870002.1
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: EP 01870003.9
/ PRIOR FILING DATE: 2001-01-09

NUMBER OF SEQ ID NOS: 732
SOFTWARE: Patentin version 3.1
SEQ ID NO 614
LENGTH: 103
TYPE: PRT
ORGANISM: Candida albicans
US-10-451-467A-614

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 22

US-09-954-342-62
Sequence 62, Application US/09954342
Publication No. US20030170838A1

GENERAL INFORMATION:

APPLICANT: MISHRA, VISHNU S.
APPLICANT: SPYTER, KIMBERLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: VERNET, CORINE A.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: GORMAN, LINDA
APPLICANT: TCHERNEV, VELIZAR T.
APPLICANT: MALYANKAR, URIEL M.
APPLICANT: SHENOY, SURESH
APPLICANT: PADIGARU, MURALIDHARA
APPLICANT: GERLACH, VALERIE L.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: SMITHSON, GLENNDA
APPLICANT: MILLET, ISABELLE
APPLICANT: PEYMAN, JOHN
APPLICANT: STONE, DAVID
APPLICANT: GUNTHER, ERIK
APPLICANT: ELLERMAN, KAREN
APPLICANT: LI, LI
APPLICANT: RASTELLI, LUCA
APPLICANT: ZERHUSEN, BRYAN
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 21402-114
CURRENT APPLICATION NUMBER: US/09/954,342
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,382
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 60/240,498
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/260,284
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/260,973
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/264,794
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: 60/238,398
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/232,675
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/274,862
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/233,801
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/232,676
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/233,960
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/233,402
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 60/233,521
PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/233,522
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/232,679
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 62
LENGTH: 104
TYPE: PRT
ORGANISM: Ovis aries
US-09-954-342-62

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 23

US-09-954-342-63
Sequence 63, Application US/09954342
Publication No. US20030170838A1

GENERAL INFORMATION:

APPLICANT: MISHRA, VISHNU S.
APPLICANT: SPYTER, KIMBERLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: VERNET, CORINE A.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: GORMAN, LINDA
APPLICANT: TCHERNEV, VELIZAR T.
APPLICANT: MALYANKAR, URIEL M.
APPLICANT: SHENOY, SURESH
APPLICANT: PADIGARU, MURALIDHARA
APPLICANT: GERLACH, VALERIE L.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: SMITHSON, GLENNDA
APPLICANT: MILLET, ISABELLE
APPLICANT: PEYMAN, JOHN
APPLICANT: STONE, DAVID
APPLICANT: GUNTHER, ERIK
APPLICANT: ELLERMAN, KAREN
APPLICANT: LI, LI
APPLICANT: RASTELLI, LUCA
APPLICANT: ZERHUSEN, BRYAN
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 21402-114
CURRENT APPLICATION NUMBER: US/09/954,342
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,382
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 60/240,498
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/260,284
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/238,398
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/232,675
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/274,862
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/233,801
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/232,676
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/233,960
PRIOR FILING DATE: 2000-09-20

;; PRIOR APPLICATION NUMBER: 60/233,402
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 60/233,521
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 60/233,522
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 60/232,679
;; PRIOR FILING DATE: 2000-09-15
;; NUMBER OF SEQ ID NOS: 104
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 63
;; LENGTH: 104
;; TYPE: PRT
;; ORGANISM: Bos taurus
US-09-954-342-63

Query Match 100.0%; Score 47; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 24
US-09-954-342-64
;; Sequence 64, Application US/09954342
;; Publication No. US20030170838A1
;; GENERAL INFORMATION:
;; APPLICANT: MISHRA, VISHNU S.
;; APPLICANT: SPYTER, KIMBERLY ANN
;; APPLICANT: TAUPIER, RAYMOND J.
;; APPLICANT: VERNET, CORINE A.
;; APPLICANT: COLMAN, STEVEN D.
;; APPLICANT: GORMAN, LINDA
;; APPLICANT: TCHERNEY, VELIZAR T.
;; APPLICANT: MALYANKAR, URIEL M.
;; APPLICANT: SHENOY, SURESH
;; APPLICANT: PADIGARU, MURALIDHARA
;; APPLICANT: GERLACH, VALERIE L.
;; APPLICANT: MACDOUGALL, JOHN R.
;; APPLICANT: SMITHSON, GLENNDA
;; APPLICANT: MILLER, ISABELLE
;; APPLICANT: PEYMAN, JOHN
;; APPLICANT: STONE, DAVID
;; APPLICANT: GUNTHER, ERIK
;; APPLICANT: ELLERMAN, KAREN
;; APPLICANT: LI, LI
;; APPLICANT: RASTELLI, LUCA
;; APPLICANT: ZERHUSEN, BRYAN
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
;; FILE REFERENCE: 21402-114
;; CURRENT APPLICATION NUMBER: US/09/954,342
;; PRIOR FILING DATE: 2001-09-17
;; PRIOR APPLICATION NUMBER: 60/233,382
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 60/240,498
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/260,284
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: 60/260,973
;; PRIOR FILING DATE: 2001-01-11
;; PRIOR APPLICATION NUMBER: 60/264,794
;; PRIOR FILING DATE: 2001-01-29
;; PRIOR APPLICATION NUMBER: 60/238,398
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/232,675
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 60/274,862
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 60/233,801
;; PRIOR FILING DATE: 2000-09-19

;; PRIOR APPLICATION NUMBER: 60/232,676
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 60/233,960
;; PRIOR FILING DATE: 2000-09-20
;; PRIOR APPLICATION NUMBER: 60/233,402
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 60/233,521
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 60/233,522
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 60/232,679
;; PRIOR FILING DATE: 2000-09-15
;; NUMBER OF SEQ ID NOS: 104
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 64
;; LENGTH: 104
;; TYPE: PRT
;; ORGANISM: Macaca mulatta
US-09-954-342-64

Query Match 100.0%; Score 47; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 25
US-09-954-342-65
;; Sequence 65, Application US/09954342
;; Publication No. US20030170838A1
;; GENERAL INFORMATION:
;; APPLICANT: MISHRA, VISHNU S.
;; APPLICANT: SPYTER, KIMBERLY ANN
;; APPLICANT: TAUPIER, RAYMOND J.
;; APPLICANT: VERNET, CORINE A.
;; APPLICANT: COLMAN, STEVEN D.
;; APPLICANT: GORMAN, LINDA
;; APPLICANT: TCHERNEY, VELIZAR T.
;; APPLICANT: MALYANKAR, URIEL M.
;; APPLICANT: SHENOY, SURESH
;; APPLICANT: PADIGARU, MURALIDHARA
;; APPLICANT: GERLACH, VALERIE L.
;; APPLICANT: MACDOUGALL, JOHN R.
;; APPLICANT: SMITHSON, GLENNDA
;; APPLICANT: MILLER, ISABELLE
;; APPLICANT: PEYMAN, JOHN
;; APPLICANT: STONE, DAVID
;; APPLICANT: GUNTHER, ERIK
;; APPLICANT: ELLERMAN, KAREN
;; APPLICANT: LI, LI
;; APPLICANT: RASTELLI, LUCA
;; APPLICANT: ZERHUSEN, BRYAN
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
;; FILE REFERENCE: 21402-114
;; CURRENT APPLICATION NUMBER: US/09/954,342
;; PRIOR FILING DATE: 2001-09-17
;; PRIOR APPLICATION NUMBER: 60/233,382
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 60/240,498
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/260,284
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: 60/260,973
;; PRIOR FILING DATE: 2001-01-11
;; PRIOR APPLICATION NUMBER: 60/264,794
;; PRIOR FILING DATE: 2001-01-29
;; PRIOR APPLICATION NUMBER: 60/238,398
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/232,675
;; PRIOR FILING DATE: 2000-09-15

```

1 PRIOR APPLICATION NUMBER: 60/274,862
2 PRIOR FILING DATE: 2001-03-09
3 PRIOR APPLICATION NUMBER: 60/233,801
4 PRIOR FILING DATE: 2000-09-19
5 PRIOR APPLICATION NUMBER: 60/233,676
6 PRIOR FILING DATE: 2000-09-15
7 PRIOR APPLICATION NUMBER: 60/233,966
8 PRIOR FILING DATE: 2000-09-20
9 PRIOR APPLICATION NUMBER: 60/233,402
10 PRIOR FILING DATE: 2000-09-18
11 PRIOR APPLICATION NUMBER: 60/233,521
12 PRIOR FILING DATE: 2000-09-19
13 PRIOR APPLICATION NUMBER: 60/233,522
14 PRIOR FILING DATE: 2000-09-19
15 PRIOR APPLICATION NUMBER: 60/233,522
16 PRIOR FILING DATE: 2000-09-15
17 NUMBER OF SEQ ID NOS: 104
18 SOFTWARE: PatentIn Ver. 2.1
19 SEQ ID NO 65
20 LENGTH: 104
21 TYPE: DRT
22 ORGANISM: Rattus norvegicus
23 US-09-954-342-65

```

Query Match	100.0%;	Score 47;	DB 3;	Length 104;
Best Local Similarity	100.0%;	Pred. No. 12;		
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0

	1	6
QY		
Db	30	35

```

RESULT 26
US-10-032-2018-146
: Sequence 146, Application US/10032201B
: Publication No. US20030167524A1
: GENERAL INFORMATION:
: APPLICANT: Van Rooijen, GJ's
: APPLICANT: Deckers, Harm
: APPLICANT: Heifetz, Peter Bernard
: APPLICANT: Briggs, Steven
: APPLICANT: Dalmia, Bipin Kumar
: APPLICANT: Del Val, Greg
: APPLICANT: Zaplachinski, Steve
: APPLICANT: Moloney, Maurice
: TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
: TITLE OF INVENTION: COMPOSITIONS
: FILE REFERENCE: 38814 351B
: CURRENT APPLICATION NUMBER: US/10/032,201B
: CURRENT FILING DATE: 2001-12-19
: NUMBER OF SEQ ID NOS: 313
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 146
: LENGTH: 104
: TYPE: PRT
: ORGANISM: Bos taurus
US-10-032-2018-146

```

Query Match	100.0%;	Score 47;	DB 4;	Length 104;
Best Local Similarity	100.0%;	Pred. No. 12;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0

QY	1	WCGPCK	6
Db	30	WCGPCK	35

```

RESULT 27
US-10-032-201B-150
; Sequence 150, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Gallus gallus
; US-10-032-201B-150

```

Query Match	100.0%;	Score 47;	DB 4;	Length 104;
Best Local Similarity	100.0%;	Pred. No. 12;		
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0

QY	1	WCGPCK	6
Db	30	WCGPCK	35

```

US-10-032-2015_152
: Sequence 152, Application US/10032201B
: Publication No. US20030167524A1
: GENERAL INFORMATION:
: APPLICANT: Van Rooijen, Gijs
: APPLICANT: Deckers, Harm
: APPLICANT: Helfetz, Peter Bernard
: APPLICANT: Briggs, Steven
: APPLICANT: Dalma, Bipin Kumar
: APPLICANT: Del Val, Greg
: APPLICANT: Zaplachinski, Steve
: APPLICANT: Moloney, Maurice
: TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
: TITLE OF INVENTION: COMPOSITIONS
: FILE REFERENCE: 38614 351B
: CURRENT APPLICATION NUMBER: US/10/032,201B
: CURRENT FILING DATE: 2001-12-19
: NUMBER OF SEQ ID NOS: 313
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 152
: LENGTH: 104
: TYPE: PRT
: ORGANISM: Homo sapien
US-10-032-201B-152

```

Query Match	100.0%;	Score 47;	DB 4;	Length 104;
Best Local Similarity	100.0%;	Pred. No. 12;		
Matches	6;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps	0

QY	1	WC	GP	CK	6
Db	30	WC	GP	CK	35

```

RESULTS29
US-10-032-201B-154
; Sequence 154, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helftetz, Peter Bernard

```

```

; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-032-201B-154

```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
    |||||
Db 30 WCGPCK 35

```

```

RESULT 30
US-10-032-201B-155
; Sequence 155, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-032-201B-155

```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
    |||||
Db 30 WCGPCK 35

```

```

RESULT 31
US-10-032-201B-158
; Sequence 158, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg

```

```

; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-032-201B-158

```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
    |||||
Db 30 WCGPCK 35

```

```

RESULT 32
US-10-032-201B-159
; Sequence 159, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-032-201B-159

```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
    |||||
Db 30 WCGPCK 35

```

```

RESULT 33
US-10-032-201B-161
; Sequence 161, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED

```

```

; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 104
; TYPE: PRF
; ORGANISM: Ovis aries
US-10-032-201B-161
```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       30 WCGPCK 35
```

```

RESULT 34
US-10-032-201B-276
; Sequence 276, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggis, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 104
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-10-032-201B-276
```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       28 WCGPCK 33
```

```

RESULT 35
US-10-424-599-282588
; Sequence 282588, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282588
; LENGTH: 104
```

```

; TYPE: PRF
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97199C.1.pep
US-10-424-599-282588
```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       54 WCGPCK 59
```

```

RESULT 36
US-10-451-467A-188
; Sequence 188, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEMANS, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 732
; SEQ ID NO 188
; LENGTH: 104
; TYPE: PRF
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-188
```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       30 WCGPCK 35
```

```

RESULT 37
US-09-954-342-61
; Sequence 61, Application US/09954342
; Publication No. US20030170838A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, VISHNU S.
; APPLICANT: SPYTER, KIMBERLY ANN
; APPLICANT: TAUPIER, RAYMOND J.
; APPLICANT: VERNET, CORINE A.
; APPLICANT: COLMAN, STEVEN D.
; APPLICANT: GORMAN, LINDA
; APPLICANT: TCHERNYEV, VELIZAR T.
; APPLICANT: MALYANKAR, URIEL M.
; APPLICANT: SHENOY, SURESH
; APPLICANT: PADIGARU, MURALIDHARA
; APPLICANT: GERLAGH, VALERIE L.
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; APPLICANT: MILLET, ISABELLE
; APPLICANT: PEYMAN, JOHN
; APPLICANT: STONE, DAVID
```

```
/ APPLICANT: GUNTHER, ERIK
/ APPLICANT: ELLERMAN, KAREN
/ APPLICANT: LI, LI
/ APPLICANT: RASTELLI, LUCA
/ APPLICANT: ZERHUSEN, BRYAN
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
/ FILE REFERENCE: 21402-114
/ CURRENT APPLICATION NUMBER: US/09/954,342
/ PRIOR FILING DATE: 2001-09-17
/ PRIOR APPLICATION NUMBER: 60/233,382
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: 60/240,498
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: 60/260,284
/ PRIOR FILING DATE: 2001-01-08
/ PRIOR APPLICATION NUMBER: 60/260,973
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/264,794
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: 60/238,398
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/232,675
/ PRIOR FILING DATE: 2000-09-15
/ PRIOR APPLICATION NUMBER: 60/274,862
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/233,801
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/232,676
/ PRIOR FILING DATE: 2000-09-15
/ PRIOR APPLICATION NUMBER: 60/233,960
/ PRIOR FILING DATE: 2000-09-20
/ PRIOR APPLICATION NUMBER: 60/233,402
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: 60/233,521
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/233,522
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/232,679
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 61
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Equus caballus
US-09-954-342-61

Query Match          100.0%; Score 47; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      31 WCGPCK 36

RESULT 38
US-10-171-311-226
/ Sequence 226, Application US/10171311
/ Publication No. US20030087270A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Chen, Yan
/ APPLICANT: Zhao, Xumei
/ APPLICANT: Monahan, John
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Glatt, Karen
/ APPLICANT: Gannavarapu, Manjula
/ APPLICANT: Hoerish, Sebastian
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
/ FILE REFERENCE: MRI-035
```

```
/ CURRENT APPLICATION NUMBER: US/10/171,311
/ CURRENT FILING DATE: 2002-06-12
/ PRIOR APPLICATION NUMBER: US 60/298,159
/ PRIOR FILING DATE: 2001-06-13
/ PRIOR APPLICATION NUMBER: US 60/298,155
/ PRIOR FILING DATE: 2001-06-13
/ PRIOR APPLICATION NUMBER: US 60/335,936
/ PRIOR FILING DATE: 2001-11-14
/ NUMBER OF SEQ ID NOS: 238
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 226
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-171-311-226

Query Match          100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      31 WCGPCK 36

RESULT 39
US-10-316-253-291
/ Sequence 291, Application US/10316253
/ Publication No. US20030162706A1
/ GENERAL INFORMATION:
/ APPLICANT: The Procter & Gamble Company
/ APPLICANT: Peters, Kevin
/ APPLICANT: Thompson, Larry
/ APPLICANT: Wang, Feng
/ APPLICANT: Greis, Kenneth
/ TITLE OF INVENTION: Angiogenesis Modulating Proteins
/ FILE REFERENCE: 8865M
/ CURRENT APPLICATION NUMBER: US/10/316,253
/ CURRENT FILING DATE: 2002-12-10
/ PRIOR APPLICATION NUMBER: US 60/355,295
/ PRIOR FILING DATE: 2002-02-08
/ NUMBER OF SEQ ID NOS: 308
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 291
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-10-316-253-291

Query Match          100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      31 WCGPCK 36

RESULT 40
US-10-032-201B-47
/ Sequence 47, Application US/10032201B
/ Publication No. US20030167524A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Rooijen, Gijb
/ APPLICANT: Deckers, Harm
/ APPLICANT: Heiletz, Peter Bernard
/ APPLICANT: Briggs, Steven
/ APPLICANT: Dalwala, Bipin Kumar
/ APPLICANT: Del Val, Greg
/ APPLICANT: Zaplachinski, Steve
/ APPLICANT: Moloney, Maurice
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
/ TITLE OF INVENTION: COMPOSITIONS
```

FILE REFERENCE: 38814 351B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 105
TYPE: PRT
ORGANISM: Homo Sapien
US-10-032-201B-47

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 41

US-10-032-201B-106
Sequence 106, Application US/10032201B
Publication No. US20030167524A1
GENERAL INFORMATION:
APPLICANT: Van Rooijen, G.J.s
APPLICANT: Deckers, Harm
APPLICANT: Heifetz, Peter Bernard
APPLICANT: Briggs, Steven
APPLICANT: Dalmla, Bipin Kumar
APPLICANT: Del Val, Greg
APPLICANT: Zaplachinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 38814 351B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 106
LENGTH: 105
TYPE: PRT
ORGANISM: Corynebacterium nephridii
US-10-032-201B-106

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 29 WCGPCK 34

RESULT 42

US-10-424-599-237784
Sequence 237784, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 237784
LENGTH: 105
TYPE: PRT

ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(105)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_56744C.1.dep
US-10-424-599-237784

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 57 WCGPCK 62

RESULT 43

US-10-351-891-127
Sequence 127, Application US/10351891
Publication No. US2004004811A1
GENERAL INFORMATION:
APPLICANT: PAUL D. KASSNER
APPLICANT: DANA ADLT-RICHER
TITLE OF INVENTION: USE OF COLLECTIONS OF BINDING SITES FOR SAMPLE PROFILING AND OTHE
TITLE OF INVENTION: APPLICATIONS
FILE REFERENCE: 25885-1753
CURRENT APPLICATION NUMBER: US/10/351,891
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: US 60/352,011
PRIOR FILING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 127
LENGTH: 105
TYPE: PRT
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank BAA04881
DATABASE ENTRY DATE: 2002-12-25
US-10-351-891-127

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 44

US-10-408-765A-2019
Sequence 2019, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2019
LENGTH: 105

TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-2019

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 45

US-10-660-118A-8
Sequence 8, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 105
TYPE: PRT
ORGANISM: Gallus gallus
US-10-660-118A-8

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 46

US-10-660-118A-9
Sequence 9, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 105
TYPE: PRT
ORGANISM: Mus musculus
US-10-660-118A-9

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 47

US-10-660-118A-10
Sequence 10, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 105
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-660-118A-10

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 48

US-10-660-118A-11
Sequence 11, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 105
TYPE: PRT
ORGANISM: Bos taurus
US-10-660-118A-11

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 49

US-10-660-118A-12
Sequence 12, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A

/ CURRENT FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 12
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-660-118A-12

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 50
US-10-451-467A-684
/ Sequence 684, Application US/10451467A
/ Publication No. US20040161840A1
/ GENERAL INFORMATION:
/ APPLICANT: CONTRERAS, ROLAND HENRI
/ APPLICANT: EBERHARDT, INES
/ APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
/ APPLICANT: REEKMAN, RIEKA JOSEPHINA
/ TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
/ TITLE OF INVENTION: YEAST AND FUNGI
/ FILE REFERENCE: JAB-1667
/ CURRENT APPLICATION NUMBER: US/10/451,467A
/ CURRENT FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: EP 00870318.3
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: EP 01870002.1
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: EP 01870003.9
/ PRIOR FILING DATE: 2001-01-09
/ NUMBER OF SEQ ID NOS: 732
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 684
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-451-467A-684

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 51
US-10-699-113-32
/ Sequence 32, Application US/10699113
/ Publication No. US200402411748A1
/ GENERAL INFORMATION:
/ APPLICANT: AULT-RICHE, Dana
/ APPLICANT: Kumble, Krishanand
/ APPLICANT: Schultz, Rainier
/ APPLICANT: Schultz, Kenneth
/ TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
/ FILE REFERENCE: 25885-1755
/ CURRENT APPLICATION NUMBER: US/10/699,113
/ CURRENT FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/446,687

/ PRIOR FILING DATE: 2003-02-10
/ NUMBER OF SEQ ID NOS: 948
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 32
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: Genbank BAA04881
/ DATABASE ENTRY DATE: 2002-12-25
US-10-699-113-32

Query Match 100.0%; Score 47; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 52
US-10-970-370-2
/ Sequence 2, Application US/10970370
/ Publication No. US20050208037A1
/ GENERAL INFORMATION:
/ APPLICANT: DASHNAMOORTHY, RAVI
/ APPLICANT: DAS, KUMUDA C.
/ TITLE OF INVENTION: THIORODOXIN INCREASES REDOX-CYCLING OF ANTICANCER
/ TITLE OF INVENTION: AGENTS THEREBY SENSITIZES CANCER CELLS TO APOPTOSIS
/ FILE REFERENCE: UTSN:025US
/ CURRENT APPLICATION NUMBER: US/10/970,370
/ CURRENT FILING DATE: 2004-10-21
/ PRIOR APPLICATION NUMBER: 60/513,134
/ PRIOR FILING DATE: 2003-10-21
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-970-370-2

Query Match 100.0%; Score 47; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 53
US-10-970-370-6
/ Sequence 6, Application US/10970370
/ Publication No. US20050208037A1
/ GENERAL INFORMATION:
/ APPLICANT: DASHNAMOORTHY, RAVI
/ APPLICANT: DAS, KUMUDA C.
/ TITLE OF INVENTION: THIORODOXIN INCREASES REDOX-CYCLING OF ANTICANCER
/ TITLE OF INVENTION: AGENTS THEREBY SENSITIZES CANCER CELLS TO APOPTOSIS
/ FILE REFERENCE: UTSN:025US
/ CURRENT APPLICATION NUMBER: US/10/970,370
/ CURRENT FILING DATE: 2004-10-21
/ PRIOR APPLICATION NUMBER: 60/513,134
/ PRIOR FILING DATE: 2003-10-21
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Macaca mulatta
US-10-970-370-6

Query Match 100.0%; Score 47; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 54
US-10-032-201B-123
; Sequence 123, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-032-201B-123

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 55
US-10-032-201B-132
; Sequence 132, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Penicillium chrysogenum
US-10-032-201B-132

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 56
US-10-032-201B-137
; Sequence 137, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Streptomyces aureofaciens
US-10-032-201B-137

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 57
US-10-032-201B-176
; Sequence 176, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-032-201B-176

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

Db 31 WCGPCK 36

RESULT 58

US-10-335-977-6752
; Sequence 6752, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031

CORRESPONDENCE ADDRESS:

ADDRESS: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977

FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002

FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 6752:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Helicobacter pylori

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1..106

SEQUENCE DESCRIPTION: SEQ ID NO: 6752:

US-10-335-977-6752

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 59

US-10-628-391-1

; Sequence 1, Application US/10628391

; Publication No. US20040146526A1

; GENERAL INFORMATION:

APPLICANT: WINDLE, Henry J.

APPLICANT: O'TOOLE, Dermot

APPLICANT: KELLEHER, Dermot

APPLICANT: ABDEL-LATIF, Mohamed M.

; TITLE OF INVENTION: INHIBITION OF NF-kappaB ACTIVATION

; FILE REFERENCE: P69048US0

; CURRENT APPLICATION NUMBER: US/10/628,391

; CURRENT FILING DATE: 2003-07-29

; PRIOR APPLICATION NUMBER: PCT/IE02/00011

; PRIOR FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 106

; TYPE: PRT

; ORGANISM: H. pylori

US-10-628-391-1

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 60

US-10-425-115-365910

; Sequence 365910, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

APPLICANT: LA ROSA, Thomas J.

APPLICANT: KOVALIC, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 365910

LENGTH: 106

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_96874C.1.pcp

US-10-425-115-365910

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 61

US-11-097-143-7479

; Sequence 7479, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CL000728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR FILING DATE: 1999-10-28

```
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7479
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-11-097-143-7479
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Query Match      100.0%; Score 47; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 WCGPCK 6
        |||||
Db       31 WCGPCK 36
```

RESULT 62

```
US-10-032-201B-109
/ Sequence 109, Application US/10032201B
/ Publication No. US20030167524A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Rooijen, Gijb
/ APPLICANT: Deckers, Harm
/ APPLICANT: Heifetz, Peter Bernard
/ APPLICANT: Briggs, Steven
/ APPLICANT: Dalma, Bipin Kumar
/ APPLICANT: Del Val, Greg
/ APPLICANT: Zaplachinski, Steve
/ APPLICANT: Moloney, Maurice
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
/ TITLE OF INVENTION: COMPOSITIONS
/ FILE REFERENCE: 38814 351B
/ CURRENT APPLICATION NUMBER: US/10/032,201B
/ CURRENT FILING DATE: 2001-12-19
/ NUMBER OF SEQ ID NOS: 313
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 109
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Chromatium vinosum
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: 17, 38, 42, 55, 58, 60, 72, 107
/ OTHER INFORMATION: Xaa = Any Amino Acid
US-10-032-201B-109
```

```
Query Match      100.0%; Score 47; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 WCGPCK 6
        |||||
Db       31 WCGPCK 36
```

RESULT 63

```
US-10-032-201B-121
/ Sequence 121, Application US/10032201B
/ Publication No. US20030167524A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Rooijen, Gijb
/ APPLICANT: Deckers, Harm
```

```
/ APPLICANT: Heifetz, Peter Bernard
/ APPLICANT: Briggs, Steven
/ APPLICANT: Dalma, Bipin Kumar
/ APPLICANT: Del Val, Greg
/ APPLICANT: Zaplachinski, Steve
/ APPLICANT: Moloney, Maurice
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
/ TITLE OF INVENTION: COMPOSITIONS
/ FILE REFERENCE: 38814 351B
/ CURRENT APPLICATION NUMBER: US/10/032,201B
/ CURRENT FILING DATE: 2001-12-19
/ NUMBER OF SEQ ID NOS: 313
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 121
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Haemophilus influenzae
US-10-032-201B-121
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```
Query Match      100.0%; Score 47; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       31 WCGPCK 36
```

RESULT 64

```
US-10-032-201B-151
/ Sequence 151, Application US/10032201B
/ Publication No. US20030167524A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Rooijen, Gijb
/ APPLICANT: Deckers, Harm
/ APPLICANT: Heifetz, Peter Bernard
/ APPLICANT: Briggs, Steven
/ APPLICANT: Dalma, Bipin Kumar
/ APPLICANT: Del Val, Greg
/ APPLICANT: Zaplachinski, Steve
/ APPLICANT: Moloney, Maurice
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
/ TITLE OF INVENTION: COMPOSITIONS
/ FILE REFERENCE: 38814 351B
/ CURRENT APPLICATION NUMBER: US/10/032,201B
/ CURRENT FILING DATE: 2001-12-19
/ NUMBER OF SEQ ID NOS: 313
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 151
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-10-032-201B-151
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```
Query Match      100.0%; Score 47; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       30 WCGPCK 35
```

RESULT 65

```
US-10-335-977-6753
/ Sequence 6753, Application US/10335977
/ Publication No. US20040052799A1
/ GENERAL INFORMATION:
/ APPLICANT: DOUGLAS SMITH et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
/ RELATING TO HELICOBLACTER PYLORI FOR
/ DIAGNOSTICS AND THERAPEUTICS
/ NUMBER OF SEQUENCES: 10031
```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6753:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...107
; SEQUENCE DESCRIPTION: SEQ ID NO: 6753:
US-10-335-977-6753
Query Match 100.0%; Score 47; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 30 WCGPCK 35
RESULT 66
US-11-097-143-8226
; Sequence 8226, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8226
; LENGTH: 107
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-8226
Query Match 100.0%; Score 47; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 30 WCGPCK 35
RESULT 67
US-09-812-777-16
; Sequence 16, Application US/09812777
; Patent No. US20020115827A1
; GENERAL INFORMATION:
; APPLICANT: KIM, KEY-SUN
; APPLICANT: LEE, DUCK YEON
; TITLE OF INVENTION: A METHOD OF PROTEIN STABILIZATION
; FILE REFERENCE: 05823, 0195-0000
; CURRENT APPLICATION NUMBER: US/09/812,777
; CURRENT FILING DATE: 2001-03-18
; PRIOR APPLICATION NUMBER: KR 00-63596
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-812-777-16
Query Match 100.0%; Score 47; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
RESULT 68
US-10-032-201B-117
; Sequence 117, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zapiachinski, Steve
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 117

LENGTH: 108
TYPE: PRT
ORGANISM: E coli, salmonella typhimurium
US-10-032-201B-117

Query Match 100.0%; Score 47; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 69
US-10-032-201B-133

Sequence 133, Application US/10032201B
Publication No. US20030167524A1
GENERAL INFORMATION:
APPLICANT: Van Rooijen, Gij's
APPLICANT: Deckers, Harm
APPLICANT: Helfetz, Peter Bernard
APPLICANT: Briggs, Steven
APPLICANT: Dalma, Bipin Kumar
APPLICANT: Del Val, Greg
APPLICANT: Zaplachinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
FILE REFERENCE: 38814 351B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 133
LENGTH: 108
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-032-201B-133

Query Match 100.0%; Score 47; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 70

US-10-032-201B-142
Sequence 142, Application US/10032201B
Publication No. US20030167524A1
GENERAL INFORMATION:
APPLICANT: Van Rooijen, Gij's
APPLICANT: Deckers, Harm
APPLICANT: Helfetz, Peter Bernard
APPLICANT: Briggs, Steven
APPLICANT: Dalma, Bipin Kumar
APPLICANT: Del Val, Greg
APPLICANT: Zaplachinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
FILE REFERENCE: 38814 351B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 142
LENGTH: 108
TYPE: PRT
ORGANISM: Thibacillus ferrooxidans

US-10-032-201B-142

Query Match 100.0%; Score 47; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

Search completed: February 23, 2006, 00:47:55
Job time : 125.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 00:44:02 ; Search time 11.5 Seconds
(without alignments)
7.767 Million cell updates/sec

Title: US-10-660-118A-3
Perfect score: 47
Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : Published Applications AA.New:*
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppaa/FCF_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	6	US-11-090-916-3	Sequence 3, Appl1
2	47	100.0	75	US-11-131-744-2	Sequence 2, Appl1
3	47	100.0	91	US-11-131-744-1	Sequence 1, Appl1
4	47	100.0	103	US-11-074-176-286	Sequence 286, Appl
5	47	100.0	103	US-11-090-916-7	Sequence 7, Appl1
6	47	100.0	105	US-10-821-234-1371	Sequence 1371, Ap
7	47	100.0	105	US-11-090-916-8	Sequence 8, Appl1
8	47	100.0	105	US-11-090-916-9	Sequence 9, Appl1
9	47	100.0	105	US-11-090-916-10	Sequence 10, Appl
10	47	100.0	105	US-11-090-916-11	Sequence 11, Appl
11	47	100.0	105	US-11-106-796-11	Sequence 12, Appl
12	47	100.0	105	US-11-106-796-13	Sequence 13, Appl
13	47	100.0	105	US-11-144-301A-9	Sequence 9, Appl
14	47	100.0	105	US-11-144-301A-10	Sequence 10, Appl
15	47	100.0	105	US-11-032-773-943	Sequence 943, App
16	47	100.0	109	US-11-090-916-4	Sequence 4, Appl
17	47	100.0	127	US-11-106-796-11	Sequence 11, Appl
18	47	100.0	127	US-11-106-796-12	Sequence 12, Appl
19	47	100.0	129	US-10-467-657-4354	Sequence 4354, Ap
20	47	100.0	177	US-11-131-744-3	Sequence 3, Appl1
21	47	100.0	273	US-11-131-744-6	Sequence 6, Appl1
22	47	100.0	440	US-11-131-744-7	Sequence 7, Appl1
23	44	93.6	103	US-11-090-916-6	Sequence 6, Appl1
24	44	93.6	104	US-11-090-916-5	Sequence 5, Appl1
25	44	93.6	107	US-11-098-686-10612	Sequence 10612, A

26	44	93.6	122	7	US-11-195-459-12	Sequence 12, Appl
27	44	93.6	122	7	US-11-195-459-16	Sequence 16, Appl
28	44	93.6	122	7	US-11-195-459-19	Sequence 19, Appl
29	44	93.6	123	7	US-11-195-459-10	Sequence 10, Appl
30	44	93.6	134	7	US-11-090-916-13	Sequence 13, Appl
31	44	93.6	134	7	US-11-195-459-8	Sequence 8, Appl1
32	44	93.6	167	7	US-11-090-916-14	Sequence 14, Appl
33	44	93.6	172	7	US-11-090-916-15	Sequence 15, Appl
34	44	93.6	209	6	US-10-467-657-8494	Sequence 8494, Ap
35	43	91.5	126	6	US-10-995-561-703	Sequence 703, App
36	43	91.5	747	6	US-10-131-826A-426	Sequence 426, App
37	42	89.4	183	6	US-10-467-657B-6	Sequence 6, Appl1
38	38	80.9	176	6	US-10-821-234-860	Sequence 860, App
39	38	80.9	269	7	US-11-000-463-344	Sequence 344, App
40	38	80.9	324	6	US-10-878-556A-114	Sequence 114, App
41	38	80.9	361	6	US-10-523-503-70	Sequence 70, Appl
42	38	80.9	414	6	US-10-878-556A-1	Sequence 1, Appl1
43	38	80.9	440	6	US-10-821-234-1282	Sequence 1282, Ap
44	38	80.9	505	6	US-10-821-234-1287	Sequence 1287, Ap
45	38	80.9	645	6	US-10-821-234-1409	Sequence 1409, Ap
46	36	76.6	32	6	US-10-895-064-976	Sequence 976, App
47	36	76.6	32	7	US-11-129-741-976	Sequence 976, App
48	36	76.6	32	7	US-11-129-741-3972	Sequence 3972, Ap
49	36	76.6	107	6	US-10-689-742-19	Sequence 19, Appl
50	36	76.6	127	7	US-11-106-796-10	Sequence 10, Appl
51	36	76.6	128	7	US-11-195-459-2	Sequence 2, Appl1
52	36	76.6	128	7	US-11-195-459-4	Sequence 4, Appl1
53	36	76.6	129	7	US-11-072-512-2145	Sequence 2145, Ap
54	36	76.6	163	6	US-10-510-386-126	Sequence 126, App
55	36	76.6	354	7	US-11-054-281-58	Sequence 58, Appl
56	36	76.6	373	7	US-11-054-281-59	Sequence 59, Appl
57	36	76.6	380	7	US-11-090-439-52	Sequence 52, Appl
58	36	76.6	380	7	US-11-090-439-54	Sequence 54, Appl
59	36	76.6	380	7	US-11-054-281-60	Sequence 60, Appl
60	36	76.6	572	6	US-10-763-712A-10	Sequence 10, Appl
61	36	76.6	572	6	US-10-763-712A-11	Sequence 11, Appl
62	36	76.6	572	6	US-10-763-712A-37	Sequence 37, Appl
63	36	76.6	572	6	US-10-763-712A-109	Sequence 109, App
64	36	76.6	572	6	US-10-763-712A-110	Sequence 110, App
65	36	76.6	654	6	US-10-055-877-253	Sequence 253, App
66	36	76.6	660	6	US-10-055-877-254	Sequence 254, App
67	36	76.6	660	6	US-10-055-877-254	Sequence 254, App
68	36	76.6	1857	6	US-10-055-877-73	Sequence 73, Appl
69	36	76.6	2084	6	US-10-055-877-73	Sequence 73, Appl
70	36	76.6	2098	6	US-10-055-877-253	Sequence 253, App
71	36	76.6	2109	6	US-10-055-877-251	Sequence 251, App
72	35	74.5	153	6	US-10-467-657-1704	Sequence 1704, Ap
73	34	72.3	75	7	US-11-174-996A-75	Sequence 75, Appl
74	34	72.3	857	6	US-11-072-512-3810	Sequence 3810, Ap
75	34	72.3	857	6	US-10-453-372-652	Sequence 652, App
76	34	72.3	905	6	US-10-453-372-658	Sequence 658, App
77	34	72.3	905	6	US-10-453-372-662	Sequence 662, App
78	34	72.3	905	6	US-10-453-372-664	Sequence 664, App
79	33	70.2	122	6	US-10-467-657-1392	Sequence 1392, Ap
80	33	70.2	216	7	US-11-106-399-8	Sequence 8, Appl1
81	33	70.2	227	6	US-10-980-388-86	Sequence 86, Appl
82	33	70.2	358	7	US-11-072-512-3307	Sequence 3307, Ap
83	33	70.2	504	7	US-11-087-100-32	Sequence 32, Appl
84	33	70.2	504	7	US-11-087-084-32	Sequence 32, Appl
85	33	70.2	510	7	US-11-087-085-32	Sequence 32, Appl
86	33	70.2	510	7	US-11-087-100-26	Sequence 26, Appl
87	33	70.2	510	7	US-11-087-084-26	Sequence 26, Appl
88	33	70.2	510	7	US-11-087-085-26	Sequence 26, Appl
89	33	70.2	577	7	US-11-074-176-184	Sequence 184, App
90	33	70.2	604	6	US-10-995-561-839	Sequence 839, App
91	33	70.2	604	6	US-11-124-368A-771	Sequence 771, App
92	33	70.2	747	6	US-10-131-826A-212	Sequence 212, App
93	33	70.2	747	6	US-10-995-561-840	Sequence 840, App
94	33	70.2	747	7	US-11-124-368A-270	Sequence 270, App
95	33	70.2	1041	6	US-10-995-561-780	Sequence 780, App
96	33	70.2	1041	6	US-10-995-561-782	Sequence 782, App
97	33	70.2	1097	6	US-10-995-561-781	Sequence 781, App
98	33	70.2	1193	7	US-11-022-478-8	Sequence 8, Appl1

99	33	70.2	1218	7	US-11-078-735-20	Sequence 20, Appl	172	31	66.0	232	7	US-11-211-724-5	Sequence 5, Appl1
100	33	70.2	1218	7	US-11-050-346-65	Sequence 65, Appl	173	31	66.0	232	7	US-11-233-119-7	Sequence 7, Appl1
101	33	70.2	1218	7	US-11-103-077-20	Sequence 20, Appl	174	31	66.0	232	7	US-11-075-047A-91	Sequence 91, Appl
102	33	70.2	1218	7	US-11-072-175-155	Sequence 155, App	175	31	66.0	291	6	US-10-511-538-225	Sequence 225, App
103	33	70.2	1218	7	US-11-022-478-4	Sequence 4, Appl1	176	31	66.0	300	7	US-11-154-257-2	Sequence 2, Appl1
104	33	70.2	1503	7	US-11-087-100-6	Sequence 6, Appl1	177	31	66.0	325	5	US-09-978-360A-406	Sequence 406, App
105	33	70.2	1503	7	US-11-087-084-6	Sequence 6, Appl1	178	31	66.0	430	7	US-11-072-512-2204	Sequence 2204, Ap
106	33	70.2	1503	7	US-11-087-085-6	Sequence 6, Appl1	179	31	66.0	447	6	US-10-967-527A-14	Sequence 14, Appl
107	33	70.2	2059	7	US-11-087-100-4	Sequence 4, Appl1	180	31	66.0	448	6	US-10-967-527A-16	Sequence 16, Appl
108	33	70.2	2059	7	US-11-087-084-4	Sequence 4, Appl1	181	31	66.0	448	6	US-11-182-016-24	Sequence 24, Appl
109	33	70.2	2059	7	US-11-087-085-4	Sequence 4, Appl1	182	31	66.0	509	7	US-11-124-367A-447	Sequence 447, App
110	33	70.2	2144	7	US-11-043-889-2	Sequence 2, Appl1	183	31	66.0	539	7	US-11-043-788-464	Sequence 464, App
111	32	68.1	46	7	US-11-000-463-844	Sequence 844, App	184	31	66.0	549	7	US-11-043-788-467	Sequence 467, App
112	32	68.1	51	7	US-11-172-571-29	Sequence 29, Appl	185	31	66.0	549	7	US-11-043-788-468	Sequence 468, App
113	32	68.1	76	7	US-11-172-571-28	Sequence 28, Appl	186	31	66.0	574	6	US-10-763-712A-1	Sequence 1, Appl1
114	32	68.1	282	7	US-11-186-284-85	Sequence 85, Appl	187	31	66.0	574	6	US-10-763-712A-6	Sequence 6, Appl1
115	32	68.1	371	7	US-11-186-284-16	Sequence 16, Appl	188	31	66.0	574	6	US-10-763-712A-102	Sequence 102, App
116	32	68.1	410	6	US-10-467-657-2312	Sequence 2312, Ap	189	31	66.0	612	7	US-11-098-686-10678	Sequence 10678, A
117	32	68.1	450	7	US-11-186-284-14	Sequence 14, Appl	190	31	66.0	654	6	US-10-510-947-6	Sequence 6, Appl1
118	32	68.1	502	6	US-10-966-483-23	Sequence 23, Appl	191	31	66.0	780	6	US-10-878-556A-197	Sequence 197, App
119	32	68.1	502	7	US-11-021-441-7	Sequence 7, Appl1	192	31	66.0	884	7	US-11-098-686-11426	Sequence 11426, A
120	32	68.1	563	6	US-10-966-483-25	Sequence 25, Appl	193	31	66.0	884	6	US-10-467-657-2302	Sequence 2302, Ap
121	32	68.1	563	7	US-11-021-441-9	Sequence 9, Appl1	194	31	66.0	905	7	US-11-072-512-2728	Sequence 2728, Ap
122	32	68.1	574	6	US-10-966-483-31	Sequence 31, Appl	195	31	66.0	954	6	US-10-467-962B-31	Sequence 31, Appl
123	32	68.1	574	6	US-11-021-441-15	Sequence 15, Appl	196	31	66.0	1238	7	US-11-078-735-21	Sequence 21, Appl
124	32	68.1	581	6	US-10-966-483-27	Sequence 27, Appl	197	31	66.0	1238	7	US-11-050-346-66	Sequence 66, Appl
125	32	68.1	581	6	US-10-966-483-29	Sequence 29, Appl	198	31	66.0	1238	7	US-11-103-077-21	Sequence 21, Appl
126	32	68.1	581	7	US-11-021-441-11	Sequence 11, Appl	199	31	66.0	1257	7	US-11-022-478-6	Sequence 6, Appl1
127	32	68.1	581	7	US-11-021-441-13	Sequence 13, Appl	200	30	63.8	37	6	US-10-467-657-1382	Sequence 1382, Ap
128	32	68.1	755	7	US-11-067-121-6	Sequence 6, Appl1	201	30	63.8	58	7	US-11-123-896-228	Sequence 228, App
129	32	68.1	757	7	US-11-067-121-16	Sequence 16, Appl	202	30	63.8	58	7	US-11-123-896-231	Sequence 231, App
130	32	68.1	757	7	US-11-186-284-41	Sequence 41, Appl	203	30	63.8	58	7	US-11-123-896-234	Sequence 234, App
131	32	68.1	976	6	US-10-966-483-2	Sequence 2, Appl1	204	30	63.8	86	7	US-11-123-896-227	Sequence 227, App
132	32	68.1	976	6	US-10-511-273-1	Sequence 1, Appl1	205	30	63.8	86	7	US-11-123-896-230	Sequence 230, App
133	32	68.1	976	7	US-11-233-796-2	Sequence 2, Appl1	206	30	63.8	86	7	US-11-123-896-233	Sequence 233, App
134	32	68.1	976	7	US-11-072-175-138	Sequence 138, Appl	207	30	63.8	134	7	US-11-188-281-13	Sequence 13, Appl
135	32	68.1	1035	6	US-10-966-483-20	Sequence 20, Appl	208	30	63.8	217	7	US-11-188-281-18	Sequence 18, Appl
136	32	68.1	1035	7	US-11-021-441-4	Sequence 4, Appl1	209	30	63.8	227	6	US-10-515-720A-2	Sequence 2, Appl1
137	32	68.1	1075	7	US-11-174-150-34	Sequence 34, Appl	210	30	63.8	230	6	US-10-515-720A-1	Sequence 1, Appl1
138	32	68.1	1114	7	US-11-174-150-35	Sequence 35, Appl	211	30	63.8	230	7	US-11-188-281-4	Sequence 4, Appl1
139	31.5	67.0	294	7	US-11-055-822-480	Sequence 480, App	212	30	63.8	514	6	US-10-498-026-97	Sequence 97, Appl
140	31.5	67.0	294	7	US-11-055-822-880	Sequence 880, App	213	30	63.8	514	6	US-10-498-026-98	Sequence 98, Appl
141	31	66.0	4	7	US-11-090-916-1	Sequence 1, Appl1	214	30	63.8	1049	6	US-10-131-826A-358	Sequence 358, App
142	31	66.0	4	7	US-11-144-301A-8	Sequence 8, Appl1	215	30	63.8	1398	6	US-10-055-877-46	Sequence 46, Appl
143	31	66.0	4	7	US-11-223-405-1	Sequence 1, Appl1	216	30	63.8	1398	6	US-10-453-372-872	Sequence 872, App
144	31	66.0	4	7	US-11-223-547-1	Sequence 1, Appl1	217	30	63.8	1403	6	US-10-055-877-52	Sequence 52, Appl
145	31	66.0	4	7	US-11-058-926-2	Sequence 2, Appl1	218	30	63.8	1403	6	US-10-453-372-878	Sequence 878, App
146	31	66.0	6	7	US-11-090-916-2	Sequence 2, Appl1	219	30	63.8	1404	6	US-10-053-877-44	Sequence 44, Appl
147	31	66.0	27	6	US-10-895-064-1084	Sequence 1084, Ap	220	30	63.8	1404	6	US-10-453-372-870	Sequence 870, App
148	31	66.0	27	7	US-11-129-741-1084	Sequence 1084, Ap	221	30	63.8	1433	7	US-11-114-962-1	Sequence 1, Appl1
149	31	66.0	84	6	US-10-467-657-5372	Sequence 5372, Ap	222	30	63.8	1547	6	US-10-453-372-886	Sequence 886, App
150	31	66.0	113	7	US-11-072-512-3199	Sequence 3199, Ap	223	30	63.8	1577	6	US-10-055-877-54	Sequence 54, Appl
151	31	66.0	137	7	US-11-098-686-11212	Sequence 11212, A	224	30	63.8	1577	6	US-10-453-372-882	Sequence 882, App
152	31	66.0	143	5	US-09-978-360A-641	Sequence 641, App	225	30	63.8	1577	6	US-10-453-372-884	Sequence 884, App
153	31	66.0	146	6	US-11-226-657-47	Sequence 47, Appl	226	30	63.8	1594	6	US-10-453-372-886	Sequence 886, App
154	31	66.0	189	6	US-10-995-561-643	Sequence 643, App	227	30	63.8	1620	6	US-10-453-372-888	Sequence 888, App
155	31	66.0	191	6	US-10-995-561-642	Sequence 642, App	228	30	63.8	1653	6	US-10-453-372-866	Sequence 866, App
156	31	66.0	191	7	US-11-064-774A-2	Sequence 2, Appl1	229	30	63.8	2556	7	US-11-050-346-67	Sequence 67, Appl
157	31	66.0	191	7	US-11-075-400-2	Sequence 2, Appl1	230	29	61.7	63	7	US-11-183-914-1	Sequence 1, Appl1
158	31	66.0	191	7	US-11-226-005-4	Sequence 4, Appl1	231	29	61.7	155	7	US-11-013-592-24	Sequence 24, Appl
159	31	66.0	191	7	US-11-129-076-9	Sequence 9, Appl1	232	29	61.7	253	7	US-11-179-977-13	Sequence 13, Appl
160	31	66.0	191	7	US-11-145-494-2	Sequence 2, Appl1	233	29	61.7	262	7	US-11-072-512-2276	Sequence 2276, Ap
161	31	66.0	191	7	US-11-075-047A-81	Sequence 81, Appl	234	29	61.7	279	7	US-11-098-686-10882	Sequence 10882, A
162	31	66.0	197	7	US-11-098-686-11017	Sequence 11017, A	235	29	61.7	523	7	US-11-072-512-2046	Sequence 2046, Ap
163	31	66.0	209	6	US-10-995-561-640	Sequence 640, App	236	29	61.7	613	6	US-10-467-657-5786	Sequence 5786, Ap
164	31	66.0	215	6	US-10-995-561-645	Sequence 645, App	237	29	61.7	838	7	US-11-072-512-2819	Sequence 2819, Ap
165	31	66.0	215	6	US-10-995-561-646	Sequence 646, App	238	29	61.7	1026	7	US-11-072-512-2509	Sequence 2509, Ap
166	31	66.0	215	7	US-11-149-462-3	Sequence 3, Appl1	239	29	61.7	1150	6	US-10-821-234-1083	Sequence 1083, Ap
167	31	66.0	224	7	US-11-072-512-3343	Sequence 3343, Ap	240	28	59.6	16	6	US-10-929-988-108	Sequence 108, App
168	31	66.0	232	6	US-10-995-561-644	Sequence 641, App	241	28	59.6	53	6	US-10-914-391A-7	Sequence 7, Appl1
169	31	66.0	232	6	US-10-995-561-644	Sequence 644, App	242	28	59.6	58	7	US-11-068-783-54	Sequence 54, Appl
170	31	66.0	232	7	US-11-153-880-7	Sequence 7, Appl1	243	28	59.6	70	6	US-10-506-192-8	Sequence 8, Appl1
171	31	66.0	232	7	US-11-064-774A-147	Sequence 147, App	244	28	59.6	81	6	US-10-131-826A-150	Sequence 150, App

245	28	59.6	106	7	US-11-074-176-288	Sequence 288, App	318	27	57.4	72	7	US-11-114-979-2	Sequence 2, Appl
246	28	59.6	126	7	US-11-195-459-14	Sequence 14, Appl	319	27	57.4	88	6	US-10-467-657-6627	Sequence 8627, Ap
247	28	59.6	134	6	US-10-498-026-37	Sequence 37, Appl	320	27	57.4	96	6	US-10-467-657-6627	Sequence 4198, Ap
248	28	59.6	155	7	US-11-098-686-1859	Sequence 10859, A	321	27	57.4	102	7	US-11-000-463-327	Sequence 327, App
249	28	59.6	188	7	US-11-024-953-304	Sequence 304, App	322	27	57.4	121	5	US-09-978-360A-614	Sequence 614, App
250	28	59.6	188	7	US-11-024-959-307	Sequence 307, App	323	27	57.4	132	6	US-10-821-234-1676	Sequence 1676, Ap
251	28	59.6	233	7	US-11-150-533-45	Sequence 45, Appl	324	27	57.4	135	6	US-10-467-657-6348	Sequence 8348, Ap
252	28	59.6	236	7	US-11-008-727-4	Sequence 4, Appl	325	27	57.4	142	6	US-10-856-751-37	Sequence 37, Appl
253	28	59.6	249	7	US-11-072-512-2058	Sequence 2058, Ap	326	27	57.4	162	5	US-09-978-360A-615	Sequence 615, App
254	28	59.6	303	7	US-11-186-284-133	Sequence 193, App	327	27	57.4	167	7	US-11-072-512-3290	Sequence 3290, Ap
255	28	59.6	309	6	US-10-714-887-42	Sequence 42, Appl	328	27	57.4	202	7	US-11-072-512-3317	Sequence 3317, Ap
256	28	59.6	318	7	US-11-021-305-168	Sequence 168, App	329	27	57.4	225	6	US-10-670-009-5	Sequence 5, Appl
257	28	59.6	336	6	US-10-467-657-4390	Sequence 4390, Ap	330	27	57.4	226	6	US-10-670-009-6	Sequence 6, Appl
258	28	59.6	365	7	US-11-087-177-5	Sequence 5, Appl	331	27	57.4	226	7	US-11-148-012-2	Sequence 2, Appl
259	28	59.6	390	6	US-10-467-657-3212	Sequence 3212, Ap	332	27	57.4	227	6	US-10-670-009-4	Sequence 4, Appl
260	28	59.6	438	7	US-11-183-136-40	Sequence 40, Appl	333	27	57.4	227	6	US-10-670-009-7	Sequence 7, Appl
261	28	59.6	470	7	US-11-008-727-20	Sequence 20, Appl	334	27	57.4	228	6	US-10-670-009-2	Sequence 2, Appl
262	28	59.6	470	7	US-11-121-438-35	Sequence 35, Appl	335	27	57.4	229	7	US-11-014-629-1	Sequence 1, Appl
263	28	59.6	476	7	US-11-008-727-22	Sequence 22, Appl	336	27	57.4	232	7	US-11-072-512-3111	Sequence 3111, Ap
264	28	59.6	490	6	US-10-763-712A-65	Sequence 65, Appl	337	27	57.4	249	7	US-11-010-239-107	Sequence 107, App
265	28	59.6	490	7	US-11-072-512-2640	Sequence 2640, Ap	338	27	57.4	255	6	US-10-660-499A-2	Sequence 2, Appl
266	28	59.6	509	7	US-11-008-727-16	Sequence 16, Appl	339	27	57.4	273	7	US-11-072-512-2703	Sequence 2703, Ap
267	28	59.6	513	7	US-11-000-463-458	Sequence 458, App	340	27	57.4	276	7	US-11-183-355-5	Sequence 5, Appl
268	28	59.6	519	7	US-11-033-033-442	Sequence 442, App	341	27	57.4	280	6	US-10-967-457-75	Sequence 75, Appl
269	28	59.6	530	7	US-11-183-136-44	Sequence 44, Appl	342	27	57.4	284	7	US-11-037-243-112	Sequence 112, App
270	28	59.6	539	7	US-11-183-136-38	Sequence 38, Appl	343	27	57.4	304	6	US-10-821-234-1540	Sequence 1540, Ap
271	28	59.6	578	7	US-11-083-800-2	Sequence 2, Appl	344	27	57.4	307	5	US-09-978-360A-550	Sequence 550, App
272	28	59.6	673	7	US-11-072-512-2774	Sequence 2774, Ap	345	27	57.4	307	5	US-09-978-360A-693	Sequence 693, App
273	28	59.6	710	7	US-11-169-041-203	Sequence 203, App	346	27	57.4	327	7	US-11-098-686-10271	Sequence 10271, A
274	28	59.6	742	6	US-10-658-986-2	Sequence 2, Appl	347	27	57.4	344	7	US-11-052-554A-43	Sequence 43, Appl
275	28	59.6	746	6	US-10-828-831-5	Sequence 5, Appl	348	27	57.4	349	6	US-10-131-826A-124	Sequence 424, App
276	28	59.6	777	6	US-10-658-986-4	Sequence 4, Appl	349	27	57.4	372	6	US-10-131-826A-106	Sequence 106, App
277	28	59.6	801	6	US-10-793-626-90	Sequence 90, Appl	350	27	57.4	378	7	US-11-244-219-7	Sequence 7, Appl
278	28	59.6	837	7	US-11-094-519A-43	Sequence 43, Appl	351	27	57.4	398	6	US-10-544-501-4	Sequence 4, Appl
279	28	59.6	844	6	US-10-453-372-852	Sequence 852, App	352	27	57.4	398	6	US-11-024-959-336	Sequence 336, App
280	28	59.6	845	6	US-10-453-372-856	Sequence 856, App	353	27	57.4	399	7	US-11-077-386-18	Sequence 18, Appl
281	28	59.6	845	6	US-11-094-519A-42	Sequence 42, Appl	354	27	57.4	400	7	US-11-183-205-46	Sequence 46, Appl
282	28	59.6	1011	6	US-10-877-346-137	Sequence 127, App	355	27	57.4	415	7	US-11-183-294-6	Sequence 6, Appl
283	28	59.6	1041	6	US-10-828-831-9	Sequence 9, Appl	356	27	57.4	415	6	US-10-821-234-1375	Sequence 1375, Ap
284	28	59.6	1198	6	US-10-877-346-35	Sequence 35, Appl	357	27	57.4	435	7	US-11-077-386-19	Sequence 19, Appl
285	28	59.6	1205	6	US-10-877-346-36	Sequence 36, Appl	358	27	57.4	450	7	US-11-077-386-20	Sequence 20, Appl
286	28	59.6	1306	6	US-10-467-657-5406	Sequence 5406, Ap	359	27	57.4	458	6	US-10-763-712A-32	Sequence 32, Appl
287	28	59.6	1428	6	US-10-877-346-33	Sequence 33, Appl	360	27	57.4	459	7	US-11-014-842A-23	Sequence 23, Appl
288	28	59.6	1428	6	US-10-877-346-34	Sequence 34, Appl	361	27	57.4	491	7	US-11-195-739-20	Sequence 20, Appl
289	28	59.6	1616	6	US-10-821-234-1497	Sequence 1497, Ap	362	27	57.4	502	7	US-11-226-701-4	Sequence 4, Appl
290	28	59.6	3712	7	US-11-019-711-48	Sequence 48, Appl	363	27	57.4	515	7	US-11-124-367A-480	Sequence 480, App
291	28	59.6	4128	6	US-10-770-726-77	Sequence 77, Appl	364	27	57.4	529	7	US-11-033-039-487	Sequence 487, App
292	28	59.6	4128	6	US-10-055-877-332	Sequence 332, App	365	27	57.4	529	7	US-11-155-288-1	Sequence 1, Appl
293	27.5	58.5	140	6	US-11-045-024-463	Sequence 463, App	366	27	57.4	560	7	US-11-040-218-7	Sequence 7, Appl
294	27	57.4	8	7	US-11-045-024-6174	Sequence 6174, Ap	367	27	57.4	566	7	US-11-065-695-2	Sequence 2, Appl
295	27	57.4	8	7	US-11-045-024-6174	Sequence 6174, Ap	368	27	57.4	576	7	US-11-040-218-9	Sequence 9, Appl
296	27	57.4	8	7	US-11-045-024-10930	Sequence 10930, A	369	27	57.4	580	7	US-11-183-136-6	Sequence 6, Appl
297	27	57.4	9	7	US-11-045-024-5123	Sequence 5123, Ap	370	27	57.4	580	7	US-11-046-653-2	Sequence 2, Appl
298	27	57.4	9	7	US-11-045-024-7020	Sequence 7020, Ap	371	27	57.4	581	7	US-11-236-198-7	Sequence 7, Appl
299	27	57.4	9	7	US-11-045-024-13608	Sequence 13608, A	372	27	57.4	589	7	US-11-183-136-42	Sequence 42, Appl
300	27	57.4	10	7	US-11-045-024-777	Sequence 777, App	373	27	57.4	589	7	US-11-040-218-5	Sequence 5, Appl
301	27	57.4	11	7	US-11-045-024-917	Sequence 917, App	374	27	57.4	595	6	US-10-510-386-240	Sequence 240, App
302	27	57.4	11	7	US-11-045-024-6135	Sequence 6135, Ap	375	27	57.4	601	7	US-11-065-695-8	Sequence 8, Appl
303	27	57.4	15	6	US-10-939-890-200	Sequence 200, App	376	27	57.4	602	6	US-10-493-909-51	Sequence 51, Appl
304	27	57.4	15	6	US-10-939-890-367	Sequence 367, App	377	27	57.4	630	7	US-11-236-198-5	Sequence 5, Appl
305	27	57.4	15	6	US-10-939-890-707	Sequence 707, App	378	27	57.4	649	7	US-11-236-198-3	Sequence 3, Appl
306	27	57.4	17	7	US-11-129-741-3980	Sequence 3980, Ap	379	27	57.4	682	7	US-11-072-512-2390	Sequence 2390, Ap
307	27	57.4	21	6	US-10-939-890-549	Sequence 549, App	380	27	57.4	683	7	US-11-065-695-6	Sequence 6, Appl
308	27	57.4	23	6	US-10-939-890-321	Sequence 321, App	381	27	57.4	684	6	US-10-714-781A-55	Sequence 55, Appl
309	27	57.4	23	6	US-10-939-890-323	Sequence 323, App	382	27	57.4	684	6	US-10-714-781A-57	Sequence 57, Appl
310	27	57.4	23	6	US-10-939-890-367	Sequence 367, App	383	27	57.4	684	6	US-10-714-781A-61	Sequence 61, Appl
311	27	57.4	23	6	US-10-939-890-707	Sequence 707, App	384	27	57.4	703	6	US-10-714-781A-59	Sequence 59, Appl
312	27	57.4	23	6	US-10-939-890-708	Sequence 708, App	385	27	57.4	703	6	US-10-821-234-1412	Sequence 1412, Ap
313	27	57.4	23	6	US-10-939-890-710	Sequence 710, App	386	27	57.4	703	7	US-11-065-695-4	Sequence 4, Appl
314	27	57.4	23	6	US-10-939-890-711	Sequence 711, App	387	27	57.4	798	7	US-11-107-028-2	Sequence 2, Appl
315	27	57.4	23	6	US-10-939-890-838	Sequence 838, App	388	27	57.4	830	6	US-10-995-561-899	Sequence 899, App
316	27	57.4	52	7	US-11-111-900-4	Sequence 4, Appl	389	27	57.4	833	6	US-10-537-971-2	Sequence 2, Appl
317	27	57.4	56	7	US-11-145-861-166	Sequence 166, App	390	27	57.4	938	7	US-11-109-157A-18	Sequence 18, Appl

391	27	57.4	1001	7	US-11-132-285-40	Sequence 40, Appl	464	26	55.3	55	6	US-10-467-657-5614	Sequence 5614, Ap
392	27	57.4	1013	6	US-10-131-826A-38	Sequence 38, Appl	465	26	55.3	57	7	US-11-000-463-710	Sequence 710, App
393	27	57.4	1047	7	US-11-124-367A-388	Sequence 388, App	466	26	55.3	55	7	US-11-000-463-883	Sequence 883, App
394	27	57.4	1058	7	US-11-124-367A-386	Sequence 386, App	467	26	55.3	58	6	US-10-467-657-5394	Sequence 5394, Ap
395	27	57.4	1062	7	US-11-124-367A-387	Sequence 387, App	468	26	55.3	75	7	US-11-174-996A-57	Sequence 57, Appl
396	27	57.4	1184	7	US-11-065-695-10	Sequence 10, Appl	469	26	55.3	86	5	US-09-978-360A-96	Sequence 496, App
397	27	57.4	1196	6	US-10-613-744-9	Sequence 19, Appl	470	26	55.3	85	5	US-09-978-360A-612	Sequence 612, App
398	27	57.4	1221	7	US-11-109-157A-17	Sequence 17, Appl	471	26	55.3	88	7	US-11-018-868-8	Sequence 8, Appl
399	27	57.4	1330	6	US-10-453-372-260	Sequence 260, App	472	26	55.3	93	6	US-10-467-657-6162	Sequence 6162, Ap
400	27	57.4	1342	6	US-10-453-372-258	Sequence 258, App	473	26	55.3	103	6	US-10-467-657-2150	Sequence 2150, Ap
401	27	57.4	1442	6	US-10-453-372-266	Sequence 266, App	474	26	55.3	104	7	US-11-072-512-2562	Sequence 2562, Ap
402	27	57.4	1542	6	US-10-453-372-280	Sequence 280, App	475	26	55.3	107	7	US-11-072-512-2218	Sequence 2218, Ap
403	27	57.4	1566	7	US-11-124-367A-481	Sequence 481, App	476	26	55.3	106	7	US-11-072-512-2122	Sequence 2122, Ap
404	27	57.4	3433	6	US-10-714-781A-67	Sequence 67, Appl	477	26	55.3	109	6	US-10-467-657-562	Sequence 562, App
405	26	55.3		8	US-11-045-024-3194	Sequence 3194, Ap	478	26	55.3	116	6	US-10-467-657-7486	Sequence 7486, Ap
406	26	55.3		8	US-11-045-024-3195	Sequence 3195, Ap	479	26	55.3	117	7	US-11-103-957-74	Sequence 74, Appl
407	26	55.3		8	US-11-045-024-4415	Sequence 4415, Ap	480	26	55.3	118	7	US-11-073-605-7	Sequence 7, Appl
408	26	55.3		8	US-11-045-024-4416	Sequence 4416, Ap	481	26	55.3	118	7	US-11-140-284-19	Sequence 19, Appl
409	26	55.3		8	US-11-045-024-5812	Sequence 5812, Ap	482	26	55.3	126	7	US-11-098-688-81	Sequence 81, Appl
410	26	55.3		8	US-11-045-024-9768	Sequence 9768, Ap	483	26	55.3	137	7	US-11-124-367A-509	Sequence 509, App
411	26	55.3		8	US-11-045-024-10009	Sequence 10009, A	484	26	55.3	140	7	US-11-084-591-4	Sequence 4, Appl
412	26	55.3		8	US-11-045-024-11748	Sequence 11748, A	485	26	55.3	146	7	US-11-226-657-80	Sequence 80, Appl
413	26	55.3		8	US-11-045-024-11916	Sequence 11916, A	486	26	55.3	146	7	US-11-072-512-3316	Sequence 3316, Ap
414	26	55.3		8	US-11-045-024-12718	Sequence 12718, A	487	26	55.3	158	7	US-11-072-512-3047	Sequence 3047, Ap
415	26	55.3		8	US-11-045-024-12754	Sequence 12754, A	488	26	55.3	159	7	US-11-072-512-3714	Sequence 3714, Ap
416	26	55.3		9	US-11-045-024-1989	Sequence 1989, Ap	489	26	55.3	162	7	US-11-033-037-246	Sequence 246, App
417	26	55.3		9	US-11-045-024-1990	Sequence 1990, Ap	490	26	55.3	170	6	US-10-467-657-104	Sequence 104, App
418	26	55.3		9	US-11-045-024-4558	Sequence 4558, Ap	491	26	55.3	172	7	US-10-467-657-8078	Sequence 8078, Ap
419	26	55.3		9	US-11-045-024-4559	Sequence 4559, Ap	492	26	55.3	172	7	US-11-098-688-10841	Sequence 10841, A
420	26	55.3		9	US-11-045-024-4560	Sequence 4560, Ap	493	26	55.3	174	7	US-11-009-658-16	Sequence 16, Appl
421	26	55.3		9	US-11-045-024-4561	Sequence 4561, Ap	494	26	55.3	178	7	US-11-072-512-3886	Sequence 3886, Ap
422	26	55.3		9	US-11-045-024-5871	Sequence 5871, Ap	495	26	55.3	179	6	US-10-467-657-1115	Sequence 1115, A
423	26	55.3		9	US-11-045-024-12712	Sequence 12712, A	496	26	55.3	179	6	US-10-467-657-3138	Sequence 3138, Ap
424	26	55.3		9	US-11-045-024-12752	Sequence 12752, A	497	26	55.3	179	6	US-10-467-657-3350	Sequence 3350, Ap
425	26	55.3		9	US-11-045-024-13842	Sequence 13842, A	498	26	55.3	182	6	US-10-467-657-3510	Sequence 3510, Ap
426	26	55.3		9	US-11-045-024-13899	Sequence 13899, A	499	26	55.3	193	7	US-11-072-512-3833	Sequence 3833, Ap
427	26	55.3		10	US-11-045-024-2224	Sequence 2224, Ap	500	26	55.3	202	6	US-10-467-657-8154	Sequence 8154, Ap
428	26	55.3		10	US-11-045-024-2225	Sequence 2225, Ap	501	26	55.3	206	6	US-11-072-512-2066	Sequence 2066, Ap
429	26	55.3		10	US-11-045-024-4709	Sequence 4709, Ap	502	26	55.3	208	6	US-10-467-657-3050	Sequence 3050, Ap
430	26	55.3		10	US-11-045-024-4710	Sequence 4710, Ap	503	26	55.3	208	6	US-11-072-512-2002	Sequence 2002, Ap
431	26	55.3		10	US-11-045-024-4711	Sequence 4711, Ap	504	26	55.3	208	6	US-10-467-657-7468	Sequence 7468, Ap
432	26	55.3		10	US-11-045-024-4712	Sequence 4712, Ap	505	26	55.3	213	6	US-11-098-688-11115	Sequence 11115, A
433	26	55.3		10	US-11-045-024-5378	Sequence 5378, Ap	506	26	55.3	214	7	US-11-098-688-11115	Sequence 2356, Ap
434	26	55.3		10	US-11-045-024-5378	Sequence 5378, Ap	507	26	55.3	217	6	US-10-467-657-8046	Sequence 8044, Ap
435	26	55.3		10	US-11-045-024-9675	Sequence 9675, Ap	508	26	55.3	232	7	US-11-072-512-3777	Sequence 3777, Ap
436	26	55.3		10	US-11-045-024-10000	Sequence 10000, A	509	26	55.3	244	7	US-11-072-512-3205	Sequence 3205, Ap
437	26	55.3		10	US-11-045-024-11679	Sequence 11679, A	510	26	55.3	248	7	US-11-152-811-7	Sequence 7, Appl
438	26	55.3		10	US-11-045-024-11909	Sequence 11909, A	511	26	55.3	251	7	US-11-072-175-223	Sequence 223, App
439	26	55.3		10	US-11-045-024-12715	Sequence 12715, A	512	26	55.3	255	7	US-11-140-284-40	Sequence 40, Appl
440	26	55.3		10	US-11-045-024-12753	Sequence 12753, A	513	26	55.3	257	7	US-11-009-658-42	Sequence 42, Appl
441	26	55.3		11	US-11-045-024-368	Sequence 368, App	514	26	55.3	258	7	US-11-058-924-6	Sequence 6, Appl
442	26	55.3		11	US-11-045-024-369	Sequence 369, App	515	26	55.3	258	7	US-11-072-512-3590	Sequence 3590, Ap
443	26	55.3		11	US-11-045-024-4871	Sequence 4871, Ap	516	26	55.3	263	6	US-10-467-657-1403	Sequence 1403, Ap
444	26	55.3		11	US-11-045-024-4872	Sequence 4872, Ap	517	26	55.3	263	6	US-10-821-234-1403	Sequence 45, Appl
445	26	55.3		11	US-11-045-024-5410	Sequence 5410, Ap	518	26	55.3	263	6	US-10-954-468-45	Sequence 45, Appl
446	26	55.3		11	US-11-045-024-5411	Sequence 5411, Ap	519	26	55.3	263	6	US-11-102-883-36	Sequence 36, Appl
447	26	55.3		11	US-11-045-024-7639	Sequence 7639, Ap	520	26	55.3	263	7	US-11-102-883-36	Sequence 2, Appl
448	26	55.3		11	US-11-045-024-7794	Sequence 7794, Ap	521	26	55.3	266	6	US-11-155-114A-2	Sequence 2, Appl
449	26	55.3		14	US-11-188-552-6	Sequence 6, Appl	522	26	55.3	266	6	US-10-663-703-2	Sequence 2, Appl
450	26	55.3		15	US-11-045-024-13186	Sequence 13186, A	523	26	55.3	267	7	US-11-102-240-2	Sequence 2, Appl
451	26	55.3		15	US-11-045-024-13243	Sequence 13243, A	524	26	55.3	267	5	US-09-978-360A-702	Sequence 702, App
452	26	55.3		16	US-10-929-988-81	Sequence 81, Appl	525	26	55.3	274	7	US-11-102-883-34	Sequence 34, Appl
453	26	55.3		17	US-10-939-890-108	Sequence 108, App	526	26	55.3	282	7	US-11-058-924-9	Sequence 9, Appl
454	26	55.3		17	US-11-149-757-23	Sequence 23, Appl	527	26	55.3	284	6	US-10-467-657-3920	Sequence 3920, Ap
455	26	55.3		25	US-11-119-293-27	Sequence 27, Appl	528	26	55.3	286	6	US-10-467-657-8	Sequence 8, Appl
456	26	55.3		28	US-11-129-741-3998	Sequence 3998, App	529	26	55.3	290	7	US-11-240-769-65	Sequence 65, Appl
457	26	55.3		29	US-10-986-501-269	Sequence 269, App	530	26	55.3	291	6	US-10-527-500-47	Sequence 43, Appl
458	26	55.3		33	US-11-121-301-79	Sequence 78, Appl	531	26	55.3	293	6	US-10-527-500-77	Sequence 77, Appl
459	26	55.3		33	US-11-121-301-79	Sequence 79, Appl	532	26	55.3	296	7	US-11-102-928-7	Sequence 7, Appl
460	26	55.3		49	US-11-145-861-307	Sequence 307, App	533	26	55.3	300	7	US-11-058-924-7	Sequence 7, Appl
461	26	55.3		51	US-09-978-360A-625	Sequence 625, App	534	26	55.3	305	7	US-11-000-463-391	Sequence 391, App
462	26	55.3		51	US-10-467-657-1730	Sequence 1730, App	535	26	55.3	305	7	US-11-000-463-863	Sequence 863, App
463	26	55.3		54	US-11-196-670-64	Sequence 64, Appl	536	26	55.3	308	7	US-11-098-688-10572	Sequence 10572, A

537	26	55.3	308	7	US-11-072-512-3715	Sequence 3715, Ap	610	26	55.3	557	6	US-10-718-264-8	Sequence 8, Appl
538	26	55.3	315	7	US-11-037-243-60	Sequence 60, Appl	611	26	55.3	557	6	US-10-718-264-8	Sequence 8, Appl
539	26	55.3	317	6	US-10-954-468-43	Sequence 43, Appl	612	26	55.3	562	7	US-11-072-512-3214	Sequence 3214, Ap
540	26	55.3	317	7	US-11-155-114A-3	Sequence 3, Appl	613	26	55.3	576	7	US-11-098-686-10763	Sequence 10763, A
541	26	55.3	318	7	US-11-072-512-3654	Sequence 3654, Ap	614	26	55.3	615	7	US-11-231-599-57	Sequence 57, Appl
542	26	55.3	320	6	US-10-467-657-424	Sequence 424, App	615	26	55.3	622	7	US-11-199-124-12	Sequence 12, Appl
543	26	55.3	322	7	US-11-052-554A-219	Sequence 219, App	616	26	55.3	636	7	US-11-072-512-3366	Sequence 3366, Ap
544	26	55.3	322	7	US-11-073-605A-4	Sequence 4, Appl	617	26	55.3	642	6	US-10-995-561-631	Sequence 631, App
545	26	55.3	322	7	US-11-140-284-6	Sequence 6, Appl	618	26	55.3	644	7	US-11-120-544B-2	Sequence 2, Appl
546	26	55.3	323	6	US-10-525-674-8	Sequence 8, Appl	619	26	55.3	645	7	US-11-072-512-2845	Sequence 2845, Ap
547	26	55.3	332	6	US-10-131-826A-386	Sequence 386, App	620	26	55.3	657	6	US-10-995-561-622	Sequence 622, App
548	26	55.3	334	7	US-11-055-822-644	Sequence 644, App	621	26	55.3	657	7	US-11-193-561-27	Sequence 27, Appl
549	26	55.3	341	7	US-11-156-084-127	Sequence 127, App	622	26	55.3	657	7	US-11-193-717-27	Sequence 27, Appl
550	26	55.3	342	7	US-11-072-512-2985	Sequence 2985, Ap	623	26	55.3	657	7	US-11-193-789-27	Sequence 27, Appl
551	26	55.3	344	7	US-11-120-308-100	Sequence 100, App	624	26	55.3	657	7	US-11-193-806-27	Sequence 27, Appl
552	26	55.3	345	6	US-10-131-826A-286	Sequence 286, App	625	26	55.3	657	7	US-11-193-857-27	Sequence 27, Appl
553	26	55.3	345	7	US-11-073-605-6	Sequence 6, Appl	626	26	55.3	660	7	US-11-186-284-125	Sequence 125, App
554	26	55.3	345	7	US-11-064-774A-149	Sequence 149, App	627	26	55.3	682	7	US-11-098-686-10487	Sequence 10487, A
555	26	55.3	345	7	US-11-075-400-12	Sequence 12, Appl	628	26	55.3	688	7	US-11-131-035-2	Sequence 2, Appl
556	26	55.3	345	7	US-11-076-427A-22	Sequence 22, Appl	629	26	55.3	693	7	US-11-098-686-11343	Sequence 11343, A
557	26	55.3	345	7	US-11-098-686-10120	Sequence 10120, A	630	26	55.3	702	6	US-10-467-657-7230	Sequence 7230, Ap
558	26	55.3	345	7	US-11-072-175-191	Sequence 191, App	631	26	55.3	708	6	US-10-821-234-917	Sequence 917, App
559	26	55.3	345	7	US-11-073-605A-103	Sequence 103, App	632	26	55.3	712	6	US-10-995-561-984	Sequence 984, App
560	26	55.3	345	7	US-11-140-284-32	Sequence 32, Appl	633	26	55.3	743	7	US-11-149-513-2	Sequence 2, Appl
561	26	55.3	347	6	US-10-131-826A-18	Sequence 18, Appl	634	26	55.3	746	7	US-11-024-959-346	Sequence 346, App
562	26	55.3	348	6	US-10-878-556A-111	Sequence 111, App	635	26	55.3	750	7	US-11-070-627-1	Sequence 1, Appl
563	26	55.3	349	7	US-11-098-686-10115	Sequence 10115, A	636	26	55.3	750	7	US-11-070-627-2	Sequence 2, Appl
564	26	55.3	362	7	US-11-152-569-16	Sequence 16, Appl	637	26	55.3	750	7	US-11-070-627-3	Sequence 3, Appl
565	26	55.3	364	6	US-10-131-826A-186	Sequence 186, App	638	26	55.3	750	7	US-11-070-627-4	Sequence 4, Appl
566	26	55.3	364	7	US-11-140-284-38	Sequence 38, Appl	639	26	55.3	750	7	US-11-070-627-6	Sequence 6, Appl
567	26	55.3	370	7	US-11-073-605-2	Sequence 2, Appl	640	26	55.3	751	6	US-10-821-234-1007	Sequence 1007, Ap
568	26	55.3	370	7	US-11-075-400-14	Sequence 14, Appl	641	26	55.3	763	7	US-11-144-985-6	Sequence 6, Appl
569	26	55.3	370	7	US-11-140-284-8	Sequence 8, Appl	642	26	55.3	765	7	US-11-120-308-84	Sequence 84, Appl
570	26	55.3	370	7	US-11-140-284-36	Sequence 36, Appl	643	26	55.3	769	6	US-10-995-561-985	Sequence 985, App
571	26	55.3	376	7	US-11-055-822-152	Sequence 152, App	644	26	55.3	769	6	US-10-995-561-986	Sequence 986, App
572	26	55.3	376	7	US-11-072-512-3484	Sequence 3484, Ap	645	26	55.3	769	7	US-11-107-028-5	Sequence 5, Appl
573	26	55.3	376	6	US-10-467-657-680	Sequence 680, App	646	26	55.3	770	7	US-11-070-627-8	Sequence 8, Appl
574	26	55.3	377	6	US-10-467-657-4946	Sequence 4946, Ap	647	26	55.3	770	7	US-11-070-627-10	Sequence 10, Appl
575	26	55.3	377	7	US-11-240-769-67	Sequence 67, Appl	648	26	55.3	770	7	US-10-821-234-1134	Sequence 1134, Ap
576	26	55.3	379	7	US-11-054-281-45	Sequence 45, Appl	649	26	55.3	774	6	US-11-070-627-7	Sequence 7, Appl
577	26	55.3	381	7	US-11-054-281-2	Sequence 2, Appl	650	26	55.3	779	7	US-11-072-512-3386	Sequence 3386, Ap
578	26	55.3	381	7	US-11-054-281-41	Sequence 41, Appl	651	26	55.3	782	6	US-10-821-234-1592	Sequence 1592, Ap
579	26	55.3	381	7	US-11-054-281-42	Sequence 42, Appl	652	26	55.3	782	7	US-11-149-513-4	Sequence 4, Appl
580	26	55.3	381	7	US-11-054-281-43	Sequence 43, Appl	653	26	55.3	782	7	US-11-177-506-38	Sequence 38, Appl
581	26	55.3	381	7	US-11-054-281-44	Sequence 44, Appl	654	26	55.3	786	7	US-11-070-627-9	Sequence 9, Appl
582	26	55.3	381	7	US-11-169-041-152	Sequence 152, App	655	26	55.3	807	7	US-11-124-367A-112	Sequence 112, App
583	26	55.3	401	7	US-11-055-822-336	Sequence 336, App	656	26	55.3	807	7	US-11-124-367A-113	Sequence 113, App
584	26	55.3	408	7	US-11-052-554A-383	Sequence 383, App	657	26	55.3	815	6	US-10-523-503-64	Sequence 64, Appl
585	26	55.3	413	7	US-11-071-686-4	Sequence 4, Appl	658	26	55.3	816	7	US-11-072-512-2341	Sequence 2341, Ap
586	26	55.3	415	7	US-11-072-512-2624	Sequence 2624, Ap	659	26	55.3	818	7	US-11-070-627-10	Sequence 10, Appl
587	26	55.3	437	7	US-11-199-124-2	Sequence 2, Appl	660	26	55.3	826	6	US-10-878-556A-68	Sequence 68, Appl
588	26	55.3	437	7	US-11-043-544-22	Sequence 22, Appl	661	26	55.3	835	7	US-11-098-686-10397	Sequence 10397, A
589	26	55.3	437	7	US-11-199-124-10	Sequence 10, Appl	662	26	55.3	842	6	US-10-645-441-2	Sequence 2, Appl
590	26	55.3	440	7	US-11-043-544-20	Sequence 20, Appl	663	26	55.3	882	7	US-11-169-041-137	Sequence 137, App
591	26	55.3	443	6	US-10-523-503-12	Sequence 12, Appl	664	26	55.3	912	7	US-11-042-988-12	Sequence 12, Appl
592	26	55.3	444	7	US-11-052-554A-67	Sequence 67, Appl	665	26	55.3	912	7	US-11-042-988-12	Sequence 12, Appl
593	26	55.3	445	7	US-11-043-544-37	Sequence 37, Appl	666	26	55.3	931	7	US-11-121-438-14	Sequence 14, Appl
594	26	55.3	451	6	US-10-131-826A-126	Sequence 126, App	667	26	55.3	953	7	US-11-037-243-66	Sequence 66, Appl
595	26	55.3	452	7	US-11-098-686-10203	Sequence 10203, A	668	26	55.3	984	6	US-10-995-561-629	Sequence 629, App
596	26	55.3	460	7	US-11-182-016-26	Sequence 26, Appl	669	26	55.3	992	7	US-11-098-686-10761	Sequence 10761, A
597	26	55.3	466	7	US-11-127-877-41	Sequence 41, Appl	670	26	55.3	1053	6	US-10-517-939-52	Sequence 52, Appl
598	26	55.3	493	7	US-11-071-686-2	Sequence 2, Appl	671	26	55.3	1073	6	US-11-121-438-4	Sequence 4, Appl
599	26	55.3	502	6	US-10-131-826A-548	Sequence 548, App	672	26	55.3	1073	6	US-10-821-234-102	Sequence 102, Ap
600	26	55.3	502	6	US-10-689-742-148	Sequence 148, App	673	26	55.3	1104	6	US-10-517-939-144	Sequence 144, App
601	26	55.3	504	6	US-10-999-782-2	Sequence 2, Appl	674	26	55.3	1132	7	US-11-120-544B-3	Sequence 3, Appl
602	26	55.3	515	7	US-11-093-274-38	Sequence 38, Appl	675	26	55.3	1132	7	US-11-110-082-29	Sequence 29, Appl
603	26	55.3	541	7	US-11-000-463-238	Sequence 238, App	676	26	55.3	1149	7	US-10-517-939-306	Sequence 306, Appl
604	26	55.3	542	6	US-11-098-686-11331	Sequence 11331, A	677	26	55.3	1234	6	US-10-493-909-89	Sequence 89, Appl
605	26	55.3	545	6	US-10-718-264-2	Sequence 2, Appl	678	26	55.3	1256	6	US-10-493-909-90	Sequence 90, Appl
606	26	55.3	545	6	US-10-718-264-2	Sequence 2, Appl	679	26	55.3	1359	7	US-11-152-569-20	Sequence 20, Appl
607	26	55.3	548	6	US-10-467-657-6000	Sequence 6000, Ap	680	26	55.3				
608	26	55.3	550	6	US-10-878-556A-166	Sequence 166, App	681	26	55.3				
609	26	55.3	550	6	US-10-878-556A-166	Sequence 166, App	682	26	55.3				

683	26	55.3	1366	7	US-11-169-041-174	Sequence 174, App	756	25	53.2	36	6	US-10-983-120-15	Sequence 15, Appl
684	26	55.3	1373	7	US-11-098-686-11150	Sequence 1150, A	757	25	53.2	39	6	US-10-895-064-295	Sequence 295, App
685	26	55.3	1377	6	US-10-821-234-1070	Sequence 1070, Ap	758	25	53.2	39	7	US-11-129-741-295	Sequence 295, App
686	26	55.3	1379	7	US-11-114-962-4	Sequence 4, Appl1	759	25	53.2	39	7	US-11-129-741-327	Sequence 327, Ap
687	26	55.3	1704	7	US-11-072-175-213	Sequence 213, App	760	25	53.2	41	6	US-10-511-314-2	Sequence 2, Appl1
688	26	55.3	2176	7	US-11-193-561-25	Sequence 25, Appl	761	25	53.2	41	6	US-10-511-314-2	Sequence 2, Appl1
689	26	55.3	2176	7	US-11-193-561-25	Sequence 25, Appl	762	25	53.2	41	7	US-11-226-657-206	Sequence 206, Appl
690	26	55.3	2176	7	US-11-193-789-25	Sequence 25, Appl	763	25	53.2	48	7	US-11-116-746-8	Sequence 8, Appl
691	26	55.3	2176	7	US-11-193-857-25	Sequence 25, Appl	764	25	53.2	57	6	US-10-467-657-7390	Sequence 7390, Ap
692	26	55.3	2176	7	US-11-193-857-25	Sequence 25, Appl	765	25	53.2	63	7	US-11-174-996A-51	Sequence 51, Appl
693	26	55.3	2176	7	US-11-193-857-25	Sequence 25, Appl	766	25	53.2	64	7	US-11-174-996A-89	Sequence 89, Appl
694	26	55.3	2217	7	US-11-193-561-38	Sequence 38, Appl	767	25	53.2	75	7	US-11-174-996A-91	Sequence 91, Appl
695	26	55.3	2217	7	US-11-193-771-38	Sequence 38, Appl	768	25	53.2	75	7	US-11-174-996A-97	Sequence 97, Appl
696	26	55.3	2217	7	US-11-193-806-38	Sequence 38, Appl	769	25	53.2	77	7	US-11-174-996A-53	Sequence 53, Appl
697	26	55.3	2217	7	US-11-193-857-38	Sequence 38, Appl	770	25	53.2	84	5	US-09-978-360A-69	Sequence 69, Appl
698	26	55.3	2223	7	US-11-193-561-2	Sequence 2, Appl1	771	25	53.2	84	5	US-09-978-360A-716	Sequence 716, App
699	26	55.3	2223	7	US-11-193-771-2	Sequence 2, Appl1	772	25	53.2	86	6	US-10-511-314-1	Sequence 1, Appl1
700	26	55.3	2223	7	US-11-193-789-2	Sequence 2, Appl1	773	25	53.2	86	6	US-10-511-722-1	Sequence 1, Appl1
701	26	55.3	2223	7	US-11-193-806-2	Sequence 2, Appl1	774	25	53.2	87	7	US-11-184-574-8	Sequence 8, Appl1
702	26	55.3	2223	7	US-11-193-857-2	Sequence 2, Appl1	775	25	53.2	91	6	US-10-511-538-56	Sequence 56, Appl1
703	26	55.3	2296	6	US-10-995-561-633	Sequence 633, App	776	25	53.2	106	7	US-11-072-512-2975	Sequence 2975, Ap
704	26	55.3	2296	7	US-11-193-561-23	Sequence 23, Appl	777	25	53.2	112	7	US-11-129-741-423	Sequence 4223, Ap
705	26	55.3	2296	7	US-11-193-771-23	Sequence 23, Appl	778	25	53.2	114	6	US-10-986-501-190	Sequence 190, App
706	26	55.3	2296	7	US-11-193-789-23	Sequence 23, Appl	779	25	53.2	115	7	US-11-155-288-11	Sequence 11, Appl
707	26	55.3	2296	7	US-11-193-806-23	Sequence 23, Appl	780	25	53.2	118	7	US-11-072-512-2212	Sequence 2212, Ap
708	26	55.3	2296	7	US-11-193-857-23	Sequence 23, Appl	781	25	53.2	120	6	US-10-793-626-2214	Sequence 2214, Ap
709	26	55.3	2330	7	US-11-193-561-21	Sequence 21, Appl	782	25	53.2	132	7	US-11-072-512-2462	Sequence 2462, Ap
710	26	55.3	2330	7	US-11-193-771-21	Sequence 21, Appl	783	25	53.2	132	7	US-11-098-686-10468	Sequence 10468, A
711	26	55.3	2330	7	US-11-193-789-21	Sequence 21, Appl	784	25	53.2	132	7	US-11-072-512-2099	Sequence 2099, Ap
712	26	55.3	2330	7	US-11-193-806-21	Sequence 21, Appl	785	25	53.2	132	7	US-11-072-512-3315	Sequence 3315, Ap
713	26	55.3	2330	7	US-11-193-857-21	Sequence 21, Appl	786	25	53.2	144	6	US-10-534-486-2	Sequence 2, Appl1
714	26	55.3	2355	6	US-10-995-561-623	Sequence 623, App	787	25	53.2	145	6	US-10-821-234-1331	Sequence 1231, Ap
715	26	55.3	2355	6	US-10-995-561-627	Sequence 627, App	788	25	53.2	146	7	US-11-226-657-63	Sequence 63, Appl
716	26	55.3	2355	7	US-11-193-561-19	Sequence 19, Appl	789	25	53.2	147	7	US-11-226-657-205	Sequence 205, Appl
717	26	55.3	2355	7	US-11-193-771-19	Sequence 19, Appl	790	25	53.2	156	6	US-10-821-234-1397	Sequence 1397, Ap
718	26	55.3	2355	7	US-11-193-789-19	Sequence 19, Appl	791	25	53.2	161	7	US-11-154-257-3	Sequence 3, Appl1
719	26	55.3	2355	7	US-11-193-806-19	Sequence 19, Appl	792	25	53.2	166	7	US-11-226-657-204	Sequence 204, App
720	26	55.3	2355	7	US-11-193-857-19	Sequence 19, Appl	793	25	53.2	182	5	US-09-978-360A-174	Sequence 174, App
721	26	55.3	2384	6	US-10-821-234-1545	Sequence 1545, Ap	794	25	53.2	182	6	US-10-131-826A-177	Sequence 177, App
722	26	55.3	2386	6	US-10-995-561-626	Sequence 626, App	795	25	53.2	183	6	US-10-467-657-6906	Sequence 6906, Ap
723	26	55.3	2421	7	US-11-193-561-17	Sequence 17, Appl	796	25	53.2	204	6	US-11-080-991-8	Sequence 8, Appl1
724	26	55.3	2421	7	US-11-193-771-17	Sequence 17, Appl	797	25	53.2	205	6	US-10-533-310-1	Sequence 1, Appl1
725	26	55.3	2421	7	US-11-193-789-17	Sequence 17, Appl	798	25	53.2	205	6	US-10-533-310-3	Sequence 3, Appl1
726	26	55.3	2421	7	US-11-193-806-17	Sequence 17, Appl	799	25	53.2	205	6	US-10-533-310-4	Sequence 4, Appl1
727	26	55.3	2421	7	US-11-193-857-17	Sequence 17, Appl	800	25	53.2	205	6	US-10-533-310-5	Sequence 5, Appl1
728	26	55.3	2477	7	US-11-193-561-15	Sequence 15, Appl	801	25	53.2	205	7	US-11-072-512-3758	Sequence 3758, Ap
729	26	55.3	2477	7	US-11-193-771-15	Sequence 15, Appl	802	25	53.2	207	7	US-11-214-199-36	Sequence 36, Appl
730	26	55.3	2477	7	US-11-193-789-15	Sequence 15, Appl	803	25	53.2	207	7	US-11-072-512-2278	Sequence 2278, Ap
731	26	55.3	2477	7	US-11-193-806-15	Sequence 15, Appl	804	25	53.2	211	7	US-11-072-512-3219	Sequence 3219, Ap
732	26	55.3	2477	7	US-11-193-857-15	Sequence 15, Appl	805	25	53.2	221	7	US-11-080-628-2	Sequence 2, Appl1
733	26	55.3	3623	6	US-10-995-561-593	Sequence 593, App	806	25	53.2	221	7	US-11-055-822-342	Sequence 342, App
734	26	55.3	3748	7	US-11-132-686-8	Sequence 8, Appl1	807	25	53.2	228	6	US-10-793-626-1662	Sequence 1662, Ap
735	26	55.3	3749	7	US-11-132-686-6	Sequence 6, Appl1	808	25	53.2	229	6	US-09-978-360A-753	Sequence 753, App
736	26	55.3	3749	7	US-11-132-686-12	Sequence 12, Appl	809	25	53.2	229	6	US-10-131-826A-522	Sequence 522, App
737	26	55.3	3912	7	US-11-132-686-5	Sequence 5, Appl1	810	25	53.2	232	6	US-10-821-234-1023	Sequence 1023, Ap
738	26	55.3	3913	7	US-11-132-686-5	Sequence 5, Appl1	811	25	53.2	239	7	US-11-072-512-2603	Sequence 2603, Ap
739	26	55.3	3913	7	US-11-132-686-9	Sequence 9, Appl1	812	25	53.2	241	6	US-10-467-657-4474	Sequence 4474, Ap
740	26	55.3	8695	7	US-11-305-109-15	Sequence 15, Appl	813	25	53.2	245	6	US-10-878-556A-182	Sequence 182, App
741	25	54.3	126	7	US-11-113-424-184	Sequence 184, App	814	25	53.2	246	7	US-11-072-512-2232	Sequence 2232, Ap
742	25	54.3	131	7	US-11-141-678-2	Sequence 704, App	815	25	53.2	246	7	US-11-072-512-2243	Sequence 2243, Ap
743	25	54.3	174	7	US-11-090-617-704	Sequence 704, App	816	25	53.2	247	7	US-11-072-512-1998	Sequence 1998, Ap
744	25	54.3	259	6	US-10-821-234-1561	Sequence 1561, Ap	817	25	53.2	247	7	US-11-072-512-2790	Sequence 2790, App
745	25	54.3	353	7	US-11-137-465-44	Sequence 44, Appl	818	25	53.2	250	5	US-09-978-360A-473	Sequence 473, App
746	25	54.3	403	6	US-10-453-372-1170	Sequence 1170, Ap	819	25	53.2	255	6	US-10-170-997-2	Sequence 2, Appl1
747	25	54.3	488	7	US-11-137-465-45	Sequence 45, Appl	820	25	53.2	255	7	US-11-182-946-11	Sequence 11, Appl
748	25	54.3	898	7	US-11-174-150-43	Sequence 43, Appl	821	25	53.2	255	7	US-11-108-257-2	Sequence 2, Appl1
749	25	54.3	1033	6	US-10-921-415-1	Sequence 914, App	822	25	53.2	259	6	US-10-131-826A-300	Sequence 300, Appl1
750	25	54.3	1532	6	US-10-821-234-914	Sequence 914, App	823	25	53.2	259	7	US-11-182-946-2	Sequence 2, Appl1
751	25	53.2	11	7	US-11-145-861-324	Sequence 324, App	824	25	53.2	261	6	US-11-116-746-1	Sequence 1, Appl1
752	25	53.2	12	6	US-10-511-314-3	Sequence 3, Appl1	825	25	53.2	261	6	US-10-467-657-5896	Sequence 5896, Ap
753	25	53.2	12	6	US-10-511-722-3	Sequence 3, Appl1	826	25	53.2	265	7	US-11-098-686-10630	Sequence 10630, A
754	25	53.2	28	6	US-10-895-064-984	Sequence 984, App	827	25	53.2	276	7	US-11-020-602-224	Sequence 224, App
755	25	53.2	28	7	US-11-129-741-984	Sequence 984, App	828	25	53.2	277	7	US-11-132-285-3	Sequence 3, Appl1

829	25	53.2	277	7	US-11-182-946-12	Sequence 12, Appl	902	25	53.2	537	7	US-11-144-236-6	Sequence 6, Appl1
830	25	53.2	280	5	US-09-978-360A-809	Sequence 809, App	903	25	53.2	539	6	US-10-793-626-340	Sequence 340, App
831	25	53.2	280	6	US-10-131-826A-458	Sequence 458, App	904	25	53.2	555	6	US-10-949-720-387	Sequence 387, App
832	25	53.2	280	6	US-10-689-742-160	Sequence 160, App	905	25	53.2	557	7	US-11-072-512-2707	Sequence 2707, App
833	25	53.2	280	6	US-10-821-234-1300	Sequence 1300, App	906	25	53.2	570	6	US-10-949-720-386	Sequence 386, App
834	25	53.2	289	7	US-11-037-243-70	Sequence 70, Appl	907	25	53.2	570	6	US-10-949-720-412	Sequence 412, App
835	25	53.2	292	5	US-09-978-360A-674	Sequence 674, App	908	25	53.2	578	6	US-10-763-712A-34	Sequence 34, Appl
836	25	53.2	292	6	US-10-967-527A-19	Sequence 19, Appl	909	25	53.2	588	6	US-10-763-712A-95	Sequence 95, Appl
837	25	53.2	299	7	US-10-538-343-4	Sequence 4, Appl1	910	25	53.2	595	7	US-11-072-512-2714	Sequence 2714, App
838	25	53.2	299	6	US-11-116-746-3	Sequence 3, Appl1	911	25	53.2	602	6	US-10-453-372-1064	Sequence 1064, App
839	25	53.2	309	6	US-10-524-647-128	Sequence 128, App	912	25	53.2	610	6	US-10-608-302-1	Sequence 1, Appl1
840	25	53.2	309	6	US-10-524-972-116	Sequence 116, App	913	25	53.2	619	7	US-11-098-666-10196	Sequence 10196, A
841	25	53.2	318	6	US-10-511-538-163	Sequence 163, App	914	25	53.2	622	6	US-10-453-372-1184	Sequence 1184, App
842	25	53.2	318	7	US-11-190-188-21	Sequence 21, App	915	25	53.2	626	7	US-11-072-512-2199	Sequence 2199, App
843	25	53.2	319	6	US-10-131-826A-134	Sequence 134, App	916	25	53.2	634	6	US-10-633-150-26	Sequence 26, Appl
844	25	53.2	336	6	US-10-467-657-5848	Sequence 5848, App	917	25	53.2	634	7	US-11-073-457-26	Sequence 26, Appl
845	25	53.2	336	6	US-10-453-372-640	Sequence 640, App	918	25	53.2	634	7	US-11-073-460-26	Sequence 26, Appl
846	25	53.2	338	6	US-11-000-463-445	Sequence 445, App	919	25	53.2	638	7	US-11-072-512-2626	Sequence 2626, App
847	25	53.2	341	6	US-10-821-234-1628	Sequence 1628, App	920	25	53.2	643	7	US-11-137-465-54	Sequence 54, Appl
848	25	53.2	342	7	US-11-098-686-10943	Sequence 10943, A	921	25	53.2	645	7	US-11-072-512-2588	Sequence 2588, App
849	25	53.2	344	6	US-10-467-657-6546	Sequence 6546, App	922	25	53.2	653	7	US-11-137-465-55	Sequence 55, Appl
850	25	53.2	344	6	US-11-000-463-917	Sequence 917, App	923	25	53.2	655	7	US-11-045-802-29	Sequence 29, Appl
851	25	53.2	348	6	US-10-520-820-5	Sequence 5, Appl1	924	25	53.2	655	7	US-11-072-512-2502	Sequence 2502, App
852	25	53.2	349	7	US-11-182-946-13	Sequence 13, Appl	925	25	53.2	656	6	US-10-821-234-1121	Sequence 1121, App
853	25	53.2	350	6	US-10-063-703-8	Sequence 8, Appl1	926	25	53.2	656	7	US-11-234-786-379	Sequence 379, App
854	25	53.2	350	7	US-11-132-285-41	Sequence 41, Appl	927	25	53.2	671	7	US-11-234-786-380	Sequence 380, App
855	25	53.2	350	7	US-11-102-240-8	Sequence 8, Appl1	928	25	53.2	687	6	US-10-055-877-203	Sequence 203, App
856	25	53.2	353	7	US-11-072-512-2052	Sequence 2052, App	929	25	53.2	692	7	US-11-103-957-29	Sequence 29, Appl
857	25	53.2	354	7	US-11-108-528-50	Sequence 50, Appl	930	25	53.2	697	6	US-10-821-234-905	Sequence 905, App
858	25	53.2	355	6	US-10-967-527A-22	Sequence 22, Appl	931	25	53.2	698	7	US-11-177-506-46	Sequence 46, Appl
859	25	53.2	355	7	US-11-182-946-14	Sequence 14, Appl	932	25	53.2	721	7	US-11-072-512-2605	Sequence 2605, App
860	25	53.2	362	7	US-11-072-512-2384	Sequence 2384, App	933	25	53.2	728	7	US-11-072-512-3399	Sequence 3399, App
861	25	53.2	363	7	US-11-169-041-216	Sequence 216, App	934	25	53.2	729	7	US-11-130-821-4	Sequence 4, Appl1
862	25	53.2	369	7	US-11-105-268-60	Sequence 60, Appl	935	25	53.2	750	7	US-11-132-285-2	Sequence 2, Appl1
863	25	53.2	380	7	US-11-144-236-1	Sequence 1, Appl1	936	25	53.2	771	6	US-10-949-720-389	Sequence 389, App
864	25	53.2	386	6	US-10-131-826A-340	Sequence 340, App	937	25	53.2	776	7	US-11-072-512-3117	Sequence 3117, App
865	25	53.2	386	7	US-11-185-878-2	Sequence 2, Appl1	938	25	53.2	783	7	US-11-037-243-67	Sequence 67, Appl
866	25	53.2	387	7	US-11-099-135-1	Sequence 1, Appl1	939	25	53.2	793	6	US-10-995-561-925	Sequence 925, App
867	25	53.2	396	7	US-11-072-512-2769	Sequence 2769, App	940	25	53.2	794	7	US-11-218-986-2	Sequence 2, Appl1
868	25	53.2	400	6	US-10-948-053-4	Sequence 4, Appl1	941	25	53.2	795	7	US-11-072-512-2810	Sequence 2810, App
869	25	53.2	400	6	US-10-948-053-5	Sequence 5, Appl1	942	25	53.2	799	7	US-11-074-176-348	Sequence 348, App
870	25	53.2	401	6	US-10-949-720-419	Sequence 419, App	943	25	53.2	804	6	US-10-453-372-650	Sequence 650, App
871	25	53.2	401	6	US-10-510-876-2	Sequence 2, Appl1	944	25	53.2	805	6	US-10-485-517-198	Sequence 198, App
872	25	53.2	401	6	US-10-510-876-4	Sequence 4, Appl1	945	25	53.2	805	7	US-11-074-176-172	Sequence 172, App
873	25	53.2	401	6	US-10-948-053-8	Sequence 8, Appl1	946	25	53.2	820	6	US-10-821-234-1176	Sequence 1176, App
874	25	53.2	401	6	US-11-072-175-224	Sequence 224, App	947	25	53.2	825	6	US-10-453-372-644	Sequence 644, App
875	25	53.2	404	6	US-10-948-053-7	Sequence 7, Appl1	948	25	53.2	833	7	US-11-076-187-5	Sequence 5, Appl1
876	25	53.2	404	7	US-11-098-686-11329	Sequence 11329, A	949	25	53.2	834	6	US-10-453-372-658	Sequence 658, App
877	25	53.2	405	6	US-10-467-657-4964	Sequence 4964, App	950	25	53.2	843	7	US-11-129-104-89	Sequence 89, Appl
878	25	53.2	406	6	US-10-948-053-6	Sequence 6, Appl1	951	25	53.2	847	6	US-10-453-372-654	Sequence 654, App
879	25	53.2	406	7	US-11-098-686-10564	Sequence 10564, A	952	25	53.2	856	7	US-11-054-281-116	Sequence 116, App
880	25	53.2	406	7	US-11-072-512-3010	Sequence 3010, App	953	25	53.2	944	7	US-11-057-058-68	Sequence 68, Appl
881	25	53.2	407	6	US-10-948-053-3	Sequence 3, Appl1	954	25	53.2	963	6	US-10-995-561-923	Sequence 923, App
882	25	53.2	409	7	US-11-137-315A-6	Sequence 6, Appl1	955	25	53.2	966	6	US-10-453-372-660	Sequence 660, App
883	25	53.2	418	6	US-10-512-325-3	Sequence 3, Appl1	956	25	53.2	967	7	US-11-057-058-67	Sequence 67, Appl
884	25	53.2	418	7	US-11-196-919-2	Sequence 2, Appl1	957	25	53.2	967	7	US-11-171-701-4	Sequence 4, Appl1
885	25	53.2	419	7	US-11-112-982-36	Sequence 36, Appl	958	25	53.2	985	7	US-11-113-424-61	Sequence 61, Appl
886	25	53.2	419	7	US-11-166-993-6	Sequence 6, Appl1	959	25	53.2	987	6	US-10-949-720-395	Sequence 395, App
887	25	53.2	422	7	US-11-166-993-7	Sequence 7, Appl1	960	25	53.2	990	6	US-10-821-234-1301	Sequence 1201, App
888	25	53.2	431	6	US-10-949-720-410	Sequence 410, App	961	25	53.2	1012	6	US-10-453-372-646	Sequence 646, App
889	25	53.2	433	6	US-10-467-657-6876	Sequence 6876, App	962	25	53.2	1143	6	US-11-072-512-2802	Sequence 2802, App
890	25	53.2	445	7	US-11-072-512-2209	Sequence 2209, App	963	25	53.2	1187	6	US-10-821-234-955	Sequence 955, App
891	25	53.2	455	5	US-09-978-360A-523	Sequence 523, App	964	25	53.2	1250	7	US-11-137-465-62	Sequence 62, Appl
892	25	53.2	477	7	US-11-055-822-338	Sequence 338, App	965	25	53.2	1544	6	US-10-453-372-1186	Sequence 1186, App
893	25	53.2	492	6	US-10-467-657-8422	Sequence 8422, App	966	25	53.2	1565	6	US-10-453-372-1180	Sequence 1180, App
894	25	53.2	502	6	US-10-763-712A-68	Sequence 68, Appl	967	25	53.2	1566	6	US-10-453-372-1190	Sequence 1190, App
895	25	53.2	505	7	US-11-124-367A-365	Sequence 365, App	968	25	53.2	1705	7	US-11-143-984A-37	Sequence 37, Appl
896	25	53.2	507	7	US-11-124-367A-351	Sequence 351, App	969	25	53.2	1719	7	US-11-234-786-378	Sequence 378, App
897	25	53.2	509	7	US-11-135-667-34	Sequence 34, Appl	970	25	53.2	1907	7	US-11-039-338-25	Sequence 25, Appl
898	25	53.2	513	7	US-11-135-667-51	Sequence 51, Appl	971	25	53.2	2053	6	US-10-453-372-1174	Sequence 1174, App
899	25	53.2	513	7	US-11-135-667-53	Sequence 53, Appl	972	25	53.2	2107	6	US-10-995-561-827	Sequence 827, App
900	25	53.2	522	6	US-10-949-720-425	Sequence 425, App	973	25	53.2	2143	6	US-10-453-372-1188	Sequence 1188, App
901	25	53.2	537	6	US-10-949-720-424	Sequence 424, App	974	25	53.2	2440	6	US-10-766-317-10	Sequence 10, Appl

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975      25      53.2      2480      6      US-10-995-561-825      Sequence 825, App
976      25      53.2      2764      6      US-10-995-561-691      Sequence 691, App
977      25      53.2      2813      6      US-10-995-561-688      Sequence 688, App
978      25      53.2      2911      7      US-11-090-617-706      Sequence 706, App
979      25      53.2      2919      6      US-10-821-234-1133      Sequence 1133, App
980      25      53.2      3116      6      US-10-995-561-826      Sequence 826, App
981      25      53.2      3635      7      US-11-019-711-47       Sequence 47, App1
982      25      53.2      4374      7      US-11-128-572-2        Sequence 2, App1
983      25      53.2      4913      6      US-10-453-372-1142      Sequence 1142, App
984      25      53.2      4961      6      US-10-453-372-1132      Sequence 1132, App
985      24.5      52.1      162      6      US-10-453-372-876      Sequence 876, App
986      24.5      52.1      170      6      US-10-055-877-50       Sequence 50, App1
987      24.5      52.1      170      6      US-10-453-372-858      Sequence 858, App
988      24.5      52.1      170      6      US-10-453-372-888      Sequence 888, App
989      24.5      52.1      173      6      US-10-453-372-862      Sequence 862, App
990      24.5      52.1      1418      6      US-10-453-372-864      Sequence 864, App
991      24.5      52.1      1450      6      US-10-055-877-48       Sequence 48, App1
992      24.5      52.1      1450      6      US-10-453-372-874      Sequence 874, App1
993      24      51.1      16      6      US-10-929-988-301      Sequence 301, App
994      24      51.1      19      7      US-11-157-049-31       Sequence 31, App1
995      24      51.1      26      7      US-11-119-293-24       Sequence 24, App1
996      24      51.1      35      6      US-10-957-351-117      Sequence 117, App
997      24      51.1      35      6      US-10-957-351-170      Sequence 170, App
998      24      51.1      38      6      US-10-957-351-155      Sequence 155, App
999      24      51.1      41      6      US-10-957-351-356      Sequence 356, App
1000     24      51.1      45      7      US-11-123-896-165      Sequence 165, App

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ALIGNMENTS

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RESULT 1
US-11-090-916-3
; Sequence 3, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-11-090-916-3

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Query Match      100.0%; Score 47; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 WCGPCK 6
      |||||
Db      1 WCGPCK 6

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RESULT 2

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US-11-131-744-2
; Sequence 2, Application US/1131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHOD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADEGHI, MEHRNOOSH
; APPLICANT: LIANG, XIQUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: 60/621,686
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-2

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Query Match      100.0%; Score 47; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 WCGPCK 6
      |||||
Db      32 WCGPCK 37

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RESULT 3
US-11-131-744-1
; Sequence 1, Application US/1131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHOD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADEGHI, MEHRNOOSH
; APPLICANT: LIANG, XIQUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: 60/621,686
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 91

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: protein sequence
US-11-131-744-1

Query Match
Best Local Similarity 100.0%; Score 47; DB 7; Length 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 4
US-11-074-176-286
Sequence 286, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klamhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 286
LENGTH: 103
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
US-11-074-176-286

Query Match
Best Local Similarity 100.0%; Score 47; DB 7; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 27 WCGPCK 32

RESULT 5
US-11-090-916-7
Sequence 7, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/550,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 103
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-11-090-916-7

Query Match
Best Local Similarity 100.0%; Score 47; DB 7; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 6
US-10-821-234-1371
Sequence 1371, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes Version 1.0
SEQ ID NO 1371
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1371

Query Match
Best Local Similarity 100.0%; Score 47; DB 6; Length 105;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 7
US-11-090-916-8
Sequence 8, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/550,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8

LENGTH: 105
TYPE: PRT
ORGANISM: Gallus gallus
US-11-090-916-8

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 8
US-11-090-916-9
Sequence 9, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 105
TYPE: PRT
ORGANISM: Mus musculus
US-11-090-916-9

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 9
US-11-090-916-10
Sequence 10, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24

PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
LENGTH: 105
TYPE: PRT
ORGANISM: Rattus norvegicus
US-11-090-916-10

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 10
US-11-090-916-11
Sequence 11, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 11
LENGTH: 105
TYPE: PRT
ORGANISM: Bos taurus
US-11-090-916-11

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 11
US-11-090-916-12
Sequence 12, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082

;; PRIOR FILING DATE: 2003-04-11
;; PRIOR APPLICATION NUMBER: 10/660,118
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/556,516
;; PRIOR FILING DATE: 2004-03-24
;; PRIOR APPLICATION NUMBER: 60/650,865
;; PRIOR FILING DATE: 2005-02-07
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO: 12
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-090-916-12

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 12
US-11-106-796-13
;; Sequence 13, Application US/11106796
;; Publication No. US20050282191A1
;; GENERAL INFORMATION:
;; APPLICANT: SUTOVSKY, PETER
;; APPLICANT: MIRANDA-VIZUELE, ANTONIO
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
;; FILE REFERENCE: UWO:033US
;; CURRENT APPLICATION NUMBER: US/11/106,796
;; CURRENT FILING DATE: 2005-04-15
;; PRIOR APPLICATION NUMBER: 60/562,526
;; PRIOR FILING DATE: 2004-04-15
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 13
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-106-796-13

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 13
US-11-144-301A-9
;; Sequence 9, Application US/11144301A
;; Publication No. US20050288227A1
;; GENERAL INFORMATION:
;; APPLICANT: Marks, Paul A.
;; APPLICANT: Johanna, Ungerestedt
;; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
;; FILE REFERENCE: 28517-501 UTIL
;; CURRENT APPLICATION NUMBER: US/11/144,301A
;; CURRENT FILING DATE: 2005-06-03
;; PRIOR APPLICATION NUMBER: US 60/577,089
;; PRIOR FILING DATE: 2004-06-04
;; PRIOR APPLICATION NUMBER: US 10/369,094
;; PRIOR FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 60/357,383
;; PRIOR FILING DATE: 2002-02-15
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn version 3.3

;; SEQ ID NO: 9
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-301A-9

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 14
US-11-144-301A-10
;; Sequence 10, Application US/11144301A
;; Publication No. US20050288227A1
;; GENERAL INFORMATION:
;; APPLICANT: Marks, Paul A.
;; APPLICANT: Johanna, Ungerestedt
;; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
;; FILE REFERENCE: 28517-501 UTIL
;; CURRENT APPLICATION NUMBER: US/11/144,301A
;; CURRENT FILING DATE: 2005-06-03
;; PRIOR APPLICATION NUMBER: US 60/577,089
;; PRIOR FILING DATE: 2004-06-04
;; PRIOR APPLICATION NUMBER: US 10/369,094
;; PRIOR FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 60/357,383
;; PRIOR FILING DATE: 2002-02-15
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO: 10
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-301A-10

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 15
US-11-032-773-943
;; Sequence 943, Application US/11032773
;; Publication No. US20060018911A1
;; GENERAL INFORMATION:
;; APPLICANT: Levy, Ronald
;; APPLICANT: Ault-Riche, Dana
;; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
;; FILE REFERENCE: 17102-013001 / 1762
;; CURRENT APPLICATION NUMBER: US/11/032,773
;; CURRENT FILING DATE: 2005-01-11
;; PRIOR APPLICATION NUMBER: 60/536,184
;; PRIOR FILING DATE: 2004-01-12
;; PRIOR APPLICATION NUMBER: 60/557,591
;; PRIOR FILING DATE: 2004-03-29
;; NUMBER OF SEQ ID NOS: 958
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 943
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: Genbank BAA04881
;; DATABASE ENTRY DATE: 2002-12-25

US-11-032-773-943

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 16

US-11-090-916-4
; Sequence 4, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Reese
; TITLE OF INVENTION: Muscolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/550,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-11-090-916-4

Query Match 100.0%; Score 47; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 33 WCGPCK 38

RESULT 17

US-11-106-796-11
; Sequence 11, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UWO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-796-11

Query Match 100.0%; Score 47; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 18

US-11-106-796-12
; Sequence 12, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UWO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 127
; TYPE: PRT
; ORGANISM: RAT
US-11-106-796-12

Query Match 100.0%; Score 47; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 19

US-10-467-657-4354
; Sequence 4354, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 4354
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4354

Query Match 100.0%; Score 47; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 52 WCGPCK 57

RESULT 20

US-11-131-744-3
; Sequence 3, Application US/1131744

```
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHROD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
TITLE OF INVENTION: SPECTROMETRY
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 3
LENGTH: 177
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-3

Query Match      100.0%; Score 47; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        31 WCGPCK 36

RESULT 21
US-11-131-744-6
Sequence 6, Application US/11/131,744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHROD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
TITLE OF INVENTION: SPECTROMETRY
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 6
LENGTH: 273
TYPE: PRT
ORGANISM: Artificial Sequence
```

```
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-6

Query Match      100.0%; Score 47; DB 7; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        31 WCGPCK 36

RESULT 22
US-11-131-744-7
Sequence 7, Application US/11/131,744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHROD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
TITLE OF INVENTION: SPECTROMETRY
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 7
LENGTH: 440
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-7

Query Match      100.0%; Score 47; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        32 WCGPCK 37

RESULT 23
US-11-090-916-6
Sequence 6, Application US/11/090,916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2679-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/550,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-090-916-6
```

```
Query Match          93.6%; Score 44; DB 7; Length 103;
Best Local Similarity 83.3%; Pred. No. 0.74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||:
Db       27 WCGPCR 32
```

```
RESULT 24
US-11-090-916-5
; Sequence 5, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Reese
; TITLE OF INVENTION: Mucolytic and Anti-Biastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-11-090-916-5
```

```
Query Match          93.6%; Score 44; DB 7; Length 104;
Best Local Similarity 83.3%; Pred. No. 0.74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||:
Db       28 WCGPCR 33
```

```
RESULT 25
US-11-098-686-10612
; Sequence 10612, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vijay and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
```

```
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10612
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10612
```

```
Query Match          93.6%; Score 44; DB 7; Length 107;
Best Local Similarity 83.3%; Pred. No. 0.76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||:
Db       29 WCGPCR 34
```

```
RESULT 26
US-11-195-459-12
; Sequence 12, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Weeley, Robert
; APPLICANT: Hantke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; PRIOR FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Zea mays
US-11-195-459-12
```

```
Query Match          93.6%; Score 44; DB 7; Length 122;
Best Local Similarity 83.3%; Pred. No. 0.82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||:
Db       39 WCGPCR 44
```

```
RESULT 27
US-11-195-459-16
; Sequence 16, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Weeley, Robert
; APPLICANT: Hantke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS
```

```
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 16
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-11-195-459-16
```

```
Query Match          93.6%; Score 44; DB 7; Length 122;
Best Local Similarity 83.3%; Pred. No. 0.82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       45 WCGPCR 50
```

```
RESULT 28
US-11-195-459-19
; Sequence 19, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Meeley, Robert
; APPLICANT: Hancke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 19
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: misc.feature
; OTHER INFORMATION: "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c, g,
US-11-195-459-19
```

```
Query Match          93.6%; Score 44; DB 7; Length 122;
Best Local Similarity 83.3%; Pred. No. 0.82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       39 WCGPCR 44
```

```
RESULT 29
US-11-195-459-10
; Sequence 10, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Meeley, Robert
```

```
; APPLICANT: Hancke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PR
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Zea mays
US-11-195-459-10
```

```
Query Match          93.6%; Score 44; DB 7; Length 123;
Best Local Similarity 83.3%; Pred. No. 0.83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       40 WCGPCR 45
```

```
RESULT 30
US-11-090-916-13
; Sequence 13, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
```

```
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Blaetase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 13
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-090-916-13
```

```
Query Match          93.6%; Score 44; DB 7; Length 134;
Best Local Similarity 83.3%; Pred. No. 0.88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       59 WCGPCR 64
```

```
RESULT 31
US-11-195-459-8
; Sequence 8, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Mealey, Robert
; APPLICANT: Hancke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; PRIOR FILING DATE: 2005-08-02
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Zea mays
US-11-195-459-8
```

```
Query Match          93.6%; Score 44; DB 7; Length 134;
Best Local Similarity 83.3%; Pred. No. 0.88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       54 WCGPCR 59
```

```
RESULT 32
US-11-090-916-14
; Sequence 14, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Reese
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
US-11-090-916-14
```

```
Query Match          93.6%; Score 44; DB 7; Length 167;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       88 WCGPCR 93
```

```
RESULT 33
US-11-090-916-15
```

```
; Sequence 15, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Reese
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-090-916-15
```

```
Query Match          93.6%; Score 44; DB 7; Length 172;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       94 WCGPCR 99
```

```
RESULT 34
US-10-467-8494
; Sequence 8494, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIgnani Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8494
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-8494
```

```
Query Match          93.6%; Score 44; DB 6; Length 209;
Best Local Similarity 83.3%; Pred. No. 1.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       101 WCGPCR 106
```

```
RESULT 35
US-10-995-561-703
; Sequence 703, Application US/10995561
```

```
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CI001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 703
/ LENGTH: 126
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-703

Query Match          91.5%; Score 43; DB 6; Length 126;
Best Local Similarity 83.3%; Pred. No. 1.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
Db      62 WCGPCQ 67

RESULT 36
US-10-131-826A-426
/ Sequence 426, Application US/10131826A
/ Publication No. US20050245730A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: Deforge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumes, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ CURRENT FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059332
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
```

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/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 426
/ LENGTH: 747
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-426

Query Match          91.5%; Score 43; DB 6; Length 747;
Best Local Similarity 83.3%; Pred. No. 3.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
Db      653 WCGPCQ 658

RESULT 37
US-10-467-962B-6
/ Sequence 6, Application US/10467962B
/ Publication No. US20050246784A1
/ GENERAL INFORMATION:
/ APPLICANT: Plesch, Gunnar
/ APPLICANT: Blau, Astrid
/ APPLICANT: Daeschner, Klaus
/ APPLICANT: Klein, Mathieu
/ TITLE OF INVENTION: Identification of Herbicidally Active Substances
/ FILE REFERENCE: 2000 857
/ CURRENT APPLICATION NUMBER: US/10/467,962B
/ CURRENT FILING DATE: 2003-08-14
/ PRIOR APPLICATION NUMBER: PCT/EP02/01466
/ PRIOR FILING DATE: 2002-02-13
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: PatentIn Vers. 2.0
/ SEQ ID NO 6
/ LENGTH: 183
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-467-962B-6

Query Match          89.4%; Score 42; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPC 5
Db      105 WCGPC 109

RESULT 38
US-10-821-234-860
/ Sequence 860, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 860
/ LENGTH: 176
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-860

Query Match          80.9%; Score 38; DB 6; Length 176;
```

Best Local Similarity 83.3%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||
Db 93 WCGHCK 98

RESULT 39

US-11-000-463-344
; Sequence 344, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhilwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dimanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-344

Query Match 80.9%; Score 38; DB 7; Length 269;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||
Db 53 WCGHCK 58

RESULT 40

US-10-878-556A-114
; Sequence 114, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
; LENGTH: 324

; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: tr_hum/g9bvh9
; DATABASE ENTRY DATE: 2001-06-01
US-10-878-556A-114

Query Match 80.9%; Score 38; DB 6; Length 324;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||
Db 108 WCGHCK 113

RESULT 41

US-10-523-503-70
; Sequence 70, Application US/10523503
; Publication No. US20060037102A1
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS IV
; FILE REFERENCE: 16313-0236
; CURRENT APPLICATION NUMBER: US/10/523,503
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 60/400,803
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-523-503-70

Query Match 80.9%; Score 38; DB 6; Length 361;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||
Db 51 WCGHCK 56

RESULT 42

US-10-878-556A-1
; Sequence 1, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (307)-(307)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: hausp:006101-3-0
; DATABASE ENTRY DATE: 2003-02-16
US-10-878-556A-1

Query Match 80.9%; Score 38; DB 6; Length 414;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 236 WCGHCK 241

RESULT 43

US-10-821-234-1282
 ; Sequence 1282, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pc_seq_genes Version 1.0
 ; SEQ ID NO 1282
 ; LENGTH: 440
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1282

Query Match 80.9%; Score 38; DB 6; Length 440;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 189 WCGHCK 194

RESULT 44

US-10-821-234-1287
 ; Sequence 1287, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pc_seq_genes Version 1.0
 ; SEQ ID NO 1287
 ; LENGTH: 505
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1287

Query Match 80.9%; Score 38; DB 6; Length 505;
 Best Local Similarity 83.3%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 56 WCGHCK 61

RESULT 45
 US-10-821-234-1409
 ; Sequence 1409, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pc_seq_genes Version 1.0
 ; SEQ ID NO 1409
 ; LENGTH: 645
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1409

Query Match 80.9%; Score 38; DB 6; Length 645;
 Best Local Similarity 83.3%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 90 WCGHCK 95

RESULT 46
 US-10-895-064-976
 ; Sequence 976, Application US/10895064
 ; Publication No. US20060018923A1

; GENERAL INFORMATION:
 ; APPLICANT: PEIRIS, JOSEPH S.M.
 ; APPLICANT: YUEN, KWOK YUNG
 ; APPLICANT: POON, LIT MAN
 ; APPLICANT: GUAN, YI
 ; APPLICANT: CHAN, KWOK HUNG
 ; APPLICANT: NICHOLLS, JOHN M.
 ; APPLICANT: LEUNG, FREDERICK C.
 ; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
 ; FILE REFERENCE: THEROPF
 ; CURRENT APPLICATION NUMBER: US/10/895,064
 ; CURRENT FILING DATE: 2004-07-21
 ; NUMBER OF SEQ ID NOS: 2918
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 976
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Corononavirius-HKU1
 US-10-895-064-976

Query Match 76.6%; Score 36; DB 6; Length 32;
 Best Local Similarity 66.7%; Pred. No. 6.1;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 9 WCGSCR 14

RESULT 47
 US-11-129-741-976

; Sequence 976, Application US/11129741
 ; Publication No. US20060034853A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YUEN, KWOK YUNG
 ; APPLICANT: WOO, CHIU YAT PATRICK
 ; APPLICANT: LAU, KAR PUI SUSANNA
 ; APPLICANT: CHAN, KWOK HUNG
 ; APPLICANT: POON, LIT MAN

```

; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 976
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Corononavirub-HKU1
US-11-129-741-976

```

```

Query Match          76.6%; Score 36; DB 7; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
Db 9 WCGSCR 14

```

RESULT 48

```

US-11-129-741-3972
; Sequence 3972, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: MOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT WAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3972
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Corononavirub-HKU1
US-11-129-741-3972

```

```

Query Match          76.6%; Score 36; DB 7; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
Db 9 WCGSCR 14

```

RESULT 49

```

US-10-689-742-19
; Sequence 19, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: JACOBS, KENNETH
; APPLICANT: MCCOY, JOHN M
; APPLICANT: LAVAILLE, EDWARD R
; APPLICANT: RACIE, LISA A
; APPLICANT: EVANS, CHERYL
; APPLICANT: MERBERG, DAVID

```

```

; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-19

```

```

Query Match          76.6%; Score 36; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGPCK 6
Db 32 CGPCK 36

```

RESULT 50

```

US-11-106-796-10
; Sequence 10, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UMO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-796-10

```

```

Query Match          76.6%; Score 36; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGPCK 6
Db 32 CGPCK 36

```

RESULT 51

```

US-11-195-459-2
; Sequence 2, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Meeley, Robert
; APPLICANT: Hantke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PR
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03

```

; PRIOR APPLICATION NUMBER: 60/250,703
 ; PRIOR FILING DATE: 2000-12-01
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 128
 ; TYPE: PRF
 ; ORGANISM: Zea mays
 US-11-195-459-2

Query Match 76.6%; Score 36; DB 7; Length 128;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 52 WCPCK 57

RESULT 52
 US-11-195-459-4
 ; Sequence 4, Application US/11195459
 ; Publication No. US20050278803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sewalt, Vincent
 ; APPLICANT: Hastings, Craig
 ; APPLICANT: Meeley, Robert
 ; APPLICANT: Hantke, Sabine
 ; APPLICANT: Jung, Rudolf
 ; APPLICANT: Everard, John
 ; APPLICANT: Allen, Stephen
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
 ; FILE REFERENCE: 5718-119 (035718/241421)
 ; CURRENT FILING DATE: 2005-08-02
 ; PRIOR APPLICATION NUMBER: US/10/005,429
 ; PRIOR FILING DATE: 2001-12-03
 ; PRIOR APPLICATION NUMBER: 60/250,703
 ; PRIOR FILING DATE: 2000-12-01
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 4
 ; LENGTH: 128
 ; TYPE: PRF
 ; ORGANISM: Zea mays
 US-11-195-459-4

Query Match 76.6%; Score 36; DB 7; Length 128;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 52 WCPCK 57

RESULT 53
 US-11-072-512-2145
 ; Sequence 2145, Application US/11072512
 ; Publication No. US20060029945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUDA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHITO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOTYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: 084335-0191
 ; CURRENT APPLICATION NUMBER: US/11/072,512
 ; CURRENT FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/350,978
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: JP 2001-379298
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2145
 ; LENGTH: 129
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-11-072-512-2145

Query Match 76.6%; Score 36; DB 7; Length 129;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
 DB 74 CGPCK 78

RESULT 54
 US-10-510-386-126
 ; Sequence 126, Application US/10510386
 ; Publication No. US20050244922A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersen, Jens Tonne
 ; APPLICANT: Clausen, Ib Groth
 ; APPLICANT: Jorgensen, Steen Troels
 ; APPLICANT: Olsen, Peter Bjarke
 ; APPLICANT: Rasmussen, Michael Dolberg
 ; TITLE OF INVENTION: Improved Bacillus Host Cell
 ; FILE REFERENCE: 10294.204-US
 ; CURRENT APPLICATION NUMBER: US/10/510,386
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 248
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 126
 ; LENGTH: 163
 ; TYPE: PRF
 ; ORGANISM: Bacillus licheniformis
 US-10-510-386-126

Query Match 76.6%; Score 36; DB 6; Length 163;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 62 WCPCK 67

RESULT 55
 US-11-054-281-58
 ; Sequence 58, Application US/11054281
 ; Publication No. US20060013813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mezes et al.
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-240CIP
 ; CURRENT APPLICATION NUMBER: US/11/054,281
 ; CURRENT FILING DATE: 2005-02-08
 ; PRIOR APPLICATION NUMBER: 60/261,014

```
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,018
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/318,410
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 60/261,013
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,026
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,029
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/313,170
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: 10/044,564
/ PRIOR FILING DATE: 2002-01-11
/ NUMBER OF SEQ ID NOS: 324
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 58
/ LENGTH: 354
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-11-054-281-58
```

```
Query Match          76.6%; Score 36; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      144 CGPCK 148
```

```
RESULT 56
US-11-054-281-59
/ Sequence 59, Application US/11054281
/ Publication No. US20060013813A1
/ GENERAL INFORMATION:
/ APPLICANT: Mezes et al.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-240CIP
/ CURRENT APPLICATION NUMBER: US/11/054,281
/ CURRENT FILING DATE: 2005-02-08
/ PRIOR APPLICATION NUMBER: 60/261,014
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,018
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/318,410
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 60/261,013
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,026
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,029
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/313,170
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: 10/044,564
/ PRIOR FILING DATE: 2002-01-11
/ NUMBER OF SEQ ID NOS: 324
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 59
/ LENGTH: 373
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-11-054-281-59
```

```
Query Match          76.6%; Score 36; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      163 CGPCK 167
```

```
RESULT 57
US-11-090-439-52
/ Sequence 52, Application US/11090439
/ Publication No. US20050266442A1
/ GENERAL INFORMATION:
/ APPLICANT: Squillace, Rachel
/ APPLICANT: Weiner, Michael P.
/ TITLE OF INVENTION: Amniomylipoma Cell and Method of Use Thereof
/ FILE REFERENCE: 24318-502
/ CURRENT APPLICATION NUMBER: US/11/090,439
/ CURRENT FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: 60/556,344
/ PRIOR FILING DATE: 2004-03-25
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 52
/ LENGTH: 380
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-090-439-52
```

```
Query Match          76.6%; Score 36; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      170 CGPCK 174
```

```
RESULT 58
US-11-090-439-54
/ Sequence 54, Application US/11090439
/ Publication No. US20050266442A1
/ GENERAL INFORMATION:
/ APPLICANT: Squillace, Rachel
/ APPLICANT: Weiner, Michael P.
/ TITLE OF INVENTION: Amniomylipoma Cell and Method of Use Thereof
/ FILE REFERENCE: 24318-502
/ CURRENT APPLICATION NUMBER: US/11/090,439
/ CURRENT FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: 60/556,344
/ PRIOR FILING DATE: 2004-03-25
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 54
/ LENGTH: 380
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-090-439-54
```

```
Query Match          76.6%; Score 36; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      170 CGPCK 174
```

```
RESULT 59
US-11-054-281-60
/ Sequence 60, Application US/11054281
/ Publication No. US20060013813A1
/ GENERAL INFORMATION:
/ APPLICANT: Mezes et al.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-240CIP
/ CURRENT APPLICATION NUMBER: US/11/054,281
```

```

; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-281-60

Query Match
Best Local Similarity 76.6%; Score 36; DB 7; Length 380;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 CGPCK 6
        |||||
Db      170 CGPCK 174

RESULT 60
US-10-763-712A-10
; Sequence 10, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Clostridium perfringens
US-10-763-712A-10

Query Match
Best Local Similarity 76.6%; Score 36; DB 6; Length 572;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 CGPCK 6
        |||||
Db      98 CGPCK 102

RESULT 61
US-10-763-712A-11
; Sequence 11, Application US/10763712A
; Publication No. US20050266541A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Clostridium perfringens
US-10-763-712A-11

Query Match
Best Local Similarity 76.6%; Score 36; DB 6; Length 572;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 CGPCK 6
        |||||
Db      98 CGPCK 102

RESULT 62
US-10-763-712A-37
; Sequence 37, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Clostridium perfringens
US-10-763-712A-37

Query Match
Best Local Similarity 76.6%; Score 36; DB 6; Length 572;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 CGPCK 6
        |||||
Db      98 CGPCK 102

RESULT 63
US-10-763-712A-109
; Sequence 109, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
```

```

; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 572
; TYPE: PRT
; ORGANISM: C. perfringens
US-10-763-712A-109
```

```
Query Match          76.6%; Score 36; DB 6; Length 572;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      98 CGPCK 102
```

```

RESULT 64
US-10-763-712A-110
; Sequence 110, Application US/10763712A
; Publication No. US2005026541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 110
; LENGTH: 572
; TYPE: PRT
; ORGANISM: C. perfringens
US-10-763-712A-110
```

```
Query Match          76.6%; Score 36; DB 6; Length 572;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      98 CGPCK 102
```

```

RESULT 65
US-10-055-877-255
; Sequence 255, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchetnev, Velizar
; APPLICANT: Zhong, Mei
```

```

; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zehrusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkels, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 255
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-255
```

```
Query Match          76.6%; Score 36; DB 6; Length 654;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      247 CGPCK 251
```

```

RESULT 66
US-10-055-877-254
; Sequence 254, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
```

```

APPLICANT: Miller, Charles
APPLICANT: Tcherny, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eiben, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldos, Feenec
FILE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055, 877
PRIOR APPLICATION NUMBER: 60/262, 892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263, 598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263, 799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264, 117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264, 139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264, 478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263, 351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272, 870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275, 990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275, 927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 254
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-254

Query Match 76.6%; Score 36; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

CY 2 CGPCK 6
DB |||||
249 CGPCK 253

RESULT 67
US-10-831-997-4
Sequence 4, Application US/10831997
Publication No. US2005024834A1

```

```

: GENERAL INFORMATION:
: APPLICANT: Lander, Eric S.
: APPLICANT: Cargill, Michele
: APPLICANT: Ireland, James S.
: APPLICANT: Bolik, Stacey
: APPLICANT: Daley, George Q.
: APPLICANT: McCarthy, Jeanette J.
: TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
: FILE REFERENCE: 2825.1027-001
: CURRENT APPLICATION NUMBER: US/10/831.997
: CURRENT FILING DATE: 2004-04-26
: PRIOR APPLICATION NUMBER: US/09/657,472
: PRIOR FILING DATE: 2000-09-07
: PRIOR APPLICATION NUMBER: US 60/153,357
: PRIOR FILING DATE: 1999-09-10
: PRIOR APPLICATION NUMBER: US 60/220,947
: PRIOR FILING DATE: 2000-07-26
: PRIOR APPLICATION NUMBER: US 60/225,724
: PRIOR FILING DATE: 2000-08-16
: NUMBER OF SEQ ID NOS: 2551
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 961
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-831-997-4

Query Match          76.6%; Score 36; DB 6; Length 961;
Best Local Similarity 100.0%; Pred. No. 56;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0

OY      2 CGPCK 6
          |||||
Db      403 CGPCK 407

RESULT 68
US-10-055-877-252
: Sequence 252, Application US/10055877
: Publication No. US20050288241A1
: GENERAL INFORMATION:
: APPLICANT: Decristofaro, Marc
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Miller, Charles
: APPLICANT: Tcherenev, Velizar
: APPLICANT: Zhong, Mei
: APPLICANT: Anderson, David
: APPLICANT: Ballinger, Robert
: APPLICANT: Gerlach, Valerie
: APPLICANT: Spytek, Kimberly
: APPLICANT: Ratelli, Luca
: APPLICANT: Kekuda, Rameesh
: APPLICANT: Guo, Xiaojia
: APPLICANT: Zernhuenn, Bryan
: APPLICANT: Andrew, David
: APPLICANT: Mezes, Peter
: APPLICANT: Patturajan, Meera
: APPLICANT: Burgess, Catherine
: APPLICANT: Eisen, Andrew
: APPLICANT: Wolenc, Adam
: APPLICANT: Baumgartner, Jason
: APPLICANT: Shimkets, Richard
: APPLICANT: Gusev, Vladimir
: APPLICANT: Verner, Corine
: APPLICANT: Taupier Jr., Raymond
: APPLICANT: Pena, Carol
: APPLICANT: Shenoy, Suresh
: APPLICANT: Li, Li
: APPLICANT: Casman, Stacie
: APPLICANT: Boldog, Perence
: TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
: FILE REFERENCE: 21402-251
: CURRENT APPLICATION NUMBER: US/10/055,877

```

;; CURRENT FILING DATE: 2002-01-22
;; PRIOR APPLICATION NUMBER: 60/262,892
;; PRIOR FILING DATE: 2001-01-19
;; PRIOR APPLICATION NUMBER: 60/263,598
;; PRIOR FILING DATE: 2001-01-23
;; PRIOR APPLICATION NUMBER: 60/263,799
;; PRIOR FILING DATE: 2001-01-24
;; PRIOR APPLICATION NUMBER: 60/264,117
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,139
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,478
;; PRIOR FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: 60/263,351
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: 60/272,870
;; PRIOR FILING DATE: 2001-03-02
;; PRIOR APPLICATION NUMBER: 60/275,990
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/275,927
;; PRIOR FILING DATE: 2001-03-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 512
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 252
;; LENGTH: 1857
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-055-877-252

Query Match 76.6%; Score 36; DB 6; Length 1857;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
Db 65 CGPCK 69

RESULT 69
US-10-055-877-73
;; Sequence 73, Application US/10055877
;; GENERAL INFORMATION:
;; APPLICANT: Decristofaro, Marc
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Miller, Charles
;; APPLICANT: Tchernev, Velizar
;; APPLICANT: Zhong, Mei
;; APPLICANT: Anderson, David
;; APPLICANT: Ballinger, Robert
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Spytek, Kimberly
;; APPLICANT: Ratelli, Luca
;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Guo, Xiaojia
;; APPLICANT: Zerhusen, Bryan
;; APPLICANT: Andrew, David
;; APPLICANT: Mezes, Peter
;; APPLICANT: Patuturajan, Meera
;; APPLICANT: Burgess, Catherine
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;; APPLICANT: Wolenc, Adam
;; APPLICANT: Baumgartner, Jason
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;; APPLICANT: Pena, Carol
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;; APPLICANT: Uli, Li
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;; APPLICANT: Boldog, Ferenc

;; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
;; FILE REFERENCE: 21402-251
;; CURRENT APPLICATION NUMBER: US/10/055,877
;; CURRENT FILING DATE: 2002-01-22
;; PRIOR APPLICATION NUMBER: 60/262,892
;; PRIOR FILING DATE: 2001-01-19
;; PRIOR APPLICATION NUMBER: 60/263,598
;; PRIOR FILING DATE: 2001-01-23
;; PRIOR APPLICATION NUMBER: 60/263,799
;; PRIOR FILING DATE: 2001-01-24
;; PRIOR APPLICATION NUMBER: 60/264,117
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,139
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,478
;; PRIOR FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: 60/263,351
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: 60/272,870
;; PRIOR FILING DATE: 2001-03-02
;; PRIOR APPLICATION NUMBER: 60/275,990
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/275,927
;; PRIOR FILING DATE: 2001-03-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 512
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 73
;; LENGTH: 2084
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-055-877-73

Query Match 76.6%; Score 36; DB 6; Length 2084;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
Db 317 CGPCK 321

RESULT 70
US-10-055-877-253
;; Sequence 253, Application US/10055877
;; Publication No. US20050288241A1
;; GENERAL INFORMATION:
;; APPLICANT: Decristofaro, Marc
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;; APPLICANT: Miller, Charles
;; APPLICANT: Tchernev, Velizar
;; APPLICANT: Zhong, Mei
;; APPLICANT: Anderson, David
;; APPLICANT: Ballinger, Robert
;; APPLICANT: Gerlach, Valerie
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;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Guo, Xiaojia
;; APPLICANT: Zerhusen, Bryan
;; APPLICANT: Andrew, David
;; APPLICANT: Mezes, Peter
;; APPLICANT: Patuturajan, Meera
;; APPLICANT: Burgess, Catherine
;; APPLICANT: Eissen, Andrew
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;; APPLICANT: Pena, Carol
;; APPLICANT: Shenoy, Suresh

APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
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PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 253
LENGTH: 2098
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-055-877-253

Query Match 76.6%; Score 36; DB 6; Length 2098;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
|||
Db 267 CGPCK 271

Search completed: February 23, 2006, 00:48:12
Job time : 15.5 secs

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